EFFECT OF GENOTYPE x ENVIRONMENT INTERACTION ON YIELD AND YIELD COMPONENTS OF CASSAVA (*Manihot esculenta* Crantz) GENOTYPES IN THE SOUTHERN ZONE OF TANZANIA

ALOYCE CALLIST KUNDY

A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTERS OF SCIENCE IN CROP SCIENCE OF SOKOINE UNIVERSITY OF AGRICULTURE. MOROGORO, TANZANIA.

2013

ABSTRACT

Cassava (*Manihot esculenta* Crantz) is a food security crop for most of the populations in the tropical regions of the world, where it ranks fourth as a source of energy, after rice, sugar cane and maize. Twelve cassava genotypes were evaluated to assess genetic variability for root yield and its components at three locations (Naliendele, Mtopwa and Nachingwea) in the Southern zone of Tanzania, during 2011 - 2012 cropping season. This research was carried out to study the stability performance for cassava root yield and its components using a Randomized Complete Block Design under split-split plot experiment. Genotype x location interaction was significant for all the characters studied, indicating considerable influence of the environment on the expression of the traits. Stable genotypes were identified for wider environments and specific environments with high per se performance for root yield per plant. The investigation revealed that, Kiroba (21.72 t ha^{-1}) and NDL 2006/487 (19.5 t ha^{-1}) were desirable and relatively stable across the environments. The genotype NDL 2006/850 was suitable for favourable situations, while genotypes NDL 2006/104 and NDL 2006/283 were suited to poor environments for root yield. High heritability and genetic gain were observed in plant height (0.729 and 36.67%), stem girth (0.694 and 33.63%) and roots per plant (0.449 and 37.05%) suggesting that the traits are primarily under genetic control and that reliable selection with simple recurrent phenotypic selection would be rewarding. Though genotypes differed significantly for all the traits varieties Kiroba and Naliendele; genotypes NDL 2006/487, NDL 2006/283, NDL 2006/104 and NDL 2006/850 were observed to constitute a pool of germplasm with adequate

genetic variability, from which selection will bring about significant progress in cassava improvement programmes.

DECLARATION

I, ALOYCE CALLIST KUNDY do hereby declare to the Senate of Sokoine University of Agriculture that this research is the result of my own original work and that it has neither been concurrently submitted in any other institution.

_____ _____

Aloyce Callist Kundy **Date**

(MSc. Crop Science Candidate)

The above declaration is confirmed

_____ _____

Prof. R.N.Misangu **Date**

(Supervisor)

COPYRIGHT

AKNOWLEDGEMENTS

First of all I am very grateful to the almighty GOD for his guidance not only for this special case, but also for the guidance throughout my life. Secondly, my special thanks are due to my parents, the late Mr. Callist Antony Kundy and Scholastica Alexander Mlay (Mrs Callist), for their tireless efforts in directing me in many aspects not only of academics.

I thank the Government of United Republic of Tanzania, through the Department of Research and Development of Ministry of Agriculture, Food Security and Cooperatives for offering me both permission and sponsorship, through ASDP, for this study.

I am very gratefully to my supervisor, Professor R. N. Misangu for his close supervision and guidance throughout the period of my study. His concern in this investigation is highly appreciated, may the almighty GOD bless him.

I am also thankful to the members of staff and my classmates, Department of Crop Science and Production, Sokoine University of Agriculture Morogoro, for their admired cooperation.

Last but not least, I acknowledge Mr. Eleuther Halla Ghama, Mr. Hassan Libubulu and Ms Stella Mfune for their unforgettable field work assistance and heartfelt encouragements during the hard times of the whole period of my research work. I

also thank some of my fellow workers at NARI as their co-operation has in one way or another assisted me to accomplish this work successfully. Many people helped me during the whole period of my study, since it is difficult to mention them all I would like to emphasize that it would not have been possible to complete this work without their cooperation. So, I thank them all, and may almighty GOD bless them.

DEDICATION

This work is dedicated to my wife Theresia John Njau, without whom this stage wouldn't have been reached. I also dedicate this work to my children Adelino, Petronila, Laila, Bryan and Beatrice for the father loneliness they experienced during my absence.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

LIST OF ABBREVIATIONS AND SYMBOLS

ANOVA	Analysis of Variance
AOAC	Association of Official Analytical Chemists
ASDP	Agricultural Sector Development Support
CBB	Cassava Bacterial Blight
CBSD	Cassava Brown Streak Disease
CBSV	Cassava Brown Streak Virus
CIAT	International Centre for Tropical Agriculture
cm	Centimeter
CMD	Cassava Mosaic Disease
COSCA	Collaborative Study of Cassava in Africa
CP	Crude Protein
DM	Dry Matter
EACMD	East African Cassava Mosaic Disease
FAO	Food and Agricultural Organization
G x E	Genotype by Environment Interaction
HCl	Hydrochloric Acid
HCN	Hydrogen Cyanide
HI	Harvest Index
ICIPE	International Centre of Insect Physiology and Ecology
IFAD	International Fund for Agricultural Development
IITA	International Institute of Tropical Agriculture
Kg	Kilogram

masl	Meters above sea level
MSc	Master of Science
N	Nitrogen
NARI	Naliendele Agricultural Research Institute
NDL	Naliendele
NPK	Nitrogen Phosphorous and Potassium
RCBD	Randomized Complete Block Design
t ha^{-1}	Tones per hectare
TARO	Tanzania Agricultural Research Organization
TRTCP	Tanzania Root and Tuber Crops Programme
UKG	Ukiriguru

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Cassava (*Manihot esculenta* Crantz) is from the family *Euphobeaceae*. It is among the most important root crops worldwide and provides food for one billion (1,000,000,000) people (Bokanga, 2001; Nuwamanya *et al.,* 2009). It is an important food crop in developing countries, and it is the fourth source of calories, after rice, sugar cane and maize worldwide (Akinwale *et al.*, 2010). The edible roots supply energy for more than 500 million people worldwide (Ceballos *et al.*, 2006). It is a perennial crop, native to America and grown in agro ecologies which differ in rainfall, temperature regimes and soil types (Olsen and Schaal, 2001). Cassava constitutes an essential part of the diet of most tropical countries of the world (Calle *et al.*, 2005). In Africa the crop is the most important staple food grown and plays a major role in the effort to alleviate food crisis (Hann and Keyer, 1985).

Tanzania is the fifth producer of cassava in Africa and eighth cassava producer in the world (Table 1) with about 670,000 hectares of land under cassava cultivation with estimated annual production of 7,000,000 tons of fresh root (FAOSTAT, 2008). Cassava is among the most important food security crops in the country and is the most important in the Lake zone(mid altitude warm sub-humid, highland cool humid and mid altitude warm sub-humid) and in the coastal lowlands (Lowland warm sub-humid) (Kapinga *et al.*, 1997). In Tanzania it is the second most important food crop after maize in terms of volume and capita consumption (Kavishe, 1993).

Table 1: Major cassava – producing countries worldwide

Country	Production of fresh roots (tones)
1. Nigeria	41,565,000
2. Brazil	25,872,000
3. Indonesia	19,459,000
4. Thailand	16,938,000
5. Democratic Republic of Congo	14,974,000
6. Mozambique	11,458,000
7. Ghana	9,567,000
8. Tanzania	7,000,000
9. India	6,976,000
10. Uganda	5,756,000
11. Paraguay	4,785,000
12. China	15,700

Source: (FAO 2005).

Nigeria is the leading country in cassava producing countries in the world, with 41,565,000 tons of fresh roots, while China is the least, with 15,700 tons of fresh roots (FAO, 2005). The success of cassava in Africa, as a food security crop is largely because of its ability and capacity to yield well in drought-prone, marginal wastelands under poor management where other crops would fail. Despite cassava's ability to grow in marginal areas (Mkumbira *et al.,* 2003), large differential genotypic responses occur under varying environmental conditions. This phenomenon is referred to as genotype x environment interactions (G x E), which is

a routine occurrence in plant breeding programmes. Recent studies on genotype by environment interactions in some economic crops include the work by Akinyele and Osekita (2011), Sakin *et al.,* (2011), Ngeve *et al.,* (2005) and Kilic *et al.,* (2009). Both the genotype and the environment determine the phenotype of an individual. The effects of these two factors, however, are not always additive because of the interaction between them. The large G x E variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Ssemakula and Dixon, 2007). G x E due to different responses of genotypes in diverse environments, makes choosing the superior genotypes difficult in plant breeding programmes. Traditionally plant breeders tend to select genotypes that show stable performance as defined by minimal G x E effects across a number of locations and/or years. The term stability is sometimes used to characterize a genotype which shows a relatively constant yield independent of changing environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable.

This study was therefore, designed to evaluate the influence of genotype (G), environment (E) and G x E interaction on fresh root yield, root number, dry matter content, starch content, root size, plant height, number of branches per plant, stem girth, harvest index, cassava mosaic disease and cassava brown streak disease of nine (9) newly developed cassava genotypes across three agro-ecological zones of Southern Tanzania, namely; Coastal low land (Naliendele-Mtwara), Masasi-Ruangwa plains (Mkumba-Nachingwea) and Makonde plateau (Mtopwa-Newala).

The Coastal low land plains located at 10^{o} 22'S and 40^{o} 10'E, 120m above sea level receives a mean annual rainfall of 950mm with monthly mean temperature of 27^{o}C and average relative humidity of 86%; Masasi-Ruangwa plains located at 10^{o} 20′S and 38^{o}46′E, 465m above sea level has a mean annual rainfall of 850mm, mean monthly temperature of 25^{o}C and annual mean relative humidity of 78%; while Makonde plateau located at 10^{o} 41'S 39^{o} 23'E, 760m above sea level receives a mean annual rainfall of 1133mm with monthly mean temperature of 23^{o}C and mean relative humidity of 75%. All the three sites experience a mono-modal type of rainfall. These data are according to the report by the Planning Commission Dar es Salaam and Regional Commissioner's Office Mtwara (2008).

1.2 Problem Statement and Justification

Cassava being the second most important food crop after maize in Tanzania, it is however faced with production constraints from pests, diseases, poor agronomic practices and inadequacy of extension services to farmers (Lema and Hemskeerk, 1996; Msabaha *et al*., 1988). Low yield of cassava in the Southern zone of Tanzania is caused by many factors, including diseases and pests. Halima (2005) found out that, the yield of cassava under farmers' conditions was 5 – 10 t ha-1, whereas attainable yield under research conditions was above 20 t ha-1. Use of local varieties which are susceptible to diseases and with poor genetic traits are among those factors contributing to low yield. Efforts on screening for genotypes with high yield potential and tolerant to biotic and a biotic stresses have been done, resulting in production of many improved genotypes, but farmers have not yet benefited from these outcomes.

This may be due to the fact that, the performance of such improved genotypes has not been tested/evaluated for recommendations in different agro ecologies of the Southern zone (Banzigarer and Cooper, 2001; Ceccarelli *et al.,* 2003; Haugernd and Collinson, 1990; Witcombe, 1996; Baidu-Forson, 1997; Morris and Bellon, 2004). There is a lack of information on the magnitude of G x E effect on yield and yield components of improved cassava genotypes in the Southern zone of Tanzania.

The early growth and development of cassava depends very much on genetic and environmental factors. Most of the community in the Southern zone depends on cassava crop as their main source of food. At Naliendele Agricultural Research Institute (NARI) for example, many improved genotypes and few varieties have been developed, but no recommendations for cassava varieties/genotypes have been made, with exception of one variety, Naliendele. Naliendele variety was tolerant to Cassava Mosaic Disease (CMD) and Cassava Brown Streak Disease (CBSD). In recent years, Naliendele variety has lost its trait for diseases resistance, CBSD & CMD, which has caused a bad situation to the community of cassava dependent people. The newly developed genotypes at NARI are now in final stages of breeding; therefore testing them and providing recommendations of suitable ones to different agro ecologies was one step forward in solving the problem.

1.3 Objectives

1.3.1 Overall Objective

To identify stable newly developed cassava genotypes for high yield.

1.3.2 Specific Objectives

i. To assess yield performance of newly developed cassava genotypes in different agro ecological conditions

ii. To identify farmers' criteria for cassava acceptability

iii. To determine nutritional characteristics of the newly developed cassava genotypes

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and Distribution of Cassava

The crop belongs to the dicotyledon family *Euphorbiaceous*, subfamily *Crotonoideae* and tribe *Manihotae*. The *Manihot* genus is reported to have about 100 species, among which the only commercially cultivated one is *Manihot esculenta* Crantz (Alves, 2002). The exact origin of cassava is not clear, but apparently it was first domesticated somewhere in Southern Brazil. The crop was established in South and South East Asia as both staple and source of starch for export in the first half of the 19th century (Olsen and Schaal, 2001).

The crop was introduced in western and East Coast of Africa by Portuguese sailors in the 18th century. In Tanzania cassava reached the Lake Tanganyika from West Africa by the Congolese farmers, from there it moved inland Tanganyika through farmer to farmer diffusion (Carter *et al.*, 1992). The cassava continued to spread due to its ability to survive in harsh conditions and viability of the cuttings which facilitated the natural spread of the crop (Masumba, 2006).

2.2 Trend in Cassava Production

Tanzania is among the top 10 largest cassava producers in the world. Between 2001 and 2005 the country produced seven million metric tons of cassava fresh roots per year on an estimated 670,00ha of land (FAO, 2005). More than 84% of the total production was consumed as human food, about 15% as waste and the remaining was for livestock feed (Mtunda *et al.*, 2002).

Cassava production trends and land area expansion in Tanzania had been fluctuating over a period of years. In all major cassava production zones the production declined from 1985/86 to 1988/89 except in the Eastern zone where cassava production increased (FAO, 2005). Other zones the Western, Central, Northern and Southern Highlands experienced low and almost constant production (FAO, 2005). There was an increase in production in the season of 1989/1990 in all zones except eastern. The highest cassava production was reported in Southern zone in the season 1991/92, and it was over 750,000 tons of dried cassava chips. This was followed by decline of production in the subsequent seasons. The changes in production are reflected very well in the land area under cassava especially in the areas where extensive farming is practiced (IFAD and FAO, 2000).

2.3 Cassava Utilization

Cassava is an important subsistence food crop in the semi-arid areas and sometimes considered as a famine reserve when cereals fail due to its drought tolerance, and the fact that the roots can readily be stored under the ground (Msabaha *et al.,* 1988). Studies conducted by COSCA project between 1989 and 1992 showed that cassava in Tanzania is used in chips/flour form in most villages, and in fresh form and alcoholic beverages in a relatively few villages (COSCA Tanzania, 1996). Africa wide, cassava roots are used in a wide range of forms of food products which can be grouped into fresh roots (unprocessed), granules, pastes, chips/flour, starch etc. (IITA, 1990).

Analysis of the information on the farmers' rank of three major cassava products showed that the range of the products is low in Tanzania where more than 90% of the representative villages reported that their most important cassava product was chips/flour (Table 2). Other products reported as being of primary importance were starch, alcohol and fresh (unprocessed) roots (COSCA, 1996). Cooked paste was reported in one village but as of secondary importance.

In the few areas that use cassava roots in fresh form, cassava was grown in 50% of the staple land, which supply the cities with fresh cassava roots. Where cassava roots were used for alcoholic beverages, cassava was found in an average of 35% of staple land area. These two cassava products are produced for sale rather than for home consumption. In contrast, cassava chips/flour is used more for home consumption than for sale. Cassava chips production for export is however a growing activity particularly in the Southern zone of Tanzania (COSCA Tanzania, 1996).

Cassava leaves are also used both in fresh and processed form. Succulent cassava leaves are crushed or pounded and boiled/cooked before eating. For processing, cassava leaves can be sundried for 3 to 5 days to get a local vegetable known as 'sansa' (Msabaha *et al.*, 1988). This is a processed form of cassava leaves common in areas around Lake Victoria.

Table 2: Percentage distribution of representative villages by most widely used cassava food products

	Percentage distribution of villages	
Cassava production	**Africa**	**Tanzania**
Fresh root	20	6
Pastes	9	0
Clips/flour	51	91
Granules	17	0
Others	3	3*

*Starch accounts for 1%
Source: COSCA Tanzania, 1996

2.4 Constraints in Cassava Production

2.4.1 Pests and diseases

2.4.1.1 Cassava green mite

Cassava green mites (*Mononychellus* sp.) were first reported in the country in 1972 at Ukerewe islands (Msabaha, 1990). At present cassava green mites have spread throughout the country. Studies to establish the distribution of different mite species were initiated in collaboration with the International Institute of Tropical Agriculture (IITA) in Nigeria and the International Centre for Insect Physiology (ICIPE) in Kenya. It was noted that mite population density is highest during the driest periods; and high humidity conditions tends to suppress major outbreaks and damage (Msabaha, 1990). Estimated losses in yield of cassava roots in Tanzania vary from 50% to 80% (Shukla, 1976) depending on the susceptibility of cassava varieties. Cultural control measures such as early planting, intercropping with other crops, and use of NPK fertilizers appeared not effective in controlling the green mites. While breeding programmes for host-plant resistance or tolerance to cassava green mites are in progress, there are good chances for the development of resistant cultivars as

several clones showing resistance to green mites have been identified and mechanism of resistance studied.

To date the national root and tuber crops improvement programme, has selected some few varieties namely: Alpin valenca, Ali Mtumba, Liongo, Kwimba, Msitu Zanzibar, Kibaha, Kigoma-red and Maparigano that show moderate resistance to the pest (IITA, 2010). These are being multiplied under proper sanitation techniques so as to generate enough planting material for farmers.

2.4.1.2 Cassava mosaic disease (CMD)

Cassava Mosaic Virus disease is caused by mosaic begomoviruses (CMBs) transmitted by the whitefly *Bemisia tabaci* (Gennandius) and through virus infected planting material (Harrison *et al*., 1997). CMD was first reported in Tanzania under the name "Krausekrankheit" (Warburg, 1894), although was not recorded as causing serious losses until 1920s. Between 1920 and 1960, comprehensive studies were conducted in the country emphasizing the development of CMD – resistant varieties through the breeding program conducted at Amani in the Usambara Mountains (Jennings, 1994). Surveys undertaken between 1992 and 1993 to establish the distribution of CMD in the country showed that, CMD is widely distributed all over the country with much incidence along the coastal belt of Indian Ocean and the Lake zone. The two areas mentioned above have higher CMD may be due to long establishment of the crop (Raya *et al.,* 1993). These two areas are the major cassava producing areas in the country with long history of cassava cultivation.

Another reason of the persistence of the disease is due to the continuous use of affected planting materials by farmers. It was noted that CMD is mostly transmitted through cutting infection (81%) and only 19% by whitefly vector (Raya *et al*., 1993). Surveys conducted throughout the major growing areas by COSCA showed that CMD was next to cassava green mite in spread its symptoms were observed in about 70% of the villages (COSCA Tanzania, 1996) (Table 4). As of recent the East African Cassava Mosaic Disease (EACMD) was found distributed along the coastal belt of Indian Ocean and the Lake zone (Ogbe *et al.*, 1996).

2.4.1.3 Cassava brown streak disease (CBSD)

Cassava Brown Streak Disease is a viral disease that impacts cassava root quality. The disease is caused by *Cassava brown streak virus* (CBSV), Genus: *Ipomovirus*; family *Potyviridae* and it is spread both through propagation of infected cuttings and by a whitefly vector, *Bemisia tabaci* (Hillocks, 1997). Cassava Brown Streak Disease (CBSD) is known to cause devastating losses to root production and quality in the coastal areas of Tanzania, Kenya, and Mozambique and in the Lakeshore areas of Malawi (Nichols, 1950). CBSD was first reported and distinguished from the cassava mosaic disease (CMD) in Tanzania during the 1930s soon after, the whitefly, *Bemisia tabaci* was suggested as a possible vector (Storey, 1936). The CBSD was found to be endemic in all East African coastal cassava-growing areas from Kenya to the Ruvuma river that marks the southern border between Tanzania and Mozambique. The disease also occurred at lower altitude in Malawi (Nichols, 1950). Prior to 2004, CBSD had never been recorded at high incidence above 1000 metres above sea level and was primarily known as a disease of the lowland cassava-growing areas of East Africa, including the shores of lake

Malawi. However, from late 2004 onwards it became apparent that CBSD was becoming more and more widespread in parts of South-Central Uganda (Alicai *et al.*, 2007).

The survey carried out by IITA and TRTCP in 2009 identified the emergence of Cassava Brown Streak Disease as devastating disease in Lake zone of Tanzania. CBSD severely affected cassava in the following districts namely Ukerewe, Bunda, Musoma, Serengeti, Tarime, Sengerema, Muleba, Geita, Bukombe, Biharmulo, Chato, Misenyi, Ilemela/Nyamagana, Rorya, Bukoba and Ngara, and the disease is still spreading so fast to other district (IITA, 2010).

A disease survey that was conducted in Tanga region of coastal lowlands of Tanzania revealed crop losses of up to 74% (Muhanna and Mtunda, 2002) but in severely affected areas, entire fields are usually destroyed leading to 100% yield losses. Emergence of CBSD in high altitude areas like the Lake zone of Tanzania has created a new challenge to stakeholders involved in cassava research and development in the country including donors.

CBSD has been recorded to be endemic in all East African coastal cassava growing areas; its symptoms include foliar chlorosis and sometimes stem lesions. The disease also affects the tuberous roots which develop a yellow/brown, dry, corky necrosis within the starch bearing tissues, sometimes accompanied by pitting and distortion that is visible externally (Hillocks,1997). Root necrosis accounts for the quantitative and qualitative reduction in total yield through the presence of necrotic lesions or discoloration of the root, rendering them unpalatable and non- marketable.

2.4.1.4 Cassava bacterial blight

For cassava bacterial blight (CBB) the disease is sporadic in nature. In Tanzania, the disease was very much widely distributed in the 1970s (Nyango, 1980). CBB appeared to be widely spread in the lake Victoria zone this necessitated to set up quarantine measures to stop movement of planting material from these areas to other parts of the country.

Table 3: Incidence and severity of cassava plant pests/diseases

Pest/disease	Incidence		Severity score	
	% Villages[1]	% Landraces[2]	Number[3]	score[4]
Cassava mealy bug	33	11	34	1.8
Cassava green mites	92	51	157	1.3
African cassava mosaic	72	27	83	1.3
Cassava bacterial blight	23	7	22	1.1

[1] Percentage of 39 villages where problem was observed.

[2] Percentage of 308 landraces assessed infected/infested

[3] Number of landraces infected /infested,

[4] On a 14 scale

Source: COSCA Tanzania, 1996.

2.4.2 Agronomic problems

Cassava is known to be an easy crop to cultivate. Most farmers thus tend not to manage the crop properly (Masabaha *et al.*, 1988). Most of the time, cassava is planted into exhausted soils. Recent studies have established that, infertile soils produce cassava storage root yields less by 40% of the expected root yield, and the same trend was observed in cassava shoot yield (Roots and Tubers, 1994). In areas where crop rotation cycle is practiced, usually cassava is grown at the end of the cycle, when the soils have already been exhausted.

Late planting of the cassava crop is also a problem, even though cassava is drought tolerant relative to other arable crops. Studies done have shown that cassava planted earlier yields higher than that planted late. Unweeded cassava crop, especially when in monoculture is a constraint to increased cassava yields. Work done on weed management in the 1970s indicated that if weeding was not done within the first two months, there was a 70% reduction in yield. One hand weeding only at one month after planting gave 31% of the expected yield (TARO, 1983).

2.4.3 Shortage of planting materials and continuous use of low genetic potential cassava varieties

Lack of adequate planting materials is another constraint to expanding cassava land area. There is no institution in Tanzania responsible for multiplication and distribution of the improved varieties of cassava (Msabaha *et al.,* 1988). Consequently, farmers plant any materials they come across. Most of the varieties grown by farmers have been selected mainly basing on the farmers' characteristics, and such varieties have low genetic potential for yields and /or resistance to the major pests and diseases (Msabaha *et al.*, 1988).

Studies by COSCA have revealed that, shortage of planting materials is generally a constraint in dry areas where biomass production is usually low in comparison with moist areas; and when new materials such as improved varieties are being introduced for the first time (COSCA Tanzania, 1996). This is because multiplication rate is low in comparison with crops such as grains propagated by seeds. This problem has also been accelerated by lack of irrigation facilities at the

stations where multiplication is being done. This has contributed to tremendous loss of many materials particularly during the dry period and also it makes it impossible to multiply cassava planting materials for the future use.

Deliberate efforts to improve genetic potential of cassava varieties have been done and still on progress in different areas of the world. In Philippines for example germplasm maintenance, characterization, hybridization, field evaluation and variety selection has resulted to two new hybrids OMR 33 – 12 – 3 and OMR 33 – 12 – 7. In these two hybrids, yield potential increased from 10 to 60 t ha-1, root dry matter content increased from 28 to 40% and low Hydrogen Cyanide content classified as edible types was noted (FAO, 2002). In Tanzania under roots and tuber research programme different varieties with improved traits have been developed. Through germplasm maintenance, hybridization and selection the programme has developed varieties which are resistant to CBSD, resistant to CMD and high yielding. The varieties developed and released for farmer use include Kibaha, Mzungu, UKG 93/041 and NDL 90/034, which are resistant to CBSD and CMD and have good yields (18 – 20 t ha-1 of fresh roots) as compared to local varieties which give 4 -10 t ha-1 of fresh root yield (Mkamilo and Jeremiah, 2005). The genotypes employed in this trial were purposeful bred for disease resistance and high yielding. In their advanced yield trials, the yields of these genotypes ranged from 18 – 25 t ha-1 (Mkamilo *et al.,* 2010). Furthermore, cassava is known for its low protein content of about 0.7 – 2% (Diasolua *et al.,* 2002, 2003). The work done by Nassar and Dorea (1982) showed that interspecific hybridization of common cassava with low protein content and wild species of cassava resulted

into the increase of protein content of the developed hybrid. Nassar and Dorea (1982) found that, total amino acid content in the common cassava cultivar was 0.254 g per 100 g *viz. a viz.* 1.664 g per 100 g in the interspecific hybrid. The genetic variability of the profile and quantity of amino acids indicate the feasibility of selecting interspecific hybrids that are rich in both crude protein and amino acids.

2.4.4 Inadequacy of extension services to farmers

There is limited knowledge of the extension personnel, shortage of extension personnel, topped with severe logistical problems in most regions where cassava is grown. Inadequate transport makes it impossible for the extensionist to cover a number of villages. Poor farmer - research extension linkages and lack of integrated research approach have sometimes led researchers to come up with messages which are not farmer problem oriented. This ultimately leads to low adoption rate of extension messages (Lema and Hemskeerk, 1996). Even when researchers want fully involvement of extensionists in transfer of technology, but meager resources do not allow for this. Low level of interaction between researchers and extension agents has also contributed to the farmers' lack of improved varieties.

2.5 Participatory Crop Improvement

Participatory Crop Improvement (PCI) is a new approach in genetic improvement. The approach aims at fully integrating farmers and their stakeholders of the production chain into the process of variety development. It aims at ensuring the needs of small farmers living in poor and marginal areas for which conventional breeding cannot offer suitable varieties (Trouche, 2004).

Participatory crop improvement is based on the principal of sufficient knowledge of farmers' specific production needs and of the advantages and disadvantages of the local varieties they use (Trouche, 2004). The approach involves farmers in different stages of selection and evaluation of future varieties. This can be done either through "Mother" trial where researchers test advanced lines on-farm and on-station, in which groups of farmers rank cassava lines or "Baby trial" where farmers test lines on their fields using their level of management and rate the performance (Singh *et al.*, 2002).

2.6 Components of Cassava Yield

The early growth and development of cassava depends on genetic and environment factors, implying that a better understanding of the relationship between environmental factors and growth/development process is of great use. Dry weight yield accumulation and distribution among different plant organs changes sharply during growth cycle and partitioning of dry matter to their storage root, tends to be more important in determining how other factors influence the growth of the plant as a whole (Ntawurunga *et al.,* 2001). High storage root yield is one of the main goals in cassava improvement.

However, it is difficult to assess storage root yield in large populations compared to other plant traits that are phenotypically observable. Different studies have reported that storage root yield is genetically related to the number of storage roots per plant, root size, harvest index (HI), stem girth, canopy width and total number of branches

(Magoon *et al.,* 1970; Mahungu, 1983; Ntawurunga *et al.,* 1998). Tai, (1975) found that cassava yield components comprise of the number of storage roots, average storage root weight and percentage of dry matter (%DM), while Ntawuhurunga *et al.,* (2001) reported storage root number, storage root weight, storage root girth and total leaf area as yield components explaining 72% of storage yield.

2.7 Nutritional Quality of Cassava

The edible parts of cassava crop include both leaves and tubers. Most of nutritional contents are found in the tubers. Tubers are valued for their highly nutritious starch content (Welch and Graham, 2004). It is a crop with a primarily high content of carbohydrates and the protein content is low. The raw roots and leaves of cassava can be toxic due to the presence of natural nitrite compounds called cyanogenic glycosides or cyanogens (Bolhuis, 1954). Nitrite compounds upon breakdown release a toxic compound Hydrogen Cyanide (HCN) which can be harmful to consumers.

2.8 Genotype x Environment Interaction

Genotype and environment (G x E) interaction is the change in a cultivar's relative performance over environments, resulting from differential response of the cultivar, to various edaphic, climatic and biotic factors (Dixon *et al.,* 1994). Crop yield fluctuates due to suitability of varieties to different growing seasons or conditions. A specific genotype does not always exhibit the same phenotypic characteristics under all environments and different genotypes respond differently to a specific environment.

Gene expression is subject to modification by environment; therefore, genotypic expression of the phenotypic is environmentally dependent (Kang, 1998).The development of new cultivars with desired characteristics such as high economic yield, tolerance or resistance to biotic or abiotic stresses, traits that add value to the product and the stability of these traits in target environments. Inconsistent genotypic responses to environment factors such as temperatures, soil moisture soil type or fertility level from location to location or year to year are a function of genotype x environment interactions. Genotype x environment interactions has been defined as the failure of genotypes to achieve the same relative performance in different environments (Kang, 1998). Identifying yield contributing traits and knowledge of G x E interactions and yield stability are important for breeding how cultivars with improved adaptation to the environment constraints prevailing the target environments.

Therefore, an understanding of the causes of genotype x environment interaction can help to identify traits that contribute to better cultivar performance and environments that facilitate cultivar evaluation (Yan and Hunt, 2000). For an example, a study of genotype x environment interaction effects on the yield of 10 early-maturing pigeon pea (*Cajanus cajan* L. Millsp.) genotypes, in a total of seven environments spread over five regions of Kenya between 1987 and 1988 noted that the best genotype in one environment is not always so in other environments (Wamatu and Thomas, 2002). Cultivar, environment, time of harvest and their interaction has also shown significant effects on sugarcane yield and quality (Gilbert *et al.*, 2007). The understanding of casual relationship among yield components and their effect on yield can be achieved by carrying out path coefficient analysis.

2.9 Path Coefficient Analysis

Path (association) analysis is a statistical tool developed by Wright, (1921). Knowledge on the correlation between yield and its component characters themselves can improve the efficiency of selection. Because, in a complex situation selection for optimum advance should be based on judiciously computed index that to if any environmental influence is there. Correlation studies permit only a measure of relationship between two traits. Hence path coefficient analysis becomes necessary as it permits separation of direct (independent) and indirect (dependent) effects via other related characters by partitioning the correlation coefficients (Dewey and Lu, 1959). In other words, path coefficient analysis differs from simple correlation in fact that: simple correlation coefficient measures mutual association without regard to causation; while the path coefficient analysis specifies the causes and measure their relative importance (Reuben *et al.*, 1998). Therefore, the path analysis is more informative and useful in determining the nature and relationships between yield and yield components than simple correlation coefficients. However according to Singh and Chaudhary (1977), there are situations in which attention have to be paid in selecting desirable effects: (i) If the correlation coefficient is positive, but the direct effect is negligible, the indirect effects seem to be the reason for correction. In such situations, the causal factors must be considered simultaneously; and (ii) the correlation coefficient may have negative value, but its direct effect is positive and high; under such circumstances, restrictions are to be imposed to nullify the undesirable indirect effect to make use of direct effect (Singh and Chaudhary, 1977).

Nevertheless, when conducting genotype x environment interactions, more emphasis should be placed on sampling a greater number of locations than on testing of genotype ability within locations. This would improve the chances of obtaining both broadly and specifically adapted crop varieties (Mirzawan *et al.*, 1993). Moreover, the study of genotype x environment interaction requires understanding of the importance of different variables in the interaction. For an example, the major component of interaction have to be identified as a contrast, say between early and late cultivars; while a minor component can be cultivars that perform relatively well in the worst environment and relatively badly in the best environment (Eeuwijk and Elgersma, 2008).

It is suggested that in locations where genotype x environment interaction for yield frequently causes re-ranking across environments, genotypes with the least contribution to the interaction sum of squares are likely to be productive. On the whole, this supports the contention that breeding under sole-crop conditions has the potential to produce cultivars effective under intercropping conditions (Padi, 2007). A genotype is said to be stable when its performance across environments does not deviate from the average performance of a group of standard genotypes (Goncalves *et al.*, 2003). That is why whenever new varieties are proposed for commercial release, information on genotype x environment interactions and stability, clearly indicating their specific and/or general adaptations, are made available to the user (Goncalves *et al.*, 2003).

CHAPTER THREE

3.0 MATERIALS AND METHODOLOGY

3.1 Experimental Sites and Materials

The experiment was conducted during the 2011/2012 cropping season in the Southern zone of Tanzania in three agro ecologies. Coastal low land plains (in Mtwara urban) located at 10^{o} 22'S and 40^{o} 10'E, 120m above sea level; Masasi-Ruangwa plains (in Lindi rural) located at 10^{o} 20′S and 38^{o}46′E, 465m above sea level and Makonde plateau (in Mtwara rural) located at 10^{o} 41'S 39^{o} 23'E, 760m above sea level.

Nine newly improved cassava genotypes, one old improved variety (Naliendele as a control), one ex-Rufiji variety (Kiroba) and 2 landraces were used in this study (Table 4). One out of these landraces, Albert, was used both as a check and a CBSD disease spreader, while the rest of the landraces, Limbanga, was used as CMD disease spreader. Albert and Limbanga were planted around the replications as a source of inoculum (spreader of the diseases) at all locations. The improved genotypes were obtained from Naliendele Agricultural Research Institute - Mtwara, while the local ones were from farmers' fields.

Table 4:Cassava genotypes used in this study, their origin and status

	Genotype	Source	Status
1	NDL 2006/104	NARI	Tolerant to CBSD &CMD
2	NDL 2006/850	NARI	Tolerant to CBSD &CMD
3	NDL 2006/487	NARI	Tolerant to CBSD &CMD
4	NDL 2006/283	NARI	Tolerant to CBSD &CMD
5	NDL 2006/738	NARI	Tolerant to CBSD &CMD
6	NDL 2006/438	NARI	Tolerant to CBSD &CMD
7	NDL 2006/741	NARI	Tolerant to CBSD &CMD
8	NDL 2006/840	NARI	Tolerant to CBSD &CMD
9	NDL 2006/030	NARI	Tolerant to CBSD &CMD
10	NALIENDELE	NARI	Susceptible to CBSD &CMD and check
11	KIROBA	Ex-Rufiji	Tolerant to CBSD & CMD and check
12	ALBERT	Farmers	Local (Check in all sites)

3.2 Methods

3.2.1 Experimental design

A split-split plot experiment in a Randomized Complete Block Design (RCBD) was used to carry out the study. Weeding regime as a crop management practice was used in each location, weeding once (W_1) and weeding twice (W_2), in order to create micro environments for stability analysis. The experiment consisted of three factors, location as main factor A, crop management (weeding regime) as sub factor B and genotype as sub-sub factor C. Nine genotypes and three other varieties with three replications in each location spaced at 1 m x 1 m, 4 rows planted with 7 plants per row and a plot size of 7m long and 4m wide were used.

3.2.2 Data collection

Data were collected from the 2 middle rows, leaving one plant at each end of the rows. Data collected and methods used are as follows:

3.2.2.1 Disease incidence (CBSD & CMD)

Number of infected plants divided by the total number of plants in the net area times 100. This was done in 3 months interval after planting.

3.2.2.2 Disease severity (CBSD & CMD)

Scale of 1 – 5 was used in scoring the severity. Where 1 = no disease symptoms observed and 5 = very severe disease symptoms (IITA, 1990). The disease severity was calculated in terms of average of the total plant scored. Calculation of average diseased plants was computed as:

$$\text{Aver. Severity} = \frac{(\text{Diseased plants x their severity scores}) + (\text{Undiseased plants})}{\text{Total number of plants scored}}$$

This was done in 3 months interval after planting.

3.2.2.3 Plant height

Was done by measuring the height of a plant (in cm), using a modified metric ruler.

3.2.2.4 Stem girth

This was taken by measuring the radius (in cm) of the plant by using vernier caliper, at 10 – 15 cm, above the ground. Then, the stem girth/circumference was calculated using the formula:

Stem girth = πr; where: π = Constant, known as pi and r = radius of the plant.

3.2.3 Harvesting data

3.2.3.1 Number of roots per plant

A plant was uprooted followed by the counting of the number of roots/plant.

3.2.3.2 Root weight per plot

Harvested roots in the net area were collected together, and then weighed (in kg) in a table weighing balance.

3.2.3.3 Root size

This was calculated by taking the total weight (kg) of the harvested roots in the net area then divided by the total number of harvested roots in the net area.

3.2.3.4 Air weight of the roots sample

A sample of 2 – 4 kg was weighed in a special balance which acts both as normal table balance as well as spring balance. The sample was weighed while immersed in water, stretching the balance downward. Only the middle part of the roots was used in obtaining this parameter. The ends of the sample roots were cut off before weighing.

3.2.3.5 Water weight of the root samples

A sample of 2 – 4 kg was weighed in a special balance which acts both as normal table balance as well as spring balance. The sample was weighed while immersed in water, stretching the balance downward. Only the middle part of the roots was used in obtaining this parameter. The ends of the sample roots were cut off before weighing.

3.2.3.6 Shoot weight per plot

This included the total weight (kg) of all above ground plant parts, which were weighed using a spring balance, stretching the balance downward while hanging.

3.2.3.7 Harvesting index (H.I)

This is defined as the proportion of the root weight in a biomass on a (fresh weight basis), is a valuable trait in cassava breeding. Heritability for H.I is relatively high and its assessment is also relatively simple and straight forward (Kawano, 1990).

The H.I was computed as

$$H.I = \frac{\text{Weight of roots/plot}}{\text{Weight of roots/plot + weight of the above ground biomass/plot}}$$

3.2.3.8 Root taste

Cassava roots are either sweet or bitter. The bitter ones are said to be associated with high levels of hydrogen cyanide content, which is poisonous. In assessing the cassava root taste, a scale of 1 – 3 was used, where, 1 = Sweet, 2 = intermediate and 3 = bitter.

3.2.3.9 Root hardness

This parameter explains the content of dry matter in the fresh cassava root in a simple way. If the cassava root is hard when chewing in the mouth, it means that, the content of dry matter is high and vice versa. In assessing the cassava root hardness, a scale of 1 – 3 was used, where, 1 = watery, 2 = intermediate and 3 = hard.

3.2.3.10 Root necrosis

This is a symptom of the presence of CBSD in the cassava roots. Cassava roots change colour from whitish to brownish (signs of root rot) and occur in patches. A scale of 1– 5 was used in scoring the necrosis severity, where 1 = no disease symptoms at all and 5 = very severe symptoms (IITA, 1990).

3.2.3.11 Dry matter percentage (%DM)

Dry matter content was carried out by gravitational method (Use of specific gravity) as described by Kawano *et al.,* (1987).

% DM = [(Specific gravity x Constant) – 142] x 100.

Whereby:

Specific gravity = Weight of cassava roots sample in air divided by the difference between weight of cassava roots sample in air and cassava roots sample in water.

Constant = 158.3.

3.2.3.12 Starch percentage

Starch percentage content was determined by gravitational method. (Use of specific gravity) as described by Kawano *et al., (*1987).

% Starch = [(Specific gravity x Constant) – 106.4] x 100.

Whereby:

Specific gravity = Weight of cassava roots sample in air divided by the difference between weight of cassava roots sample in air and cassava roots sample in water, constant = 112.1.

3.2.3.13 Protein content

Protein content determination was carried out by *Kjeldalh* method as described by AOAC, (1990).

3.3 Data Analysis

Data was subjected to Analysis of Variance (ANOVA) using Indostat/Windostat version 8.5 statistical software package. Mean separation was done using Duncan's Multiple Range Test (DMRT) at a probability level of 5%. Correlations and stability studies were assessed using linear regression analysis (Eberhart and Russell, 1966). Path coefficient analysis was done according to Dewey and Lu, (1959) procedures.

3.3.1 Specific objective (i) to assess the yield performance of newly developed cassava genotypes in different agro ecological conditions

3.3.1.1 Analysis of variance

Single site and combined sites analysis was done using Indostat/Windostat software. The analysis was performed as per location and as well as combined analysis, using the following models.

The statistical model for each location was: $\mathbf{Y_{ijkl}=\mu + r_i +\alpha_k +r\alpha_{ik} +\gamma_l +\alpha\gamma_{kl} + \varepsilon_{ijkl}}$

For combined analysis the model used was:

$$\mathbf{Y_{ijklm} = \mu + r_{ij} + \beta_j +r\beta_{ij}(\varepsilon_a) +\alpha_k + \beta\alpha_{jk} + \gamma_l+\beta\gamma_{jl} + \alpha\gamma_{kl} + \alpha\gamma\beta_{ijk} + \varepsilon_{ijklm}}$$

Where by:

$\mathbf{Y_{ijklm}}$ = measurement for l^{th} genotype of the j^{th} and k^{th} weeding in i^{th} replication and m^{th} plot,

μ = Overall mean,

$\mathbf{r_{ij}}$ = i^{th} replication within j^{th} location**,**

$\mathbf{\beta_j}$ = j^{th} location effect,

$\mathbf{r\beta_{ij}}$ = interaction effect of i^{th} replication and j^{th} location,

$\mathbf{\alpha_k}$ = k^{th} weeding effect,

$\mathbf{\beta\alpha_{jk}}$ = interaction effect of j^{th} location and k^{th} spacing ,

$\mathbf{\gamma_l}$ = i^{th} genotype effect

$\mathbf{\beta\gamma_{jl}}$ = interaction effect of j^{th} location and i^{th} genotype

$\mathbf{\alpha\gamma_{kl}}$ = interaction of k^{th} weeding and i^{th} genotype

$\mathbf{\alpha\gamma\beta_{ijk}}$ = interaction effect of k^{th} weeding , j^{th} location and i^{th} genotype

$\mathbf{\varepsilon_{ijklm}}$ = random experimental error

3.3.1.2 Stability analysis

Stability analysis was performed using deviation from unit regression value (b - 1) and deviations mean square (S^2di) after Elberhart and Russel, (1966), using the following linear regression model;

$\mathbf{Y_{ij}} = \mu_1 + \beta_1 I_j + \delta_{ij}$

Where by:

$\mathbf{Y_{ij}}$ = observation of the i^{th} genotype at the j_{th} environment,

$\mathbf{\mu_1}$ = mean of i^{th} genotype mean over all environments,

$\mathbf{\beta_1}$ = regression coefficient that measures the response of the i^{th} genotype to varying environments,

$\mathbf{\delta_{ij}}$ = deviation from regression of the i^{th} genotype at the j^{th} environment,

$\mathbf{I_j}$ = environmental index obtained as the mean of all genotypes at the j^{th} environments.

3.3.1.3 Correlation analysis

By using Indostat/Windostat version 8.5 Software for analysis, correlations among yield and yield components for each location and across locations as a combined analysis was done.

3.3.1.4 Estimation of components of variances

Combined analysis of variance model for evaluating components of variance pooled over locations was calculated using the method given by Al- jibouri *et al.,* (1958). The observed mean squares obtained in the combined analysis of variance was used to separate out the effect of genotypes, environments and their interaction (Table 5).

Table 5: Combined ANOVA for evaluating genotypes at different locations

Source of Variation	DF	MS	Expected Mean Squares	F-Value
Locations (L)	l - 1	M1	$\sigma^2e + r\sigma^2_{GLW} + w\sigma^2_{GL} + rg\delta^2_{WL} + wg\sigma^2_{R(L)L} + sg\sigma^2_{R(L)} + sg\sigma^2_{L}$	M1/M9
Replication(R) within location (L)	l(r-1)	M2	$\sigma^2e + mg\,\sigma^2_{R(L)L} + sg\sigma^2_{R(L)}$	M2/M9
$Error_a$ R(L) x L)	l(r-1) (l-1)	M3	$\sigma^2e + wg\sigma^2_{R(L)L}$	M3/M9
Management (M)	m – 1	M4	$\sigma^2e + r\sigma^2_{GLW} + rg\sigma^2_{WL} + rl\sigma^2_{GW} + rlg\,\sigma^2_{W}$	M4/M9
M x L	(m – 1)(l – 1)	M5	$\sigma^2e + r\,\sigma^2_{GLW} + rg\sigma^2_{WL}$	M5/M9
Genotype (G)	g-1	M6	$\sigma^2e + r\,\sigma^2_{GLW} + rw\sigma^2_{GL} + rl\sigma^2_{GS} + rlw\sigma^2_{G}$	M6/M9
G x L	(g-1)(l-1)	M7	$\sigma^2e + r\,\sigma^2_{GLW} + rw\sigma^2_{GL}$	M7/M9
G x M	(g-1)(m-1)	M8	$\sigma^2e + r\,\sigma^2_{GLW} + rl\sigma^2_{GW}$	M8/M9
G x L x M	(g-1)(l-1)(m-1)	M9	$\sigma^2e + r\,\sigma^2_{GLW}$	M9/M10
Overall $Error_c$	l(r-1)(l-1)(m-1)(g-1)	M10	σ^2e	
Total	lrmg-1			

Where:

$\boldsymbol{\sigma^2_e}$ = Component of variance due to the error term,

$\boldsymbol{\sigma^2_G}$ = Component of variance due to genotypes,

$\boldsymbol{\sigma^2_L}$ = Component of variance due to locations,

$\boldsymbol{\sigma^2_W}$ = Component of variance due to crop management,

$\boldsymbol{\sigma^2_{R\,(L)}}$ = Component of variance due to replication within location,

$\boldsymbol{\sigma^2_{R\,(L)\,L}}$ = Component of variance due to replication within location x location interaction,

$\boldsymbol{\sigma^2_{GL}}$ = Component of variance due to genotype x location interaction,

$\boldsymbol{\sigma^2_{GW}}$ = Component of variance due to genotype x management interaction,

$\boldsymbol{\sigma^2_{GLW}}$ = Component of variance due to genotype x location x management interaction,

R = Replications,

L = Locations,

W = Weeding

G = Genotypes.

3.3.1.5 Analysis of phenotypic variance

Analysis of the component of phenotypic variance (δ^2_{ph}) tested in r replications and l locations were computed using the following formula:

$$\delta^2_{ph} = \sigma^2 e + \sigma^2_{GLW} + \sigma^2_{GW} + \sigma^2_{GL} + \sigma^2_{G} + \sigma^2_{WL} + \sigma^2_{S} + \sigma^2_{R\,(L)} + \sigma^2_{R/(L)} + \sigma^2_{L}$$

3.3.1.6 Broad sense heritability

Heritability (broad sense) was calculated as the ratio of genotypic variance to phenotypic variance using the formula after Hanson *et al.,* (1956);

$$h^2_b = \sigma^2_g / \sigma^2_{ph} \times 100.$$

Where:

$\mathbf{h^2_b}$ = heritability in the broad sense, $\sigma^2 g$ = the component of variance due to genotypes,

$\boldsymbol{\sigma^2_g}$ = the component of variance due to genotypes,

$\boldsymbol{\sigma^2_{ph}}$ =phenotypic component of variance.

3.3.1.7 Path coefficient analysis

Path coefficient analysis was carried out as described by Dewey and Lu, (1959). The relationships among yield and yield components were computed at each location and across locations as combined analysis. The relationship between correlation coefficients and path coefficients was established using the following path

coefficient diagram and simultaneous equations arranged in matrix form (Figure 1). The method involves solving of unknowns (path coefficients) from a series of simultaneous equations.

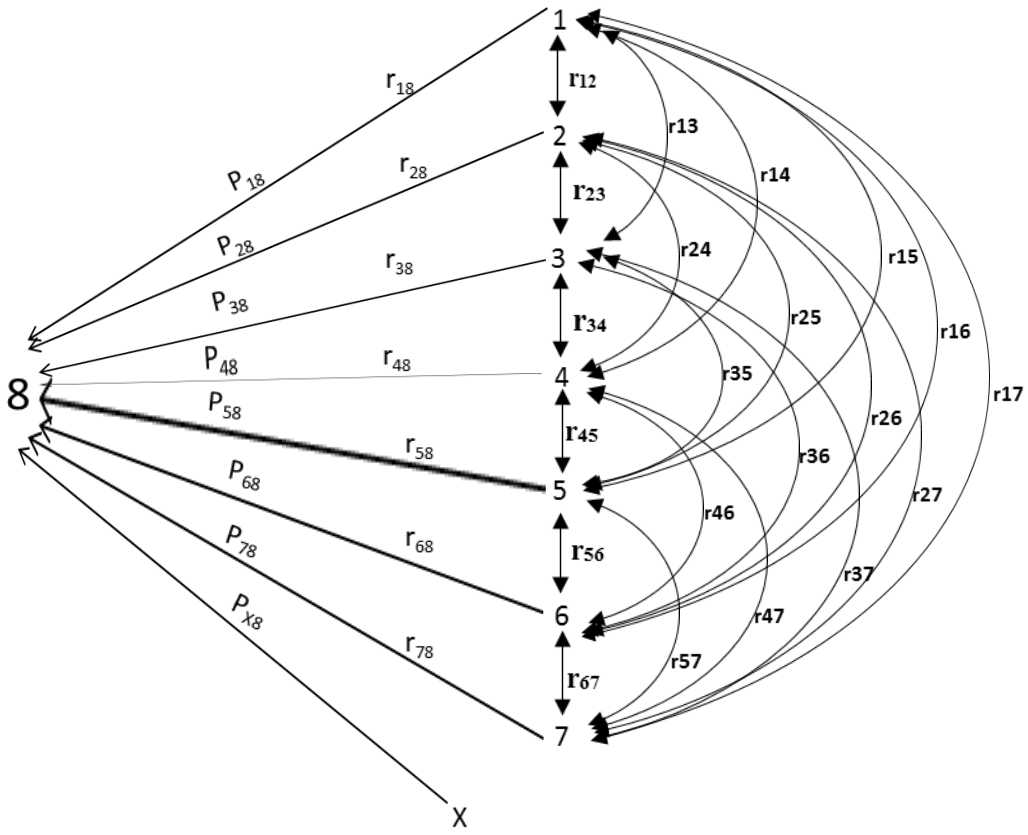


Figure 1: Path diagram showing direct and indirect effects on yield and yield components

Key: (1) = Root size; (2) = Number of roots per plant; (3) = Plant height; (4) = Number of branches per plant; (5) = Stem girth; (6) = % Dry Matter; (7) = Harvest Index; (8) = Storage root yield and (X) = Residual effect.

In the path diagram the double-arrowed lines indicate mutual associations as measured by correlation coefficients, r, and the single arrowed lines represent direct influence as measured by path coefficients P.

Simultaneous Equations used in the computation of rP's

$r_{18} = P_{18} + r_{12}P_{28} + r_{13}P_{38} + r_{14}P_{48} + r_{15}P_{58} + r_{16}P_{68} + r_{17}P_{78}$

$r_{28} = r_{12}P_{18} + P_{28} + r_{23}P_{38} + r_{24}P_{48} + r_{25}P_{58} + r_{26}P_{68} + r_{27}P_{78}$

$r_{38} = r_{13}P_{18} + r_{23}P_{28} + P_{38} + r_{34}P_{48} + r_{35}P_{58} + r_{36}P_{68} + r_{37}P_{78}$

$r_{48} = r_{14}P_{18} + r_{24}P_{28} + r_{34}P_{38} + P_{48} + r_{45}P_{58} + r_{46}P_{68} + r_{47}P_{78}$

$r_{58} = r_{15}P_{18} + r_{25}P_{28} + r_{35}P_{38} + r_{45}P_{48} + P_{58} + r_{56}P_{68} + r_{57}P_{78}$

$r_{68} = r_{16}P_{18} + r_{26}P_{28} + r_{36}P_{38} + r_{46}P_{48} + r_{56}P_{58} + P_{68} + r_{67}P_{78}$

$r_{78} = r_{17}P_{18} + r_{27}P_{28} + r_{37}P_{38} + r_{47}P_{48} + r_{57}P_{58} + + r_{67}P_{68} + P_{78}$

Computation of residual factor (Px8) was based on the following equation;

$1 = P^2X_8+P^2_{18}+P^2_{28}{}^{+}P^2_{38}+P^2_{48}+P^2_{58}+P^2_{68}+P^2_{78}+2P_{18}r_{12}P_{28}+2P_{18}r_{13}P_{38}+2P_{18}r_{14}P_{48}+$

$2P_{18}r_{15}P_{58}+2P_{18}r_{16}P_{68}+2P_{18}r_{17}P_{78}+2P_{28}r_{23}P_{38}+2P_{28}r_{24}P_{48}+2P_{28}r_{25}P_{58}+2P_{28}r_{26}P_{68}+2P_{28}r_{2}$

$_{7}P_{78}+2P_{38}r_{34}P_{48}+2P_{38}r_{35}P_{58} + 2P_{38}r_{36}P_{68} + 2P_{38}r_{37}P_{78} + 2P_{48}r_{45}P_{58} + 2P_{48}r_{46}P_{68} +$

$2P_{48}r_{47}P_{78}+2P_{58}r_{56}P_{68}+2P_{58}r_{57}P_{78}+2P_{68}r_{67}P_{78}$

The indirect effects of a variable on yield (rP's) are the product of the correlation coefficient (r) and the direct effect (P).

Explanations basing on the path model:

r_{ij} = simple correlation coefficients for measuring the mutual association of the two variable,

$\mathbf{P_{ij}}$ = path coefficients for measuring direct effects of the variables on yield

$\mathbf{r_{ij}p_{ij}}$ = indirect effects of variables upon another via other variables

$\mathbf{p_x}$ = the residue effect in the path analysis model; i and j = (1,2,3, …..8)

3.3.2 Specific objective (ii) to identify farmers' criteria for cassava acceptability

A group of farmers between 10 – 20 in each location were involved in the harvesting exercise. Before harvesting, farmers were urged to mention/describe the cassava criteria they use in selecting cassava variety. These criteria were then ranked according to the farmers' prioritization. By using "seed ranking method", criteria-wise, farmers made selection among the harvested cassava genotypes. Then genotypes were compared using 'pair-wise ranking" method.

3.3.3 Specific Objective (iii) to study nutritional characteristics of the cassava genotypes

3.3.3.1 Percentage Dry matter (DM) content determination

Dry matter comprises all remains after removing water from a cassava fresh root. Estimation of DM content in cassava bases on the principle of a linear relationship between specific gravity with DM (Kawano et *al.*, 1987). Percentage DM = 158.3x – 142,

Procedures

i. Root samples weighing 2 – 3 kg were prepared by cutting off the side parts of the roots
ii. The samples were weighed in air using a suitable balance (Wa).
iii. Then the samples were weighed in water (Ww).

iv. Computation of specific gravity

$$\text{Specific gravity} = \frac{Wa}{Wa - Ww}$$

Where:

Wa = Air weight (kg)

Ww = Water weight (kg)

3.3.3.2 Starch content determination

According to Kawano *et al.,* (1987), determination of starch content in cassava takes the same principles as those of determining % DM. In estimating the % starch, the linear relationship used was, percentage starch content = 112.1x – 106.4; where x = specific gravity.

Procedures

i. Root samples weighing 2 – 3 kg were prepared cutting off the side parts of the roots

ii. The samples were weighed in air using a suitable balance (Wa).

iii. Then the samples were weighed in water (Ww).

iv. Computation of specific gravity

$$\text{Specific gravity} = \frac{Wa}{Wa - Ww}$$

Where:

Wa = Air weight (kg)

Ww = Water weight (kg)

3.3.3.3 Protein content determination

Protein content determination was carried out by *Kjeldalh* method as described by AOAC, (1990). 1g of sample was weighed and placed to nitrogen free filter paper, then folded and dropped into a Kjeldalh digestion tube. 3.0g of digestion mixed catalyst $CuSo_4$ +Na_2So_4 and 25 mls of concentrated Na_2So_4 were added. The mixture was then transferred to the Kjeldalh digestion apparatus. This was followed by addition of 6 mls sulphuric acid. The samples were then placed in digestion chamber and heated for one hour. After one hour the samples were allowed to cool. Then, a fractional distillation was carried out to separate ammonia from the digested contents. The boric acid was used to trap up the gas into the form of ammonium borate. The ammonia solution (ammonium borate) was titrated against hydrochloric acid to obtain the actual content of ammonia. Amount of Nitrogen (N) was determined from the ammonia, which was then used to calculate the actual protein content in the sample using the formular:

$$[\%\ N = \frac{14.01 \times (Titre - Blank) \times Conc.\ HCl}{5.00 \times 10}] \times 100.$$

Whereby:

N = nitrogen

Conc. HCl = Concentrated hydrochloric acid

Crude Protein (CP) is then calculated as:

CP = %N x factor;

Factor = 6.25

CHAPTER FOUR

4.0 RESULTS

4.1 Yield and Yield Components

4.1.1 Effect of locations on root yield, plant height, number of branches per plant, stem girth, number of roots per plant, root size and harvest index on Cassava Genotypes

4.1.1.1 Root yield

Table 6 presents the means for cassava root yield at Naliendele, Mtopwa and Nachingwea. Significant variations ($P \leq 0.05$) were observed among genotypes within and across the locations. Genotype NDL 2006/487 had the highest mean root yield of 19.02 t ha^{-1} at Naliendele, while the lowest mean root yield (4.71 t ha^{-1}) was recorded on NDL 2006/840 which was not significantly different from Albert (5.00 t ha^{-1}). At Mtopwa, the genotype NDL 2006/487 also recorded the highest mean root yield (14.02 t ha^{-1}), while landrace Albert had the lowest root yield of 4.71 t ha^{-1} which did not significantly differ from genotype NDL 2006/030 (5.17 t ha^{-1}), variety Naliendele (5.33 t ha^{-1}) and genotype NDL 2006/850 (5.55 t ha^{-1}). On the other hand, the adapted variety, Kiroba, showed superiority over the rest of the genotypes by producing the highest root yield of 40.48 t ha^{-1} at Nachingwea, while at that site genotype NDL 2006/030 gave the lowest root yield of 8.97 t ha^{-1}. However this genotype (NDL 2006/030) did not differ significantly from genotype NDL 2006/104 (9.06 t ha^{-1}). The highest overall mean root yield (18.18 t ha^{-1}) was obtained at Nachingwea, while Mtopwa site gave the lowest overall mean root yield (8.1t ha^{-1}). On the other hand, Naliendele site gave an overall mean root yield of 11.62 t ha^{-1} (Table 6 and 7).

Table 6: Means for root yield in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	5.00^{h}	4.71^{f}	12.23^{efg}
KIROBA	14.11^{dc}	10.56^{c}	40.48^{a}
NALIENDELE	16.00^{b}	5.33^{f}	12.87^{ef}
NDL 2006/030	12.72^{ed}	5.17^{f}	8.97^{g}
NDL 2006/104	11.22^{fe}	5.83^{ef}	9.06^{g}
NDL 2006/283	11.42^{e}	8.02^{d}	13.20^{e}
NDL 2006/438	14.40^{c}	12.83^{b}	14.61^{e}
NDL 2006/487	19.02^{a}	14.02^{a}	19.45^{d}
NDL 2006/738	9.77^{gf}	10.15^{c}	20.50^{d}
NDL 2006/741	8.92^{g}	8.22^{d}	9.63^{fg}
NDL 2006/840	4.71^{h}	6.78^{e}	12.33^{efg}
NDL 2006/850	12.17^{e}	5.55^{f}	24.80^{c}
Overall mean	**11.62**	**8.10**	**18.18**
s.e	1.32	0.98	0.91
c.v. (%)	11.40	12.10	5.00

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Table7: Summary of location effects for the different variables

Location	RYD	PHT	BPL	SGH	RPL	RTZ	HI	CBI%	CBS	CMI%	CMS	NEC	DM%	STH%	PTN%
Nali	11.62	136.04	2.72	5.25	4.78	0.21	0.65	10.97	1.24	21.53	1.41	1.60	36.75	20.36	0.67
Mtop	8.10	96.89	2.49	3.37	3.21	0.25	0.65	11.89	1.30	8.34	1.19	1.31	37.92	21.21	0.88
Nach	18.18	158.00	2.75	4.59	5.18	0.31	0.76	11.79	1.25	11.60	1.30	1.51	38.22	21.47	0.78
Mean	**12.63**	**130.31**	**2.65**	**4.40**	**4.39**	**0.26**	**0.69**	**11.55**	**1.26**	**13.82**	**1.30**	**1.47**	**37.63**	**21.01**	**0.78**

Nali = Naliendele, Mto = Mtopwa, Nach = Nachingwea

Where: RYD = Root yield, PHT = Plant height, BPL = Branches per plant, SGH = Stem girth, RPL = Roots per plant, RTZ = Root size, HI = Harvest index, CBSI% = Cassava brown streak disease incidence, CBS = Cassava brown streak disease severity, CMI = Cassava mosaic disease incidence, NEC = Root necrosis, DM% = Dry matter, STH = Starch and PTN = Protein

The relationship between the locations and the root yield (Figure 2) indicates that, Nachingwea (mid altitude) generally recorded highest values over the other locations. The lowest root yield values were obtained at Mtopwa (relative high altitude), whereas Naliendele (low altitude) had moderately root yield values. At Nachingwea (mid altitude), Kiroba, NDL 2006/283, NDL 2006/738, NDL 2006/840 and NDL 2006/850 outperformed the similar genotypes at Naliendele (low altitude) and Mtopwa (relative high altitude). At Mtopwa (relative high altitude), varieties Kiroba and Naliendele, genotypes NDL 2006/030, NDL 2006/104, NDL 2006/283 and NDL 2006/487 showed lowest values of root yield. On the other hand, genotypes NDL 2006/438 and NDL 2006/741 almost performed similarly at all locations (Figure 2).

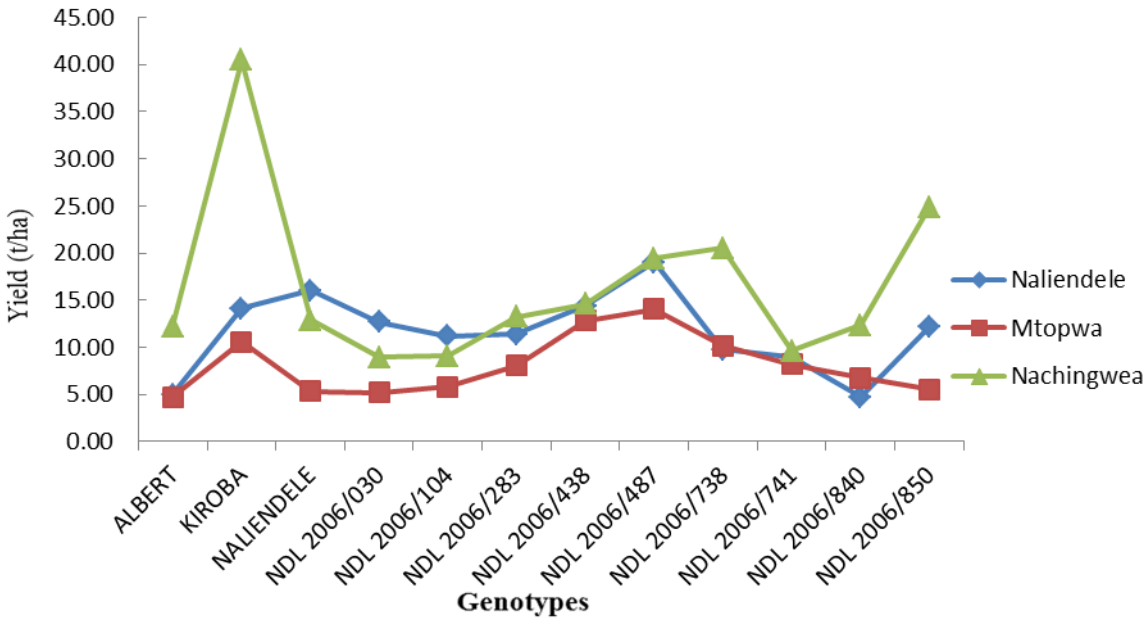


Figure 2: Effects of location on cassava root yield (t ha^{-1}) grown at Naliendele (low altitude), Nachingwea (mid altitude) and Mtopwa (high altitude)

4.1.1.2 Plant height

Significant differences ($P \leq 0.05$) existed among the means of the treatments within and across the locations (Table 8 and 7)). At Naliendele, genotype NDL 2006/487 outperformed all other treatments for plant height with (156.2 cm), while the lowest plant height (113.6 cm) was shown on genotype NDL 2006/840. At Mtopwa, although the highest value of plant height (119.7 cm) was observed on the landrace Albert, it was not significantly different from treatments NDL 2006/438 (116.43 cm) and NDL 2006/840 (113.89 cm). Kiroba recorded the least value of 80.55 cm. Treatments Naliendele (85.04 cm), NDL 2006/030 (88.33 cm), NDL 2006/104 (84.27 cm), NDL 2006/738 (85.00 cm) and NDL 2006/741 (89.38 cm), did not significantly differ in plant height. At Nachingwea the highest value for plant height (184.9 cm) was recorded on the genotype NDL 2006/438, while genotype NDL 2006/741 had the lowest value of (128.10 cm). Treatments, Albert, NDL 2006/104 and NDL 2006/283 with plant heights of 159.40 cm, 163.20 cm and 163.00 cm respectively revealed no significant differences among them. Based on locations, at Nachingwea, the highest overall mean plant height was 158.00 cm, while Mtopwa site gave the lowest overall mean plant height of (96.89 cm). Furthermore, Naliendele site gave an overall mean plant height of 136.04 cm.

Across the locations treatment NDL 2006/438 had the highest plant height at Nachingwea (184.90 cm) and Mtopwa (116.43 cm), while at Naliendele had plant height of (128.70 cm). Treatment NDL 2006/840 had almost similar plant heights at Naliendele (113.60 cm, lowest) and Mtopwa (113.89 cm, high) whereas at Nachingwea it had a medium plant height of 151.70 cm.

Table 8: Means for plant height in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	124.00^{gfe}	119.17^{a}	159.40^{cb}
KIROBA	130.50^{fed}	80.55^{d}	139.70^{fed}
NALIENDELE	150.00^{ba}	85.04^{dc}	135.00^{fe}
NDL 2006/030	134.40^{edc}	88.33^{dc}	156.10^{dc}
NDL 2006/104	143.00^{dcb}	84.27^{dc}	163.20^{cb}
NDL 2006/283	144.60^{cba}	105.69^{b}	163.00^{cb}
NDL 2006/438	128.70^{fe}	116.43^{a}	184.90^{a}
NDL 2006/487	156.20^{a}	90.63^{c}	169.40^{cba}
NDL 2006/738	134.50^{edc}	85.00^{dc}	168.00^{cba}
NDL 2006/741	120.40^{gf}	89.38^{dc}	128.10^{f}
NDL 2006/840	113.60^{g}	113.89^{a}	151.70^{edc}
NDL 2006/850	152.60^{ba}	104.27^{b}	177.90^{ba}
Overall mean	**136.04**	**96.89**	**158.00**
s.e	10.15	6.80	10.77
c.v.(%)	7.50	7.00	6.80

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.3 Number of branches per plant

Significant ($P \leq 0.05$) variations were observed among the tested genotypes at all locations (Table 9). At Naliendele, the highest number of branches per plant (3.75) was observed on the genotype NDL 2006/104 while genotype NDL 2006/487, recorded the lowest number of branches per plant (1.15). Treatments NDL 2006/283, NDL 2006/438, NDL 2006/738, NDL 2006/840 and NDL 2006/850 were not significantly different with number of branches per plant of 2.02, 2.43, 2.35, and 2.33 and 2.50 respectively. At Mtopwa, Kiroba had the highest number of branches per plant of 3.63. The lowest number of branches per plant (1.33) at Mtopwa was observed on the genotype NDL 2006/487. However, at Mtopwa, treatments Naliendele (2.35), NDL 2006/030 (2.37), NDL 2006/104 (2.17), NDL 2006/283 (2.40), NDL 2006/438 (2.51), NDL 2006/840 (2.13) NDL 2006/850 (2.10) were not

statistically different. At Nachingwea Kiroba was superior over the other treatments in number of branches per plant (4.17). The lowest number of branches per plant (1.18) was recorded on the treatment NDL 2006/487**.** However, no significant differences were observed among the treatments Naliendele (3.04), NDL 2006/030 (3.02), NDL 2006/104 (3.00), NDL 2006/283 (3.01) and NDL 2006/741 (2.83). The overall mean number of branches per plant at Nachingwea was 2.75, while Naliendele site gave the lowest overall number of branches per plant (2.72). At Mtopwa the overall mean number of branches per plant was 2.49. Across the locations treatment Kiroba had the highest number of branches per plant at Mtopwa and Nachingwea (3.63 and 4.17) respectively, while at Naliendele it had medium number of branches per plant of 3.32. The lowest number of branches per plant at Naliendele (1.15), Mtopwa (1.33) and Nachingwea (1.18) was observed on NDL 2006/487.

Table 9: Means for number of branches per plant in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	3.07^{b}	2.69^{bc}	3.03^{b}
KIROBA	3.32^{ba}	3.63^{a}	4.17^{a}
NALIENDELE	3.18^{b}	2.35^{c}	3.04^{b}
NDL 2006/030	3.01^{b}	2.37^{c}	3.02^{b}
NDL 2006/104	3.75^{a}	2.17^{c}	3.00^{b}
NDL 2006/283	2.02^{c}	2.40^{c}	3.01^{b}
NDL 2006/438	2.43^{c}	2.51^{c}	2.58^{dcb}
NDL 2006/487	1.15^{d}	1.33^{d}	1.18^{e}
NDL 2006/738	2.35^{c}	2.75^{bc}	2.68^{cb}
NDL 2006/741	3.51^{ba}	3.37^{ab}	2.83^{b}
NDL 2006/840	2.33^{c}	2.13^{c}	2.17^{d}
NDL 2006/850	2.50^{c}	2.10^{c}	2.25^{dc}
Overall mean	**2.72**	**2.49**	**2.75**
s.e	0.42	0.62	0.34
c.v. (%)	15.5	24.80	12.30

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.4 Stem girth

The results for stem girth varied significantly ($P \leq 0.05$) among genotypes within and across the locations (Table 10). Although variety Naliendele (6.17 cm) outperformed all other treatments, it showed no significant differences with the treatments Kiroba (6.03 cm), NDL 2006/283 (5.99 cm), NDL 2006/487 (5.95 cm) and NDL 2006/850 (5.96 cm). The lowest value of 4.17cm was recorded on genotype NDL 2006/840 which was not statistically different from treatment Albert with stem girth of 4.35cm. Other treatments that had statistically similar means of stem girth were NDL 2006/030 (5.15 cm), NDL 2006/104 (5.38 cm), NDL 2006/438 (5.20 cm), NDL 2006/738 (4.92 cm) and NDL 2006/741 (4.97 cm).

At Mtopwa, the widest stem girth (3.92 cm) was observed on the genotype NDL 2006/840, while the lowest stem girth (2.79 cm) was recorded on the treatment NDL 2006/438. No significant differences were observed on treatments NDL 2006/104 (3.26 cm), NDL 2006/283 (3.29 cm) and NDL 2006/738 (3.38 cm); also treatments Albert (3.55 cm) and NDL 2006/850 (5.96 cm) were not significantly different. Genotype NDL 2006/104 showed the highest mean stem girth of 5.13 cm at Nachingwea, however this treatment had no significant differences from treatmnets Kiroba (5.07 cm), NDL 2006/438 (4.96 cm), NDL 2006/738 (5.00 cm) and NDL 2006/850 (5.04 cm). Furhermore, Naliendele variety recorded the lowest stem girth of 3.58 cm which was statistically similar to treatments NDL 2006/030 (3.82 cm) and NDL 2006/283 (3.84 cm). Also no statistically significant variations were observed between Albert (4.47 cm) and NDL 2006/487 (4.49 cm); and between NDL 2006/741 (4.88 cm) and NDL 2006/840 (4.74 cm). The highest overall mean

stem girth was recorded at Naliendele (5.35 cm), while the lowest overall stem girth was recorded at Mtopwa (3.37 cm). Nachingwea recorded the overall mean stem girth of 4.59.

Across the locations Naliendele had the highest stem girth of 6.17 cm at Naliendele site, while it was the least at Nachingwea (3.58 cm). At Mtopwa, treatment Naliendele performed moderately (3.06 cm). The least stem girth across the locations was recorded on the treatment NDL 2006/438 (2.79 cm) at Mtopwa, while at Naliendele it had moderately stem girth of (5.20 cm) and at Nachingwea it had a high stem girth of (4.96 cm).

Table 10: Means for stem girth in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	4.35^{c}	3.55^{abc}	4.47^{b}
KIROBA	6.03^{a}	3.46^{abcd}	5.07^{a}
NALIENDELE	6.17^{a}	3.06^{de}	3.58^{c}
NDL 2006/030	5.15^{b}	3.24^{bcde}	3.82^{c}
NDL 2006/104	5.38^{b}	3.26^{bcd}	5.13^{a}
NDL 2006/283	5.99^{a}	3.29^{bcd}	3.84^{c}
NDL 2006/438	5.20^{b}	2.79^{e}	4.96^{a}
NDL 2006/487	5.95^{a}	3.70^{ab}	4.49^{b}
NDL 2006/738	4.92^{b}	3.38^{bcd}	5.00^{a}
NDL 2006/741	4.97^{b}	3.20^{cde}	4.88^{ab}
NDL 2006/840	4.17^{c}	3.92^{a}	4.74^{ab}
NDL 2006/850	5.96^{a}	3.62^{abc}	5.04^{a}
Overall mean	**5.35**	**3.37**	**4.59**
s.e	0.37	0.36	0.38
c.v. (%)	6.80	10.60	8.20

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.5 Number of roots per plant

The means for number of roots per plant varied significantly ($P \leq 0.05$) among the treatments within and across the locations (Table 11). Variety Naliendele gave the highest mean number of roots per plant (7.03) at Naliendele, and the lowest mean number of roots per plant was 3.23 recorded on Albert. However, genotype NDL 2006/840 with mean number of roots per plant of 3.39 did not differ significantly with Albert. Treatments Kiroba and NDL 2006/283 with number of roots per plant 5.61 and 5.45 respectively, had no significant differences, also, NDL 2006/030 (3.75) and NDL 2006/741 (3.71) were not statistically different. Other treatments that showed no significant variation between their means on number of roots per plant were NDL 2006/487 and NDL 2006/738 with number of roots per plant 5.01 and 4.99 respectively.

At Mtopwa, the genotype which outperformed the rest in the mean number of roots per plant was NDL 2006/487 (5.79) and the lowest value for number of roots per plant (1.63), was recorded on genotypes NDL 2006/741. This treatment did not vary significantly with treatments NDL 2006/104 (2.00), NDL 2006/738 (2.10), NDL 2006/741 (1.63) and NDL 2006/850 (2.04). Also treatments Albert, NDL 2006/030 and NDL 2006/283 were statistically similar with number of roots per plant of 2.90, 2.98 and 2.98 respectively. The variations of number of roots per plant were also observed at Nachingwea whereby the highest number of roots per plant 10.03 was recorded on Kiroba. The lowest number of roots per plant was 3.26 recorded on NDL 2006/030. Treatments NDL 2006/438 and NDL 2006/850 showed statistically similar means of number of roots per plant of 5.77 and 5.95 respectively.

Nachingwea was the leading site in the overall mean number of roots per plant (5.95), followed by Naliendele site 4.78 and Mtopwa site showed the lowest mean overall number of roots per plant (3.21). Across the locations, Kiroba was superior (10.03) over all other treatments at Nachingwea, while at Mtopwa was among the highest (5.45) and moderate at Naliendele (5.61).

Table 7: Means for number of roots per plant in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	3.23^{e}	2.90^{d}	4.80^{cde}
KIROBA	5.61^{cb}	5.45^{a}	10.03^{a}
NALIENDELE	7.03^{a}	3.51^{c}	5.17^{bcd}
NDL 2006/030	3.75^{ed}	2.98^{d}	3.26^{g}
NDL 2006/104	5.02^{c}	2.00^{e}	3.53^{fg}
NDL 2006/283	5.45^{cb}	2.98^{d}	4.09^{defg}
NDL 2006/438	5.01^{c}	3.17^{cd}	4.94^{bcde}
NDL 2006/487	5.92^{b}	5.79^{a}	5.77^{cb}
NDL 2006/738	4.99^{c}	2.10^{e}	4.59^{bde}
NDL 2006/741	3.71^{ed}	1.63^{e}	6.07^{b}
NDL 2006/840	3.39^{e}	4.01^{b}	3.93^{efg}
NDL 2006/850	4.23^{d}	2.04^{e}	5.95^{bc}
Overall mean	**4.78**	**3.21**	**5.18**
s.e	0.51	0.39	0.66
c.v.(%)	10.70	12.10	12.70

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.6 Root size

Significant differences ($P \leq 0.05$) were observed among the genotypes tested (Table 12). Albert variety showed the highest root size (0.26 kg) at Naliendele, whereas the least treatment in root size was NDL 2006/840 (0.11 kg). Genotypes NDL 2006/438, NDL 2006/487 and NDL 2006/738 gave equal means of root size being 0.22 kg. Treatment NDL 2006/738 outperformed all other treatments with mean root

size of 0.49 kg and was statistically different from all other treatments at Mtopwa. The variety Naliendele had the lowest mean root size (0.13 kg), which also was statistically different from all other treatments. No significant differences were observed among treatments Albert, Kiroba, NDL 2006/030, NDL 2006/283, NDL 2006/438 NDL 2006/741, NDL 2006/840 and NDL 2006/850 with mean root sizes of 0.22 kg, 0.25 kg, 0.28 kg, 0.28 kg, 0.16, 0.18 kg 0.31 kg, 0.22 kg and 0.28 kg respectively at Mtopwa. At Nachingwea, NDL 2006/840 outperformed the rest of the treatments by recording the highest mean cassava root size of 0.66 kg, while at the same location the lowest mean root size (0.16 kg) was obtained on NDL 2006/030. Treatments Albert, Naliendele, NDL 2006/104, NDL 2006/438 and NDL 2006/487 with mean root size of 0.23 kg, 0.24 kg, 0.24 kg, 0.24 kg and 0.25 kg respectively, did not differ significantly. On the other hand, treatments Kiroba (0.39 kg), NDL 2006/738 (0.42 kg) and NDL 2006/850 (0.38 kg), were statistically similar in root size. The highest overall mean root size (0.31 kg) was obtained at Nachingwea, while Mtopwa gave 0.25 kg overall mean root size and 0.21kg overall mean root size was recorded at Naliendele (Table 12). Across the locations, NDL 2006/840 was superior (0.66 kg) and was obtained at Nachingwea, but the same treatment performed worst at Naliendele (0.11 kg) and moderately at Mtopwa (0.22 kg).

Table 12: Means for root size in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	0.26^{a}	0.22^{ab}	0.23^{cd}
KIROBA	0.19^{edc}	0.25^{ab}	0.39^{b}
NALIENDELE	0.21^{dcb}	0.13^{b}	0.24^{cd}
NDL 2006/030	0.23^{cea}	0.28^{ab}	0.16^{e}
NDL 2006/104	0.17^{e}	0.16^{b}	0.24^{cd}
NDL 2006/283	0.20^{edc}	0.28^{ab}	0.26^{c}
NDL 2006/438	0.22^{dcb}	0.16^{b}	0.24^{cd}
NDL 2006/487	0.22^{dcb}	0.18^{b}	0.25^{cd}
NDL 2006/738	0.22^{dcb}	0.49^{a}	0.42^{b}
NDL 2006/741	0.18^{ed}	0.31^{ab}	0.20^{de}
NDL 2006/840	0.11^{f}	0.22^{ab}	0.66^{a}
NDL 2006/850	0.25^{ba}	0.28^{ab}	0.38^{b}
Overall mean	**0.21**	**0.25**	**0.31**
s.e	0.03	0.21	0.04
c.v. (%)	14.9	15.40	12.00

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.7 Harvest index (HI)

The results for harvest index varied significantly ($P \leq 0.05$) among genotypes within and across the locations (Table 13). Harvest index values ranged between 0.53 and 0.84. At Naliendele, variety Kiroba had the highest harvest index (0.74), and the variety Albert showed the lowest value (0.57). However treatment Albert was not significantly different from NDL 2006/487 (0.58). Naliendele and NDL 2006/104 had a similar harvest index value of 0.62. Genotypes NDL 2006/030, NDL 2006/283, NDL 2006/438, NDL 2006/741, NDL 2006/840 and NDL 2006/850 showed no significant differences with harvest index values of 0.66, 0.65, 0.64, 0.67, 0.68 and 0.68 respectively. At Mtopwa, the highest mean harvest index was observed on NDL 2006/438 which had 0.75. However this treatment did not differ significantly from treatment Albert. The lowest mean harvest index value (0.53) was recorded on the treatment NDL 2006/487. Treatments Naliendele and NDL

2006/438 did not vary significantly, and also treatments NDL 2006/030 and NDL 2006/104 were statistically similar with an equal value of 0.65 which did not vary significantly with NDL 2006/741 and NDL 2006/850. At Nachingwea, treatment NDL 2006/738 was superior over all other treatments by giving an index value of 0.84. There were no significant differences observed on mean harvest indices among the treatments NDL 2006/104, NDL 2006/283, NDL 2006/438 and NDL 2006/850. Albert and NDL 2006/487 gave the lowest equal harvest index values of 0.70. The highest overall mean harvest index (0.76) was obtained at Nachingwea, while Mtopwa and Naliendele sites gave equal overall mean harvest indices of 0.65. The highest harvest index value (0.84) was observed on NDL 2006/738 at Nachingwea, while the same treatment had moderate harvest index values of 0.71 and 0.66 at Naliendele and Mtopwa sites respectively. Treatment NDL 2006/487 had the least harvest indices in all locations.

Table 8: Means for harvest index in cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	0.57^{c}	0.74^{a}	0.70^{d}
KIROBA	0.74^{a}	0.62^{cbc}	0.81^{cba}
NALIENDELE	0.62^{cb}	0.66^{ba}	0.73^{dc}
NDL 2006/030	0.66^{cba}	0.65^{cba}	0.73^{dcb}
NDL 2006/104	0.62^{cb}	0.65^{cba}	0.75^{dcba}
NDL 2006/283	0.65^{cba}	0.68^{ba}	0.75^{dcba}
NDL 2006/438	0.64^{cba}	0.75^{a}	0.75^{dcba}
NDL 2006/487	0.58^{c}	0.53^{c}	0.70^{d}
NDL 2006/738	0.71^{ba}	0.66^{cba}	0.84^{a}
NDL 2006/741	0.67^{cba}	0.58^{cb}	0.72^{dc}
NDL 2006/840	0.68^{cba}	0.59^{cb}	0.77^{dcba}
NDL 2006/850	0.68^{cba}	0.64^{cba}	0.83^{ba}
Overall mean	**0.65**	**0.65**	**0.76**
s.e	0.08	0.09	0.07
c.v.(%)	12.30	14.50	9.00

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.1.8 Combined analysis

Mean cassava root yield varied significantly ($P \leq 0.05$) among genotypes across locations (Table 14). The mean cassava root yield ranged from 7.32 to 21.72 t ha^{-1}, recorded on Albert and Kiroba respectively. Albert differed significantly from other genotypes except NDL 2006/840 while Kiroba differed significantly from all other treatments. Treatments NDL 2006/030, NDL 2006/104 and NDL 2006/741 were not significantly different and also genotypes Naliendele and NDL 2006/283 were not statistically different. The overall mean root yield was 12.63 t ha^{-1}.

Significant variations ($P \leq 0.05$) were observed among genotypes on the mean plant height. Genotype NDL 2006/850 gave the highest overall mean plant height of 144.90 cm, but this treatment was not significantly different from treatment NDL 2006/438 (143.40 cm). The lowest mean plant height was recorded on genotype NDL 2006/741 (112.60 cm) (Table 14). Neither treatments NDL 2006/104 and NDL 2006/738 nor treatments NDL 2006/283 and NDL 2006/487 had significant variations between them. The overall mean plant height was 130.32 cm.

Table 9: Means for yield and growth parameters in cassava genotypes under combined analysis

Genotype	PHT	BRP	STG	RTP	RTS	HI	RTY
ALBERT	134.20^{bc}	2.93^{bcd}	4.12^{ef}	3.64^{fgh}	0.24^{bcd}	0.67^{bc}	7.32^{g}
KIROBA	116.90^{ef}	3.71^{a}	4.85^{a}	7.03^{a}	0.28^{bcd}	0.73^{ab}	21.72^{a}
NALIENDELE	123.40^{de}	2.86^{cd}	4.27^{def}	5.24^{c}	0.20^{d}	0.67^{bc}	11.40^{e}
NDL 2006/030	126.30^{d}	2.80^{cde}	4.07^{f}	3.33^{h}	0.22^{cd}	0.68^{abc}	8.95^{f}
NDL 2006/104	130.20^{cd}	2.97^{bc}	4.59^{bc}	3.52^{gh}	0.19^{d}	0.67^{abc}	8.71^{f}
NDL 2006/283	137.80^{ab}	2.48^{efg}	4.37^{cde}	4.17^{de}	0.25^{bcd}	0.69^{abc}	10.88^{e}
NDL 2006/438	143.40^{a}	2.51^{efg}	4.32^{def}	5.83^{b}	0.22^{cd}	0.71^{abc}	18.61^{c}
NDL 2006/487	138.80^{ab}	1.22^{h}	4.71^{ab}	4.37^{d}	0.22^{cd}	0.60^{d}	19.50^{b}
NDL 2006/738	129.20^{cd}	2.59^{def}	4.43^{cd}	3.89^{efg}	0.38^{a}	0.74^{a}	13.47^{d}
NDL 2006/741	112.60^{f}	3.24^{b}	4.35^{cde}	3.81^{efg}	0.23^{cd}	0.66^{c}	8.93^{f}
NDL 2006/840	126.40^{d}	2.21^{g}	4.28^{def}	3.77^{efg}	0.33^{ab}	0.68^{abc}	7.94^{fg}
NDL 2006/850	144.90^{a}	2.28^{fg}	4.87^{a}	4.07^{def}	0.30^{abc}	0.71^{abc}	14.17^{d}
Overall mean	**130.32**	**2.65**	**4.44**	**4.39**	**0.25**	**0.68**	**12.63**
s.e	10.36	0.48	0.36	0.59	0.13	0.08	1.49
c.v. (%)	8.00	18.10	8.10	13.40	12.10	11.90	11.80

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Key: PHT = Plant height (cm), BRP = Number of branches per plant, STG = Stem girth (cm), RTP = Number of roots per plant, RTS = Root size (kg), HI = Harvest index and RYD = Root yield (t ha^{-1}).

The mean number of branches per plant had significant variations ($P \leq 0.05$) among the tested genotypes. The results for number of branches per plant are shown in (Table 14). Across the locations, the highest number of branches per plant (3.71) was recorded on Kiroba, while genotype NDL 2006/487 showed the lowest number of branches per plant (1.22). Statistically similar treatments on number of branches per plant were observed on NDL 2006/283 (2.48) and NDL 2006/438 (2.51). The overall mean number of branches per plant in all locations was 2.65. Genotypes varied significantly different ($P \leq 0.05$) in stem girth across the sites (Table 14). The highest mean stem girth was recorded on NDL 2006/850 which had 4.87 cm.

However the genotype did not differ significantly from treatment Kiroba (4.85 cm). The lowest stem girth (4.12 cm) was recorded on Albert whereas the overall mean stem girth in the trial was 4.44 cm. There were no significant differences observed among the treatments Naliendele, NDL 2006/438 and NDL 2006/840.

Significant variabilities ($P \leq 0.05$) were observed on the mean number of roots per plant among tested genotypes. Kiroba recorded the highest mean number of roots per plant (7.03) while the lowest mean number of roots per plant (3.33) was recorded on NDL 2006/030 (Table 14). The overall mean number of roots per plant was 4.39. However there were no significant differences among treatments NDL 2006/738, NDL 2006/741 and NDL 2006/840 (Table 14).

The mean root size across locations had significant variations ($P \leq 0.05$) among the genotypes. NDL 2006/738 genotype out-performed the rest of the treatments by recording the highest overall mean root size (0.38 kg). Genotype, NDL 2006/104 had the lowest overall mean root size of (0.19 kg). However this treatment did not differ significantly from the treatment Naliendele (0.20 kg) (Table 14). Treatments Albert, Kiroba and NDL 2006/283 showed no significant variations among them and non-significant difference was observed on the genotypes NDL 2006/438 and NDL 2006/487. The overall mean root size across the locations was 0.25 kg.

Significant variations ($P \leq 0.05$) were observed on the mean plant harvest index of cassava genotypes (Table 14). NDL 2006/738 recorded the highest overall mean harvest index (0.74). The lowest overall mean harvest index (0.60) was observed on

NDL 2006/487. The genotype with the lowest harvest index differed significantly from all treatments in the experiment. However, treatments NDL 2006/030, NDL 2006/104, NDL 2006/283, NDL 2006/438 NDL 2006/840 and NDL 2006/850 were not significantly different. The overall mean harvest index across the locations was 0.68.

4.1.2 Effect of locations on cassava major diseases on the Cassava Genotypes

4.1.2.1 Cassava brown streak disease incidence

There were significant differences ($P \leq 0.05$) among the treatments and locations (Table 15) with respect to major cassava diseases. Only variety Albert and the genotype NDL 2006/283 were affected by CBSD at Naliendele. Albert showed the highest disease incidence of 96.67%, while the lowest disease incidence of 35.03% was recorded on NDL 2006/283. All other treatments had no variations on the incidence of CBSD. Most of the genotypes tested at Mtopwa were affected by cassava brown streak disease (CBSD), only variety Naliendele, genotypes NDL 2006/283 and NDL 2006/487 were not affected by the CBSD. The highest disease incidence (93.33%) at Mtopwa was recorded on Albert while the lowest disease incidence (0.17%) was recorded on the genotype Kiroba. No significant differences were observed among the treatments with exclusion of Albert. At Nachingwea, treatments Albert, Naliendele and NDL 2006/850, were the only ones affected by CBSD. The highest disease incidence (100.00%),) was obtained from Albert, while the least disease incidence (8.33%), was observed on the genotype NDL 2006/850. Albert had the highest disease incidences across the locations; while treatment NDL 2006/487 had no disease incidence at any of the locations. The overall mean cassava

brown streak disease incidences were 10.97%, 11.89% and 11.79% for Naliendele, Mtopwa and Nachingwea respectively.

Table 10: Means for Cassava brown streak disease incidence (%) at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	96.67[a]	93.33[a]	100.00[a]
KIROBA	0.00[c]	0.17[b]	0.00[d]
NALIENDELE	0.00[c]	0.00[b]	33.21[b]
NDL 2006/030	0.00[c]	4.17[b]	0.00[d]
NDL 2006/104	0.00[c]	4.17[b]	0.00[d]
NDL 2006/283	35.03[b]	0.00[b]	0.00[d]
NDL 2006/438	0.00[c]	16.67[b]	0.00[d]
NDL 2006/487	0.00[c]	0.00[b]	0.00[d]
NDL 2006/738	0.00[c]	8.33[b]	0.00[d]
NDL 2006/741	0.00[c]	7.50[b]	0.00[d]
NDL 2006/840	0.00[c]	4.17[b]	0.00[d]
NDL 2006/850	0.00[c]	4.17[b]	8.33[c]
Overall mean	**10.97**	**11.89**	**11.79**
s.e	1.95	2.34	3.99
c.v. (%)	17.80	25.50	23.80

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.2.2 Cassava brown streak disease severity

Table 16 presents the means for cassava brown streak diseases severity at Naliendele, Mtopwa and Nachingwea. Significant variations ($P \leq 0.05$) were observed among genotypes at Naliendele. Only variety Albert and the genotype NDL 2006/283 were significantly affected by CBSD at Naliendele. Albert and NDL 2006/283 showed disease severity of 2.90 and 1.96 respectively. The rest of the treatments revealed no symptoms of the disease (i.e had the lowest disease severity of 1.00) at Naliendele. Significant variations ($P \leq 0.05$) were observed among genotypes at Mtopwa. Only the variety Naliendele, genotypes NDL 2006/283 and

NDL 2006/487 were not affected by the CBSD. Albert had the highest disease severity of 2.97 while NDL 2006/850 gave the lowest disease severity of 1.13. At Nachingwea, the highest disease severity (3.00) was obtained from Albert. Genotype NDL 2006/850 recorded the lowest mean disease severity of 1.13. Also significant variations ($P \leq 0.05$) were observed among genotypes at Nachingwea. The highest mean CBSD severity (3.00) was recorded on Albert, followed by Naliendele (1.84) and NDL 2006/850 (1.13) at Nachingwea, while the rest of the genotypes showed the lowest CBSD severity of 1.00, means with no disease symptoms. Across the locations, Albert had the highest CBSD disease severity scores in all sites. Treatment NDL 2006/487 had the lowest disease severity scores of 1.00 in all sites. However treatments Naliendele, NDL 2006/104, NDL 2006/438, NDL 2006/738, NDL 2006/741 and NDL 2006/840 had disease severity score of 1.00 at Naliendele and Nachingwea, while at Mtopwa they had minor severity scores. Treatment NDL 2006/283 had disease severity of (1.96) only at Naliendele, whereas it was clean (1.00) at Mtopwa and Nachingwea. The overall means for CBSD severity at Naliendele, Mtopwa and Nachingwea were 1.24, 1.30 and 1.25 respectively.

Table 11: Means for Cassava brown streak disease severity at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	2.90[a]	2.97[a]	3.00[a]
KIROBA	1.00[c]	1.01[b]	1.00[d]
NALIENDELE	1.00[c]	1.00[b]	1.84[b]
NDL 2006/030	1.00[c]	1.17[b]	1.00[d]
NDL 2006/104	1.00[c]	1.17[b]	1.00[d]
NDL 2006/283	1.96[b]	1.00[b]	1.00[d]
NDL 2006/438	1.00[c]	1.33[b]	1.00[d]
NDL 2006/487	1.00[c]	1.00[b]	1.00[d]
NDL 2006/738	1.00[c]	1.42[b]	1.00[d]
NDL 2006/741	1.00[c]	1.18[b]	1.00[d]
NDL 2006/840	1.00[c]	1.23[b]	1.00[d]
NDL 2006/850	1.00[c]	1.13[b]	1.13[c]
Overall mean	**1.24**	**1.30**	**1.25**
s.e	0.07	0.33	0.11
c.v. (%)	5.70	19.70	8.50

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.2.3 Cassava mosaic disease incidence

Significant differences ($P \leq 0.05$) were observed within and across locations for CMD incidence (Table 17). At Naliendele, genotype NDL 2006/741 had the highest cassava mosaic disease incidence of 93.00%. Genotype NDL 2006/840 had the lowest CMD incidence of 24.08%. Albert, Kiroba and genotypes, NDL 2006/283, NDL 2006/438, NDL 2006/487, NDL 2006/104 and NDL 2006/850 were free from cassava mosaic disease (CMD). At Mtopwa the highest disease incidence of (87.50%) was recorded on NDL 2006/741 and the lowest disease incidence of 2.08% was recorded on the genotype NDL 2006/438. Cassava mosaic disease incidence at Nachingwea ranged between 1.67 and 95.83%. The highest disease incidence (95.83%) was recorded on NDL 2006/741, followed by Naliendele with disease incidence of 32.52%. The lowest disease incidence (1.67%) was recorded on Albert. Treatment NDL 2006/741 showed the highest CMD disease incidences in

all locations, while the lowest or no CMD disease incidences (1.00) were observed on the treatment Kiroba across the locations. Naliendele variety showed high disease incidences at Naliendele and Nachingwea, on the contrary at Mtopwa it had no disease incidences. The overall means for cassava mosaic disease incidences were 21.53%, 8.34% and 11.60% at Naliendele, Mtopwa and Nachingwea respectively.

Table 12: Means for Cassava mosaic disease incidence (%) at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	0.00^{e}	0.00^{c}	1.67^{c}
KIROBA	0.00^{e}	0.00^{c}	0.00^{c}
NALIENDELE	83.33^{b}	0.00^{c}	32.52^{b}
NDL 2006/030	26.31^{d}	0.00^{c}	0.00^{c}
NDL 2006/104	0.00^{e}	3.00b^{c}	4.56^{c}
NDL 2006/283	0.00^{e}	0.00^{c}	2.38^{c}
NDL 2006/438	0.00^{e}	2.08^{bc}	2.22^{c}
NDL 2006/487	0.00^{e}	0.00^{c}	0.00^{c}
NDL 2006/738	31.66^{c}	0.00^{c}	0.00^{c}
NDL 2006/741	93.00^{a}	87.50^{a}	95.83^{a}
NDL 2006/840	24.08^{d}	0.00^{c}	0.00^{c}
NDL 2006/850	0.00^{e}	7.50	0.00^{c}
Overall mean	**21.53**	**8.34**	**11.60**
s.e	3.43	2.01	2.44
c.v. (%)	15.90	30.10	28.30

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.2.4 Cassava mosaic disease severity

The means for cassava mosaic disease severity varied significantly ($P \leq 0.05$) within and across locations, maximum being 3.17 and minimum 1.00 (Table 18). The cassava mosaic disease severity ranged from 1.00 to 3.17. Naliendele variety gave the highest mean CMD severity (2.67) at Naliendele. Treatments Albert, Kiroba, NDL 2006/030, NDL 2006/104, NDL 2006/283, NDL 2006/438, NDL 2006/487 and NDL

2006/850 showed no CMD disease severity (1.00). At Mtopwa genotype NDL 2006/741 recorded the highest disease severity of 2.87. Albert, Kiroba, Naliendele, NDL 2006/283 and NDL 2006/738 had CMD disease severity of 1.00. At Nachingwea, The highest cassava mosaic disease severity (3.17) was recorded on genotype NDL 2006/741. Treatments Albert, Kiroba, NDL 2006/030, NDL 2006/487, NDL 2006/738, NDL 2006/840 and NDL 2006/850 had the lowest CMD severity of (1.00). Across the locations, genotype NDL 2006/741 had the highest CMD severity values and Kiroba was free from CMD severity. The overall means for CMD severity at Naliendele was 1.41, at Mtopwa (1.19) and at Nachingwea was 1.30.

Table 13: Means for Cassava mosaic disease severity at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	1.00^{d}	1.00^{c}	1.00^{c}
KIROBA	1.00^{d}	1.00^{c}	1.00^{c}
NALIENDELE	2.67^{b}	1.00^{c}	1.80^{b}
NDL 2006/030	1.00^{d}	1.11^{c}	1.00^{c}
NDL 2006/104	1.00^{d}	1.00^{c}	1.04^{c}
NDL 2006/283	1.00^{d}	1.04^{c}	1.11^{c}
NDL 2006/438	1.00^{d}	1.00^{c}	1.28^{c}
NDL 2006/487	1.00^{d}	1.00^{c}	1.00^{c}
NDL 2006/738	1.54^{c}	1.00^{c}	1.00^{c}
NDL 2006/741	2.48^{a}	2.87^{a}	3.17^{a}
NDL 2006/840	1.35^{c}	1.29^{b}	1.00^{c}
NDL 2006/850	1.00^{d}	1.00^{c}	1.00^{c}
Overall mean	**1.41**	**1.19**	**1.30**
s.e	0.18	0.14	0.24
c.v. (%)	13.00	11.70	18.60

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.2.5 Cassava root necrosis

The means for cassava root necrosis varied significantly ($P \leq 0.05$) within and across locations (Table 19). From the results it was observed that, Albert gave the highest mean root necrosis (3.17) at Naliendele, while variation in all locations ranged between 1 and 3.33. Genotype NDL 2006/840 recorded the root necrosis value of 1.73, whereas treatments Kiroba, NDL 2006/104, NDL 2006/030, NDL 2006/283, and NDL 2006/738 showed no signs of root necrosis. At Mtopwa, the highest root necrosis was observed on Albert (3.00) followed by NDL 2006/438 (2.00), NDL 2006/283 (1.50) and Kiroba (1.17). The rest of the treatments were free from root necrosis (i.e. had root necrosis scores of 1.00).

At Nachingwea Albert also recorded the highest mean root necrosis score (3.33), followed by Naliendele (3.00). Other genotypes NDL 2006/283 and NDL 2006/487 showed root necrosis mean score of 1.17. On the other hand variety Kiroba, genotypes NDL 2006/030, NDL 200/741, NDL 2006/104 and NDL 2006/840 showed no symptoms of cassava root necrosis (Table 19). Among the treatments, Albert gave the highest root necrosis scores across the locations. Treatment Naliendele showed same higher root necrosis score at Naliendele and Nachingwea (3.00), while it had no root necrosis at Mtopwa site (1.00). Nachingwea site, had the highest root necrosis overall mean of 1.60, Mtopwa (1.31) and Naliendele recorded (1.51).

Table 14: Means for Cassava root necrosis at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	3.17[a]	3.00[a]	3.33[a]
KIROBA	1.00[d]	1.17[cd]	1.00[c]
NALIENDELE	3.00[a]	1.00[d]	3.00[a]
NDL 2006/030	1.00[d]	1.00[d]	1.00[c]
NDL 2006/104	1.00[d]	1.00[d]	1.00[c]
NDL 2006/283	1.00[d]	1.50[c]	1.17[bc]
NDL 2006/438	1.95[c]	2.00[b]	1.50[bc]
NDL 2006/487	1.00[d]	1.00[d]	1.17[bc]
NDL 2006/738	1.00[d]	1.00[d]	1.67[b]
NDL 2006/741	2.33[b]	1.00[d]	1.00[c]
NDL 2006/840	1.73[c]	1.00[d]	1.00[c]
NDL 2006/850	1.00[d]	1.00[d]	1.33[bc]
Overall mean	**1.60**	**1.31**	**1.51**
s.e	0.22	0.36	0.50
c.v. (%)	13.50	27.80	29.00

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.2.6 CBSD, CMD and root necrosis on the cassava genotypes under combined analysis

The results for CBSD, CMD and root necrosis across the locations are presented in (Table 20). Significant variabilities ($P \leq 0.05$) were observed on the means for cassava brown streak disease incidence among genotypes. Across the locations variety Albert recorded the highest mean cassava brown streak disease incidence (96.67%) followed by Naliendele (11.68%). The overall mean disease incidence was 11.55%. Genotype NDL 2006/487 showed least disease symptoms across the locations, whereas the lowest CBSD incidence (0.06%) was recorded on NDL 2006/840. With exception of treatments Albert, Kiroba and Naliendele the rest of the treatments had no significant differences among them.

Significant variations ($P \leq 0.05$) were observed on the mean cassava brown streak disease severity of cassava genotypes. Variety Albert recorded the highest mean cassava brown streak disease severity (2.99) followed by Naliendele (1.28), while NDL 2006/487 did not show any disease symptoms. The overall mean disease severity was 1.26 (Table 19). There were no significant differences observed among treatments Kiroba, NDL 2006/030, NDL 2006/104, NDL 2006/438, NDL 2006/487, NDL 2006/741, NDL 2006/840 and NDL 2006/850.

The results on CMD incidences revealed presence of significant variations ($P \leq 0.05$) among the genotypes. The highest mean values for CMD incidence (92.11%) was observed on the genotype NDL 2006/741 followed by Naliendele (38.62%), which was significantly different from the rest of the treatments. Kiroba showed no any CMD incidence. However the treatment (Kiroba) was not significantly different from treatments Albert, NDL 2006/104, NDL 2006/283, NDL 2006/438, NDL 2006/487 and NDL 2006/ 850. The overall mean disease incidence was 13.82.

There were significant variations ($P \leq 0.05$) on mean cassava mosaic disease severity among genotypes across the locations. The highest mean value for CMD severity (2.97) was observed on the genotype NDL 2006/741 followed by variety Naliendele which had CMD severity of 1.82. The overall mean disease severity was 1.3. Kiroba was not affected by CMD but revealed no significant differences with treatments Albert, NDL 2006/030, NDL, 2006/840 and NDL 2006/850.

The means for cassava root necrosis varied significantly ($P \leq 0.05$) across the locations (Table 20). Albert showed the highest root necrosis score of 3.17 and had significant differences with the rest of the treatments. Naliendele recorded 2.33 root necrosis. On the other hand, genotypes NDL 2006/840 and NDL 2006/850 had no any symptoms of root necrosis i.e. had a root necrosis score of 1.00. Although the two genotypes had no root necrosis symptoms, they were not significantly different from the treatments Kiroba, NDL 2006/487, NDL 2006/438, NDL 2006/741 and NDL 2006/738. The overall mean root necrosis in all sites was 1.47.

Treatment Albert had consistently highest CDSDI (96.67%), CDSDS (2.96) and root necrosis (3.17) across the locations, while it had lowest scores for CMDI (0.56) and CMDS (1.01). On the other hand, treatment NDL 2006/487 showed consistently lowest mean value sores of the diseases, CDSDI (1.39), CDSDS (1.00) and root necrosis (1.11), while with regard to CMD, NDL 2006/487 had not showed disease incidence (0.00) and severity(1.00) (Table 20).

Table 20: Means for CBSD, CMD and root necrosis in cassava genotypes under combined analysis

Genotype	CBSDI	CBSDS	CMDI	CMDS	Root necrosis
ALBERT	96.67[a]	2.96[a]	0.56[d]	1.01[d]	3.17[a]
KIROBA	1.53[b]	1.00[c]	0.00[d]	1.00[d]	1.54[c]
NALIENDELE	11.68[b]	1.28[b]	38.62[b]	1.82[b]	2.33[b]
NDL 2006/030	5.56[c]	1.06[c]	8.77[c]	1.17[c]	1.50[cd]
NDL 2006/104	4.17[c]	.1.06[c]	2.52[d]	1.19[cd]	1.44[cde]
NDL 2006/283	2.78[c]	1.32[b]	0.79[d]	1.12[cd]	1.24[def]
NDL 2006/438	2.50[c]	1.11[c]	1.43[d]	1.10[cd]	1.22[ef]
NDL 2006/487	1.39[c]	1.00[c]	0.00[d]	1.00[cd]	1.11[f]
NDL 2006/738	1.39[c]	1.14[c]	10.55[c]	1.05[cd]	1.06[f]
NDL 2006/741	1.39[c]	1.06[c]	92.11[a]	2.97[a]	1.06[f]
NDL 2006/840	0.06[c]	1.08[c]	8.03[c]	1.00[d]	1.00[f]
NDL 2006/850	0.00[c]	1.08[c]	2.50[d]	1.00[d]	1.00[f]
Overall mean	**11.55**	**1.26**	**13.82**	**1.30**	**1.47**
s.e	8.34	0.26	4.35	0.19	0.38
c.v.(%)	28.80	16.20	31.40	14.80	25.70

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Key: CBSDI% = Percentage cassava brown streak disease incidence, CBSDS = Cassava brown streak disease severity, CMDI% = Percentage cassava mosaic disease incidence and CMDS = Cassava mosaic disease severity.

4.1.3 Nutritional characteristics of the studied cassava genotypes

4.1.3.1 Dry matter percentage

Significant variations ($P \leq 0.05$) in dry matter percentage were observed among genotypes within and across locations. At Naliendele, Mtopwa and Nachingwea NDL 2006/487 recorded the highest mean values of percentage dry matter of 39.16%, 40.42% and 41.78% respectively. At Naliendele, treatments Albert (35.43%), Kiroba (37.15%), NDL 2006/283 (37.17%), NDL 2006/738 (36.68%) and NDL 2006/840 (36.56%) showed no significant differences for this parameter. Also NDL 2006/104 (38.63%) and NDL 2006/741 (39.12%) were statistically similar. At

Mtopwa, neither Albert, Kiroba, Naliendele and NDL 2006/104; nor NDL 2006/283 and NDL 2006/738 showed significant differences. However at Nachingwea, treatment NDL 2006/487 was not significantly different from treatments NDL 2006/738 and NDL 2006/840 (Table 21). NDL 2006/850 had the lowest mean dry matter percentage of 33.54% recorded at Naliendele. The lowest dry matter percentage (33.68%) at Mtopwa was recorded from NDL 2006/840, which was significantly different from the rest of treatments. At Nachingwea site, the lowest percentage dry matter (35.32%) was observed on the genotype NDL 2006/850 which was not significantly different from treatments Albert, NDL 2006/030 and NDL 2006/738. Overall mean dry matter percentage of cassava genotypes across the locations were 33.75%, 21.21% and 35.32% for Naliendele, Mtopwa and Nachingwea respectively. Nachingwea had the highest overall dry matter percentage (41.78%).

Across the locations, NDL 2006/487 showed superiority over the rest of the treatments in all sites; at Naliendele (39.16%), Mtopwa (40.62%) and Nachingwea (41.78%). On the other hand, treatment NDL 2006/850, showed the least dry matter percentage at Naliendele (33.54%) and Nachingwea (35.52), while at Mtopwa it was the last but one (36.21%) (Table 21).

Table 15: Means for percentage dry matter (%) in Cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	35.43^{dcba}	39.23^{cba}	35.76^{b}
KIROBA	37.15^{dcba}	38.91^{cba}	38.23^{ab}
NALIENDELE	35.29^{dcb}	38.97^{cba}	37.92^{ab}
NDL 2006/030	34.64^{dc}	36.29^{dcb}	35.77^{b}
NDL 2006/104	38.63^{ba}	38.36^{cba}	39.05^{ab}
NDL 2006/283	37.17^{dcba}	37.33^{dcba}	40.95^{a}
NDL 2006/438	37.61^{cba}	38.42^{cba}	38.53^{ab}
NDL 2006/487	39.16^{a}	40.62^{a}	41.78^{a}
NDL 2006/738	36.68^{dcba}	36.90^{dcba}	36.02^{b}
NDL 2006/741	39.12^{ba}	40.11^{ba}	40.41^{a}
NDL 2006/840	36.56^{dcba}	33.68^{d}	38.95^{ab}
NDL 2006/850	33.54^{d}	36.21^{dc}	35.32^{b}
Overall mean	**36.75**	**37.92**	**38.22**
s.e	2.84	2.85	3.00
c.v. (%)	7.70	7.50	7.90

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.3.2 Starch percentage

The results for cassava starch percentage varied significantly ($P \leq 0.05$) among the genotypes within and across the locations (Table 22). The highest starch percentage content was 23.99% and the lowest was 18.14%. At Naliendele, genotype NDL 2006/487 recorded the highest starch percentage (22.13%), whereas the lowest starch percentage (18.14%) was recorded on NDL 2006/850. However, the treatment NDL 2006/487 did not vary significantly from NDL 2006/741 (22.10%). Treatments Kiroba, NDL 2006/104, NDL 2006/283 and NDL 2006/438 showed no significant differences with values 20.70%, 21.09%, 20.72 and 21.03% respectively. In the same site, Naliendele (19.38%) and NDL 2006/030 (18.92%) were not significantly different. The highest starch percentage content (23.17%) at Mtopwa was obtained from the genotype NDL 2006/283. Treatments Albert, Kiroba, NDL /2006104 and

NDL 2006/438 were statistically the same with starch percentage means of 21.83%, 21.56%, 21.56% and 21.61% respectively. Similarly Naliendele (22.83%) and NDL 2006/741 (22.80%) were not significantly different. Genotype NDL 2006/850 gave the lowest starch percentage values of 18.14%, 20.04% and 19.41% at Naliendele, Mtopwa and Nachingwea respectively. At Nachingwea, genotype NDL 2006/487 recorded the highest starch percentage (23.99%), however this treatment did not significantly differ from genotypes NDL 2006/283 (23.40%) and NDL 2006/741 (23.02%). The lowest starch percentage mean (19.41%) was recorded from NDL 2006/850, which was statistically similar to treatments Albert (19.72%), NDL 2006/030 (19.73%) and NDL 2006/738 (19.91%). The highest overall starch percentage mean (21.47%) was recorded at Nachingwea, while the lowest overall starch percentage mean (20.36%) was observed at Naliendele site. On the other hand, Mtopwa site recorded an overall starch percentage mean of 21.21%. Across the locations, treatment NDL 2006/487 had consistently highest starch percentage means. NDL 2006/850 recorded consistently lowest starch percentage content at Naliendele (18.14%) and Nachingwea (19.41%), while at Mtopwa it was in the range of medium values (20.04%). Treatment NDL 2006/840 had the lowest starch percentage content (18.24%) at Mtopwa and had medium starch percentage content at Naliendele (20.28%) and Nachingwea (21.68%) sites (Table 22).

Table 16: Means for percentage starch in Cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	19.49^{cb}	21.83^{cba}	19.72^{b}
KIROBA	20.70^{ba}	21.56^{cba}	21.47^{ba}
NALIENDELE	19.38^{cb}	22.83^{ba}	21.26^{ba}
NDL 2006/030	18.92^{cb}	19.47^{dc}	19.73^{b}
NDL 2006/104	21.09^{ba}	21.56^{cba}	22.06^{ba}
NDL 2006/283	20.72^{ba}	20.84^{dcba}	23.40^{a}
NDL 2006/438	21.03^{ba}	21.61^{cba}	21.68^{ba}
NDL 2006/487	22.13^{a}	23.17^{a}	23.99^{a}
NDL 2006/738	20.37^{cba}	20.53^{dcba}	19.91^{b}
NDL 2006/741	22.10^{a}	22.80^{ba}	23.02^{a}
NDL 2006/840	20.28^{cba}	18.24^{d}	21.98^{ba}
NDL 2006/850	18.14^{c}	20.04^{dcba}	19.41^{b}
Overall mean	**20.36**	**21.21**	**21.47**
s.e	1.91	2.07	2.13
c.v. (%)	9.40	9.80	9.90

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.3.3 Protein percentage

Table 23 presents the means for protein percentage in the studied cassava genotypes at Naliendele, Mtopwa and Nachingwea. Significant variations were observed among the genotypes in all locations ranged from 0.07 to 1.63. At Naliendele, genotypes NDL 2006/487, NDL 2006/738 and NDL 2006/840 recorded the same (1.13%) as the highest protein percentage content. The lowest protein percentage mean was recorded on the genotype NDL 2006/741 (0.07%), however this treatment did not vary significantly with the treatment NDL 2006/030 (0.10%). At Mtopwa, the highest protein percentage content (1.63 %) was recorded from NDL 2006/487, and showed non-significant difference with the treatment NDL 2006/850 (1.49), while the lowest protein percentage content (0.13%) was obtained from the genotype NDL 2006/030. The treatment (NDL 2006/030) was statistically similar to treatment

NDL 2006/741 (0.09 %). The highest mean protein percentage content at Nachingwea was observed on the treatment NDL 2006/487 (1.41 %), while the lowest protein percentage content (0.08 %) was recorded from NDL 2006/741. The treatments which showed non-significant differences in protein percentage content were Albert and NDL 2006/030; NDL 2006/438, NDL 2006/738 and NDL 2006/850; and NDL 2006/283 and NDL 2006/840. The overall mean protein percentage values were 0.67, 0.876 and 0.78 at Naliendele, Mtopwa and Nachingwea respectively (Table 23). Across the locations, NDL 2006/487 gave the highest protein percentage content in all sites. The lowest protein percentage contents were observed on the treatment NDL 2006/741, at Naliendele (0.07 %), at Mtopwa (0.09 %) and at Nachingwea (0.08 %).

Table 23: Means for protein percentage in Cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	0.14^{fe}	0.62^{d}	0.17^{fe}
KIROBA	0.21^{ed}	0.20^{fg}	0.27^{ed}
NALIENDELE	0.30^{d}	0.32^{f}	0.32^{d}
NDL 2006/030	0.10^{f}	0.13^{g}	0.13^{fe}
NDL 2006/104	0.80^{c}	0.91^{c}	0.92^{c}
NDL 2006/283	1.01^{b}	1.10^{e}	1.26^{ba}
NDL 2006/438	0.98^{b}	1.23^{e}	1.17^{b}
NDL 2006/487	1.13^{a}	1.63^{a}	1.41^{a}
NDL 2006/738	1.13^{a}	1.47^{ba}	1.18^{b}
NDL 2006/741	0.07^{f}	0.09^{g}	0.08^{f}
NDL 2006/840	1.13^{a}	1.29^{eb}	1.23^{ba}
NDL 2006/850	1.05^{ba}	1.49^{a}	1.17^{b}
Overall mean	**0.67**	**0.88**	**0.78**
s.e	0.08	0.16	0.16
c.v. (%)	12.30	17.70	21.20

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

4.1.3.4 Cassava root taste

Significant variations ($P \leq 0.05$) in cassava root taste were observed among genotypes within and across all locations (Table 24). The cassava root taste values ranged between 1 and 2. Genotype NDL 2006/487 was found to have the highest mean root taste value of 2.0 at Naliendele indicating that it is a bitter variety. However this genotype was not significantly different from treatments NDL 2006/738 and NDL 2006/850. On the other hand, genotypes Albert, NDL 2006/283 and NDL 2006/741 had the lowest value of root taste being 1.00. Treatments Kiroba and NDL 2006/438; Naliendele and NDL 2006/840; and NDL 2006/030 and NDL 2006/104 showed no significant variations. At Mtopwa the highest mean root taste (2.00) was recorded on NDL 2006/487 and NDL 2006/850 indicated better genotypes while the lowest value (1.00) was recorded from Albert, Kiroba, NDL 2006/030, NDL 2006/104 and NDL 2006/741 indicating the sweet genotypes. Genotypes NDL 2006/438 and NDL 2006/840 recorded equal value for root taste being 1.83. At Nachingwea the highest mean root taste (2.00) was recorded on NDL 2006/283, NDL 2006/738, and NDL 2006/840, while the lowest value (1.17) was recorded on Kiroba, Naliendele, NDL 2006/030 NDL 2006/438 and NDL 2006/74. Similarly, there were no significant differences observed among treatments Albert, NDL 2006/030, NDL 2006/487 and NDL 2006/850 (Table 24). The overall mean for cassava root taste at Naliendele, Mtopwa and Nachingwea were 1.44, 1.43 and 1.56 respectively.

Treatment NDL 2006/487 recorded the highest mean root taste score (2.00) at Naliendele and Mtopwa, while at Nachingwea it was in the medium range (1.67).

Albert and NDL 2006/741 had root taste of 1.00 at Naliendele and Mtopwa, whereas at Nachingwea, Albert tasted moderately (1.67). On the other hand NDL 2006/741 had a relatively sweet taste (1.17).

Table 17: Means for root taste in Cassava genotypes at Naliendele, Mtopwa and Nachingwea locations

Genotype	Naliendele	Mtopwa	Nachingwea
ALBERT	1.00^{c}	1.00^{d}	1.67^{ab}
KIROBA	1.50^{cba}	1.00^{d}	1.17^{b}
NALIENDELE	1.67^{ba}	1.50^{bc}	1.17^{b}
NDL 2006/030	1.167^{cb}	1.00^{d}	1.17^{b}
NDL 2006/104	1.17^{cb}	1.00^{d}	1.67^{ab}
NDL 2006/283	1.00^{c}	1.67^{cba}	2.00^{a}
NDL 2006/438	1.50^{cba}	1.83^{ab}	1.17^{b}
NDL 2006/487	2.00^{a}	2.00^{a}	1.67^{ab}
NDL 2006/738	1.83^{a}	1.33^{cd}	2.00^{a}
NDL 2006/741	1.00^{c}	1.00^{d}	1.17^{b}
NDL 2006/840	1.67^{ba}	1.83^{ab}	2.00^{a}
NDL 2006/850	1.83^{a}	2.00^{a}	1.83^{ab}
Overall mean	**1.44**	**1.43**	**1.56**
s.e	0.40	0.32	0.29
c.v. (%)	27.80	22.20	18.60

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Key: Scale used in root taste: 1 – 2; where 1 = sweet and 2 = bitter.

4.1.3.5 Combined analysis for nutritional characteristics of the studied cassava genotypes

Table 25 presents the results for the studied cassava nutritional characteristics in a combined analysis. Significant variations ($P \leq 0.05$) were observed among the genotypes for all the studied cassava nutritional characteristics. The highest overall mean dry matter percentage (40.52%) was recorded on the genotype NDL 2006/487, while the lowest overall mean dry matter percentage was recorded on the genotype

NDL 2006/850 (35.02%). Both treatments (with highest and lowest values) had significant differences from the rest of the genotypes. Albert and NDL 2006/738 were not statistically different in their dry matter percentage means. The overall dry matter percentage mean across the locations was 37.63%. Treatment NDL 2006/487 with starch percentage content (23.10%) outperformed the rest of the treatments, while the lowest starch percentage content (19.20%) was observed on the genotype NDL 2006/850, and was significantly different from all other treatments (Table 25). Treatments Kiroba, Naliendele, NDL 2006/104, NDL 2006/283 and NDL 2006/438 showed non-significant differences. Similarly, treatments Albert with dry matter (20.35%) and NDL 2006/840 (20.17 %) were not significantly different however, the overall mean percentage starch was 21.01%.

Significant variations ($P \leq 0.05$) were observed on the protein percentage mean of cassava genotypes (Table 25). Genotype NDL 2006/487 recorded the highest protein percentage mean (1.39%), which was significantly different from the rest of the treatments. The lowest value for protein percentage mean (0.08%) across the locations was obtained from the genotype NDL 2006/741, which was statistically similar to the treatment NDL 2006/030 (0.12 %). Albert (0.30%), Kiroba (0.24%) and Naliendele (0.31%) revealed existence of non – significant differences among their protein percentage means. Treatments across the locations gave an overall protein percentage mean of 0.77%.

There were significant differences ($P \leq 0.05$) on cassava root taste among the studied genotypes. Genotypes NDL 2006/487 and NDL 2006/850 were superior

over the other genotypes with root taste mean of 1.89 (Table 25). However these two treatments were not significantly different from the treatment NDL 2006/840 (1.83). The lowest root taste value (1.06) was recorded on genotype NDL 2006/741. This treatment was not significantly different from the genotype NDL 2006/030 which had a root taste value of 1.11. Across the locations treatment NDL 2006/487 had the highest values for the cassava nutritional variables studied. The lowest dry matter percentage mean of 35.02% and the lowest starch percentage mean (19.20%) were both recorded from NDL 2006/850, however this treatment had the highest value of root taste (1.89 same as NDL 2006/487) and a medium protein percentage mean of 1.23% (Table 25).

Table 18: Combined means of genotypes for cassava nutritional variables at the three sites

Genotype	Dry matter%	Starch%	Protein%	Root taste
ALBERT	36.81^{cdef}	20.35^{cd}	0.30^{e}	1.22^{ef}
KIROBA	38.10^{bcd}	21.25^{bc}	0.24^{e}	1.22^{def}
NALIENDELE	37.39^{cde}	21.16^{bc}	0.31^{e}	1.44^{cde}
NDL 2006/030	35.57^{ef}	19.37^{d}	0.12^{f}	1.11^{f}
NDL 2006/104	38.68^{abc}	21.57^{bc}	0.88^{d}	1.28^{def}
NDL 2006/283	38.49^{abcd}	21.65^{bc}	1.12^{c}	1.56^{bc}
NDL 2006/438	38.19^{bcd}	21.44^{bc}	1.13^{c}	1.50^{bcd}
NDL 2006/487	40.52^{a}	23.10^{a}	1.39^{a}	1.89^{a}
NDL 2006/738	36.53^{cdef}	20.27^{cd}	1.26^{b}	1.72^{ab}
NDL 2006/741	39.88^{ab}	22.64^{ab}	0.08^{f}	1.06^{f}
NDL 2006/840	36.39^{def}	20.17^{cd}	1.23^{b}	1.83^{a}
NDL 2006/850	35.02^{f}	19.20^{d}	1.23^{b}	1.89^{a}
Overall mean	**37.63**	**21.01**	**0.77**	**1.48**
s.e	2.91	2.05	0.13	0.38
c.v. (%)	7.70	9.80	17.20	25.70

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Key: Scale used for root taste: 1 – 2; where 1 = sweet and 2 = bitter.

The results in (Table 25 and Figure 3) show that, there is a negative relationship between protein percentage content and cassava root sweetness. It was observed that, bitter varieties/genotypes had higher protein percentage as compared to sweet ones. Genotypes NDL 2006/487 and NDL 200/850 had same highest value of root taste (1.89), indicating that they are the most bitter genotypes. The highest protein percentage content value was obtained on NDL 2006/487 (1.39) (Table 25). Genotypes NDL 2006/738 and NDL 2006/840, which had also high values of root taste, had higher protein percentage content almost similar to NDL 2006/850 (Figure 2). On the contrary, genotype NDL 2006/741 which had the lowest value of root taste, recorded the lowest protein percentage content. NDL 2006/030 had smaller root taste value (1.11), which was not significantly different from NDL 2006/741 (1.06), which also recorded the least protein percentage content (0.12%) after NDL 2006/741 (0.08) (Table 25). Varieties Albert, Kiroba and Naliendele which showed relatively low root taste values of 1.22, 1.22 and 1.44 also revealed relatively low protein percentage contents of 0.30%, 0.24% and 0.31% respectively.

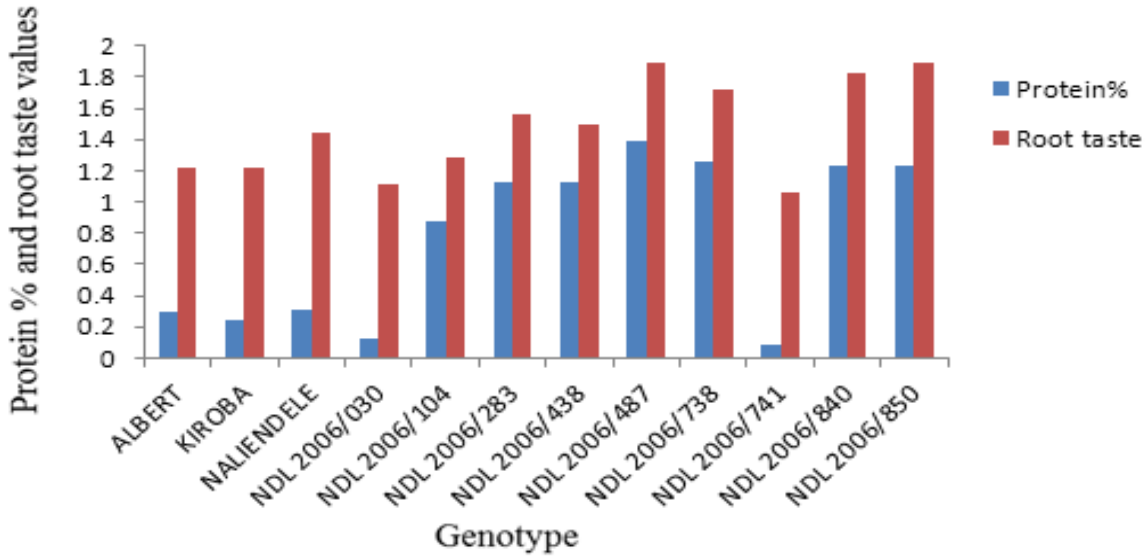


Figure 3: Relationship between cassava protein percentage content and cassava root taste

4.2 Farmers Involvement

4.2.1 Farmers' criteria for selecting cassava genotypes/varieties

Farmers were involved in the harvesting exercise, where they were given a chance of selecting cassava genotypes/varieties according to their fore discussed criteria. Twelve farmers were involved at Naliendele site whereas fifteen farmers were involved at both Mtopwa and Nachingwea sites. The criteria used by farmers in selecting cassava genotypes/varieties were almost the same at all the trial sites. Table 26 shows the criteria used by farmers and their respective ranking in order of importance. At Naliendele site, yield ranked the first while root hardness ranked fourth in order of importance. At Mtopwa yield ranked the third whereas diseases ranked first and root hardness was fourth. On the other hand, at Nachingwea yield ranked first while root taste rank was fourth in order of importance.

Table 19: Farmers criteria for selecting cassava varieties/genotypes at the trial sites

S/no.	Naliendele		Mtopwa		Nachingwea	
	Criteria	**Rank**	**Criteria**	**Rank**	**Criteria**	**Rank**
1	Yield	1	Disease	1	Yield	1
2	Disease	2	Taste	2	Disease	2
3	Taste	3	Yield	3	Hardness	3
4	Hardness	4	Hardness	4	Taste	4
5	Cookability	5	Vegetables	5	Drought	5
6	Planting material	6	Maturity	6	Planting material	6
7	Storability	7	Architecture	7	Cookability	7
8	Architecture	8	Planting material	8	Vegetables	8
9	Fibreousness	9	Cookability	9	Architecture	9
10	Flesh colour	10	Storability	10	Storability	10

From (Table 26), at Naliendele flesh colour as a criterion of selecting genotypes was of the least importance. Root fibrousness ranked second from the last followed by

plant architecture. However, at Mtopwa the least criterion (storability) in order of importance differed from the least one at Naliendele site. Storability ranked the last, followed by cookability, whereas planting material was the third from the bottom. At Nachingwea, storability ranked the last in order of importance, followed by plant architecture and vegetables production (cassava plant leaves).

The above mentioned criteria are used by farmers depending on the prevailing need(s) at a given period of time. However, according to them, they mostly use the top four ranked criteria. Among the criteria identified therefore, only the top four were used in assessing the cassava genotypes in the field. The criteria used are root yield, cassava diseases, cassava root taste and cassava root hardness.

4.2.2 Farmers' genotypes selection: based on root yield, disease, root taste and root hardness

Results for farmers' genotypes selection based on yield, disease, root hardness and root taste are shown in (Table 27). The highest yielder selected by farmers at Naliendele site was NDL 438 (32 points), followed by NDL 2006/487(31 points) and NDL 2006/283 (29 points), while Albert, NDL 200/741 and variety Naliendele were found to be inferior with score points of 14, 18 and 19 respectively. At Mtopwa the highest yielders were NDL 2006/487 (27 points) followed by NDL 2006/438 (25 points) and variety Naliendele (24 points). The least yielders were found to be NDL 2006/840, NDL 2006/741 and NDL 2006/283 with score points of 15, 16 and 17 respectively. At Nachingwea site, Kiroba, Naliendele variety and NDL 2006/487 were observed to have higher score points of 33, 31 and 30 respectively. The lower

score points were found on NDL 2006/741(17 points), NDL 2006/840 (19 points) and Albert (20 points).

At Naliendele no or minor signs of diseases were observed on genotypes NDL 2006/487 (27 points), NDL 2006/738 (26 points) and NDL 2006/840 (24 points), while most disease symptoms were observed on Albert (12 points), variety Naliendele (13 points) and NDL 2006/283 (14 points) (Table 27). Genotypes NDL 200/438, NDL 2006/850 and NDL 2006/030 were assigned the highest score points of 34, 33 and 31 respectively at Mtopwa, while genotype NDL 2006/741 was found to have clear disease symptoms, Albert (15 points), followed by variety Naliendele (17). At Nachingwea, NDL 2006/487(38 points), NDL 2006/738 (35 points) and Kiroba (34 points) (were observed as most tolerant genotypes), while the most susceptible ones were NDL 2006/741 (16 points), Albert (17 points) and Naliendele (17 points).

Root hardness as assessed by farmers at Naliendele revealed that, NDL 2006/738, had the lowest water content with (21) score points, followed by NDL 2006/487 (19 points) and Naliendele with score points of (18), while Albert, NDL 2006/741 and NDL 2006/840 scored the lowest root hardness with score points of 10, 11 and 12 respectively. At Mtopwa, variety Naliendele had the highest root hardness (34 points) followed by Kiroba (33 points) and NDL 2006/850 (32 points). Genotypes NDL 2006/283, NDL 2006/840 and NDL 2006/438 exhibited the lowest root hardness with score points of 15, 20 and 21 respectively. At Nachingwea, variety Kiroba showed the highest root hardness (35points) followed by Naliemdele

(33points) and NDL 2006/850 (32points). Genotypes NDL 2006/487, NDL 2006/840 and NDL 2006/438 gave the lowest root hardness with score points of 17, 20 and 22 respectively (Table 27).

Variety Albert was the sweetest at Naliendele site (32 points), followed by NDL 2006/438 (28 points) and NDL 2006/104 (26points) as indicated in Table 26, while the most bitter genotypes at Naliendele were NDL 2006/487 (12 points), NDL 2006/850 (14 points) and NDL 2006/738 (14points). At Mtopwa, the sweetest genotypes observed after Naliendele (38 points) were Albert (32 points), NDL 2006/104 (22 points) and NDL 2006/438 (22 points). On the other hand, most bitter genotypes, comparatively, at Mtopwa were NDL 2006/487, NDL 2006/850 and NDL 2006/738 with score points of 15, 16 and 17 respectively. At Nachingwea site, Albert was the sweetest with (27 points), while the least genotypes for sweetness were NDL 2006/487, NDL 2006/850 and NDL 2006/738 with score points of 14, 16 and 17 respectively.

Table 20: Farmers' genotypes selection based on yield, diseases, hardness and taste

	Naliendele								Mtopwa								Nachingwea							
Geno	Y	**Rank**	D	**Rank**	H	**Rank**	T	**Rank**	Y	**Rank**	D	**Rank**	H	**Rank**	T	**Rank**	Y	**Rank**	D	**Rank**	H	**Rank**	T	**Rank**
1	14	**12**	12	**12**	10	**12**	32	**1**	18	**9**	15	**11.5**	31	**4**	32	**2**	20	**10**	17	**11.5**	28	**6**	27	**1**
2	21	**9**	22	**4**	15	**7**	21	**6**	19	**7.5**	30	**4.5**	33	**2**	31	**3**	33	**1**	34	**3**	35	**1**	23	**5**
3	19	**10**	13	**11**	18	**3**	19	**8**	24	**3**	17	**10**	34	**1**	38	**1**	31	**2**	17	**11.5**	33	**2**	25	**4**
4	24	**8**	21	**5**	16	**6**	20	**7**	20	**6**	31	**3**	30	**5.5**	25	**7**	23	**7**	20	**9**	31	**4**	26	**2.5**
5	28	**5**	18	**7**	17	**4.5**	26	**3**	21	**5**	30	**4.5**	29	**7**	28	**5**	21	**9**	25	**7**	27	**7**	21	**6.5**
6	29	**3.5**	14	**10**	17	**4.5**	24	**4**	17	**10**	19	**9**	15	**12**	29	**4**	22	**8**	23	**8**	22	**9.5**	26	**2.5**
7	32	**1**	20	**6**	14	**8.5**	28	**2**	25	**2**	34	**1**	21	**10**	17	**10**	25	**6**	33	**4**	22	**9.5**	21	**6.5**
8	31	**2**	27	**1**	19	**2**	12	**12**	27	**1**	29	**6**	30	**5.5**	15	**12**	30	**3**	38	**1**	17	**12**	14	**12**
9	25	**6.5**	26	**2**	21	**1**	14	**10.5**	19	**7.5**	28	**7**	24	**9**	22	**8**	27	**4**	35	**2**	26	**8**	17	**10**
10	18	**11**	16	**8**	11	**11**	23	**5**	16	**11**	15	**11.5**	25	**8**	27	**6**	17	**12**	19	**10**	30	**5**	20	**8**
11	25	**6.5**	24	**3**	12	**10**	15	**9**	15	**12**	25	**8**	20	**11**	20	**9**	19	**11**	31	**5**	20	**11**	19	**9**
12	29	**3.5**	15	**9**	14	**8.5**	14	**10.5**	22	**4**	33	**2**	32	**3**	16	**11**	26	**5**	29	**6**	32	**3**	16	**11**

N.B: 1. The higher the number of the variables, the better the genotype
2. Yield and disease assessed by visual observation
3. Root taste and hardness scored by chew taste

KEY:
Y = Yield, D = Disease, H = Hardness and T = Taste
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

4.2.3 Farmers' pair wise matrix selection of studied genotypes based on yield

4.2.3.1 Naliendele site

At Naliendele site, twelve farmers participated in the assessment of genotypes based on yield; the results are presented in (Table 28). Genotype NDL 2006/438 was the highest yielder (11 score) followed by NDL 2006/850 and NDL 2006/283, but Albert was the least yielder (0 score) among the varieties and genotypes assessed.

Table 21: Pair wise ranking based on yield for Naliendele site

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	Score	Rank
ALBERT													0	12
KIROBA	2												4	8
NALIENDELE	3	2											3	9
NDL 2006/030	4	4	4										5	7
NDL 2006/104	5	5	5	5									7	5.5
NDL 2006/283	6	6	6	6	6								9	2.5
NDL 2006/438	7	7	7	7	7	7							11	1
NDL 2006/487	8	8	8	8	8	6	7						8	4
NDL 2006/738	9	9	9	9	5	6	7	8					7	5.5
NDL 2006/741	10	2	3	4	5	6	7	8	9				2	10
NDL 2006/840	11	2	3	4	5	6	7	8	9	10			1	11
NDL 2006/850	12	12	12	12	12	12	7	12	9	12	12		9	2.5

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

4.2.3.2 Mtopwa site

At Mtopwa and Nachingwea sites, fifteen farmers participated for the comparison of genotypes based on yield (Table 29). Based on yield at Mtopwa, genotype NDL 2006/438 (11 scores) was superior followed by NDL 2006/487 (10 score) and Kiroba (9 scores), while genotype NDL 2006/741 was the least (0 score).

Table 22: Pair wise ranking based on yield for Mtopwa site

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	Score	Rank
ALBERT													2	10
KIROBA	2												9	3
NALIENDELE	3	2											8	4
NDL 2006/030	4	2	3										3	9
NDL 2006/104	5	2	3	4									4	8
NDL 2006/283	6	2	3	6	6								7	5
NDL 2006/438	7	7	7	7	7	7							11	1
NDL 2006/487	8	8	8	8	8	8	7						5	2
NDL 2006/738	9	2	3	9	9	6	7	8					10	7
NDL 2006/741	1	2	3	4	5	6	7	8	9				0	12
NDL 2006/840	1	2	3	4	5	6	7	8	9	11			1	11
NDL 2006/850	12	2	3	12	12	6	7	8	12	12	12		6	6

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

4.2.3.3 Nachingwea site

At Nachingwea site, fifteen farmers participated for the comparison of genotypes based on yield. Based on yield at Nachingwea, Kiroba with 11 score, outperformed other genotypes followed by NDL 2006/487 (10 score) and Naliendele (9 score). Genotype NDL 2006/741 was the least genotype in terms of yield, it scored (0) (Table 30).

Table 23: Pair wise ranking for Nachingwea site.

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	Score	Rank
ALBERT													0	12
KIROBA	2												11	1
NALIENDELE	3	2											9	3
NDL 2006/030	4	2	3										5	7
NDL 2006/104	5	2	3	4									3	9
NDL 2006/283	6	2	3	6	6								7	5
NDL 2006/438	7	2	3	7	7	7							8	4
NDL 2006/487	8	2	8	8	8	8	8						10	2
NDL 2006/738	9	2	3	4	9	6	7	8					4	8
NDL 2006/741	10	2	3	4	5	6	7	8	9				1	11
NDL 2006/840	11	2	3	4	5	6	7	8	9	11			2	10
NDL 2006/850	12	2	3	12	12	6	7	8	12	12	12		6	6

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

4.3 Effect of Weeding Regimes on the Performance of Root Yield and Yield Components

Weeding once and weeding twice were used as factors that determine the root yield and or yield components of cassava. At Naliendele dry matter percentage was the only variable that showed significant differences at ($P \leq 0.05$) (Apppendix 1). The weeding regime (weeding twice) gave an overall mean of 36.94% dry matter, whereas weeding regime (weeding once) gave the overall mean of 36.56% dry matter (Table 31). The grand mean for Naliendele site was 36.75% dry matter. At Mtopwa, percentage dry matter, plant height and root yield differed significantly at ($P \leq 0.05$), ($P \leq 0.001$) and ($P \leq 0.05$) respectively (Appendix 3). Weeding twice at Mtopwa gave 37.92% dry matter, 100.38 cm plant height and root yield of 8.54 t ha-1, while where genotypes were weeded once, dry matter percentage was 38.32%, plant height was 93.36cm and root yield of 7.65t ha^{-1} (Table 30). The grand means at Mtopwa were 37.92 for dry matter percentage, 96.89 cm for plant height and 8.10 t ha^{-1} for root yield.

Plant height and root yield showed significant differences, at ($P \leq 0.01$) and ($P \leq 0.001$) respectively, at Nachingwea (Appendix 5). Weeding twice gave an overall mean of 162.5 cm for plant height (Table 30), while the overall mean for weeding once was 153.5 cm. The grand mean for plant height was 158.0 cm. Genotypes that were weeded twice at Nachingwea gave 18.91 t ha^{-1} of root yield outweighing those weeded once which gave 17.45 t ha^{-1}. The grand mean for root yield was 18.18 t ha^{-1}.

Table 24: Means of variables that showed significant differences with differing weeding regimes at the trial sites

Location	Variable	Means		
		Grand Mean	Weeding twice	Weeding once
Naliendele	% Dry Matter	36.75	36.94	36.56
	SD	2.907	2.734	3.066
	S.e	0.343	0.456	0.511
	c.v. (%)	7.911	7.367	8.426
Mtopwa	% Dry Matter	37.92	37.52	38.32
	SD	3.158	3.731	2.483
	S.e	0.372	0.622	0.414
	c.v. (%)	8.328	9.908	6.503
	Plant Height	96.89	100.38	93.36
	SD	15.34	14.172	15.475
	S.e	1.808	2.465	2.579
	c.v. (%)	15.833	14.802	16.491
	Root Yield	8.1	8.54	7.65
	SD	3.2	3.313	2.281
	S.e	0.377	0.552	0.38
	c.v. (%)	39.514	34.537	34.542
Nachingwea	Plant Height	158	162.5	153.5
	SD	20	21.391	18.788
	S.e	2.438	3.565	3.131
	c.v. (%)	13.091	13.096	12.301
	Root Yield	18.18	18.91	17.45
	SD	10.158	8.547	11.299
	S.e	1.197	1.424	1.883
	c.v. (%)	25	23	32

4.4 Genetic Correlations between Cassava Yield Components at Naliendele, Mtopwa and Nachingwea

The correlation coefficients between cassava root yield components are presented in (Table 32). At Naliendele, very highly significant positive correlations were observed between root yield and plant height (r =0.5738***); stem girth (r = 0.6902***) and roots per plant (r = 0.6237***). The results also revealed highly positive significant correlation, between plant height and stem girth (r = 0.5815***) and between stem girth and roots per plant (r = 0.6458***). A high and positive significant correlation was observed between plant height and root size (r = 0.3594**).

On the other hand, at Mtopwa only roots per plant showed a highly positive correlation (r = 0.422***) with root yield. Plant height showed negative significant correlation with root dry matter r = (- 0.2395*) and was positively and significantly correlated with roots per plant (r = 0.2395*). Another negative significant correlation (r = -0.0583*) was observed between root size and stem girth (Table 32).

As indicated in Table 32, at Nachingwea, positive highly significant correlations were observed between root yield and stem girth (r = 0.3848***), root yield and roots per plant (r = 0.7474***) and between branches per plant and roots per plant (r = 3852***). There was a negative highly significant correlation (r = -0.3813***) between plant height and branches per plant. Also, positive and highly significant correlations were observed between root size and stem girth (0.3516***); stem girth and roots per plant (0.3429**) and between root size and harvest index

(r = 0.3152**). Moreover positive significant correlations were observed between root yield and plant height (r = 0.2537*) and between stem girth and harvest index (r = 0.3006*).

Consistently positive correlation between roots and yield was observed at all locations, Naliendele (0.6902***), Mtopwa (0.422**) and Nachingwea (0.7474***). Number of branches per plant was negatively correlated with yield at Naliendele (-0.2656) and Mtopwa (-0.0151). At Naliendele and Mtopwa, harvest index had negative correlation with yield (-0.0585 and -0.1583 respectively).

Table 32: Genetic correlation between cassava traits at Naliendele, Mtopwa and Nachingwea

Location		PLHT	BRPL	RTSZ	SGTH	DM	RTPL	HI	YLD
Naliendele	PHT	1.0000	-0.168	0.3594 **	0.5815 ***	0.0091	0.4507 ***	-0.1912	0.5738***
	BPL		1.0000	-0.0224	-0.1047	-0.0612	-0.0086	0.1155	-0.2656
	RSZ			1.0000	0.1709	-0.1117	0.0407	-0.1187	0.2682
	SGH				1.0000	-0.0605	0.6458 ***	-0.0095	0.6902***
	DM					1.0000	0.0256	-0.0174	0.1378
	RPL						1.0000	0.0132	0.6237***
	HI							1.0000	-0.0585
	RYLD								1.0000
Mtopwa	PHT	1.0000	-0.1918	-0.0215	0.1342	-0.2395	0.2395*	0.1688	0.0200
	BPL		1.0000	-0.0706	-0.2853	0.0212	0.1525	0.2155	-0.0151
	RSZ			1.0000	-0.0583*	0.1184	-0.1581	-0.1930	0.0691
	SGH				1.0000	-0.2206	-0.1014	-0.1876	-0.0532
	DM					1.0000	-0.0091	0.0694	0.1687
	RPL						1.0000	0.1448	0.422***
	HI							1.0000	-0.1583
	RYLD								1.0000
Nachingwea	PHT	1.0000	-0.3813 ***	0.0298	0.1999	-0.1124	-0.1845	-0.0408	0.2537*
	BPL		1.0000	-0.1129	-0.0318	-0.0670	0.3852 ***	0.1112	0.1897
	RSZ			1.0000	0.3516 **	-0.0584	0.0772	0.3152 **	0.1896
	SGH				1.0000	-0.0293	0.3429 **	0.3006 *	0.3848***
	DM					1.0000	0.0232	-0.1698	-0.0777
	RPL						1.0000	0.2189	0.7474***
	HI							1.0000	0.2683
	RYLD								1.0000

PHT = Plant height, BPL = Branches per plant, RSZ = Root size, SGH = Stem girth, DM = Dry matter, RPL = Roots per plant, HI = Harvest index, YLD =Yield

Based on combined analysis, highly significant positive correlations existed between variables (Table 33). Positively and highly significant correlations were observed between yield and plant height (r =0.5436***), stem girth (r = 0.3874***) and harvest index (r = 0.3025***). Also positive highly significant correlations were observed between plant height and stem girth (r = 0.5900 ***), roots per plant (r = 0.4463***) and harvest index (r = 0.3005***). Other positive correlations were observed between branches per plant and roots per plant (0.2441***), stem girth and roots per plant (r = 5046***) and between roots per plant and harvest index (r = 2647***). Another positive and highly significant correlation was observed between branches per plant and harvest index (r = 0.1762**). On the other hand a negative significant correlation (-0.15480*) was observed between stem girth and dry matter. There was no any variable that gave negative correlation with in the combined analysis.

Table 25: Genetic correlations between variables influencing yield in cassava as observed in a combined analysis

	PHT	BPL	RSZ	SGH	DM	RPL	HI	YLD
PHT	1.0000	-0.02570	0.10970	0.5900 ***	-0.05730	0.4463 ***	0.3005 ***	0.5436***
BPL		1.0000	-0.06060	0.03350	-0.04100	0.2441 ***	0.1762 **	0.0947
RSZ			1.0000	-0.00620	0.07370	0.0033	0.08330	0.1969
SGH				1.0000	-0.15480 *	0.5046 ***	0.09280	0.3874***
DM					1.0000	-0.00100	0.02690	0.0472
RPL						1.0000	0.2647 ***	0.7053***
HI							1.0000	0.3025***
YLD								1.000

Significance Levels	0.05	0.01	0.005	0.001
If correlation (r = >)	0.1335	0.1749	0.1903	0.2224

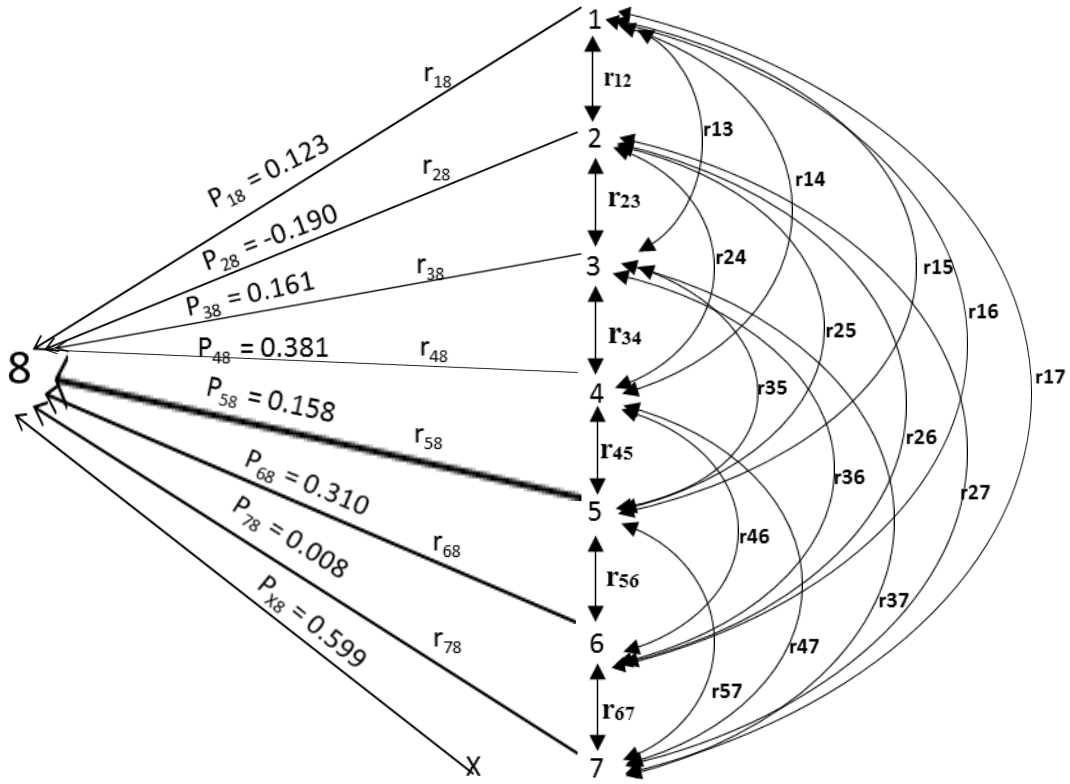
Where; PHT = Plant height, BPL = Branches per plant, RSZ = Root size, SGH = Stem girth, DM = Dry matter, RPL = Roots per plant, HI = Harvest index, YLD = Root yield

4.5 Path Analysis

4.5.1 Associations among cassava root yield influencing components at Naliendele, Mtopwa and Nachingwea

4.5.1.1 Associations at Naliendele

Results of associations among factors that influenced cassava root yield at Naliendele as described using path coefficient analysis are shown in Figure 4 and Table 34. The results indicated significant variability in causal relationships among cassava root yield influencing components. The highest genetic correlation on cassava root yield was found on plant height (r = 0.451), but the highest direct effect on cassava root yield was observed on stem girth (0.381) with genetic correlation of 0.309. The lowest genetic correlation (– 0.076) was found between branches per plant and yield. The highest indirect effect on yield (0.246) was found on roots per plant via stem girth, while the lowest was found on most variables via harvest index. These included plant height via harvest index (- 0.002), branches per plant via harvest index (0.001), root size via harvest index (- 0.001), stem girth via harvest index (0.000) indirect effect of dry matter via harvest index (0.000) and indirect effect of roots per plant via harvest index (0.000).



Where:

1 = plant height 2 = branches per plant 3 = root size 4 = stem girth
5 = dry matter 6 = roots per plant 7 = harvest index 8 = yield

X = residual P_{18} = effect of plant height P_{28} = effect of branches per plant
P_{38} = effect of root size P_{48} = effect of stem girth P_{58} = effect of dry matter
P_{68} = effects of roots per plant P_{78} = effect of harvest index P_{x8} = residual effect

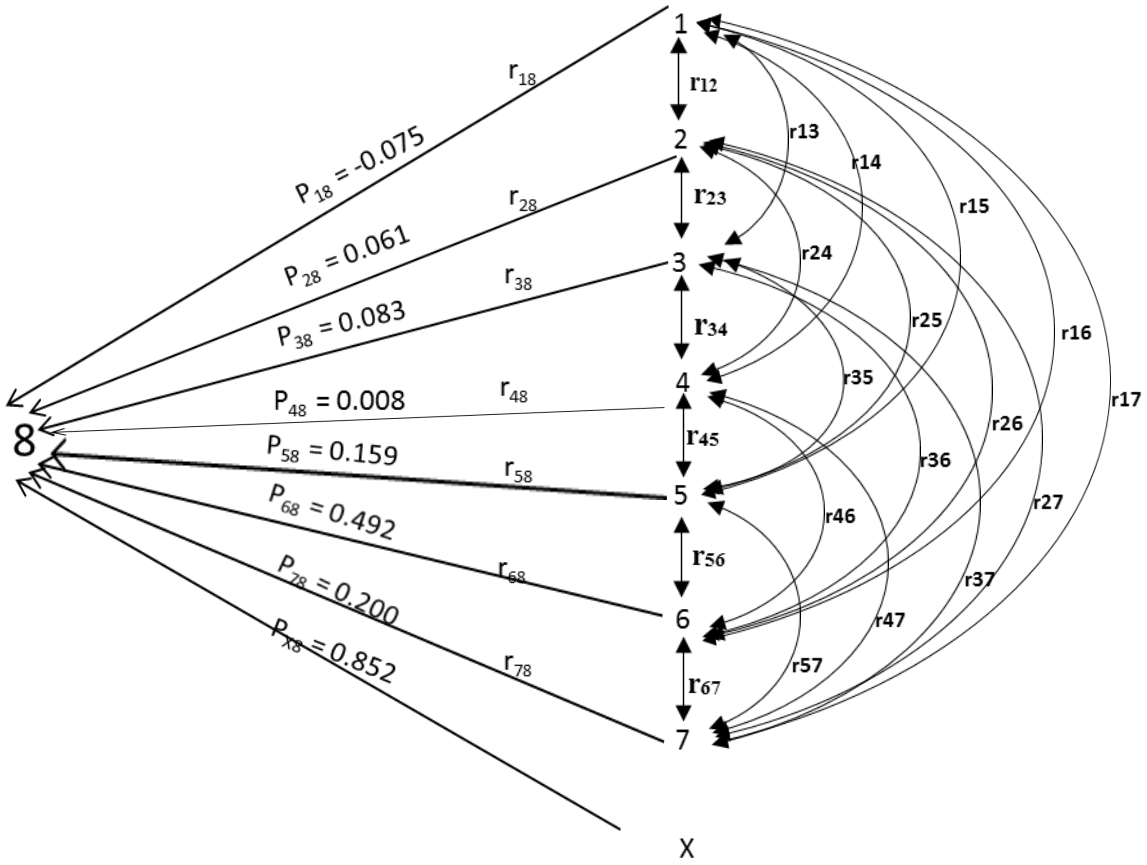
r_{18} = 0.451	r_{12} = -0.168	r_{24} = -0.105	r_{37} = -0.119
r_{28} = -0.076	r_{13} = 0.359	r_{25} = -0.0161	r_{45} = -0.061
r_{38} = 0.108	r_{14} = 0.581	r_{26} = -0.009	r_{46} = 0.646
r_{48} = 0.309	r_{15} = 0.009	r_{27} = 0.116	r_{47} = -0.01
r_{58} = -0.021	r_{16} = 0.451	r_{34} = 0.171	r_{56} = 0.026
r_{68} = 0.314	r_{17} = -0.191	r_{35} = -0.112	r_{57} = -0.017
r_{78} = -0.023	r_{23} = 0.022	r_{36} = 0.041	r_{67} = 0.013

P = Direct effect r = Correlation coefficient

Figure 4: Path diagram showing relationships between yield and yield components of cassava at Naliendele.

4.5.1.2 Associations at Mtopwa

Generally, at Mtopwa, most of genetic correlations, direct effects and indirect effects of different traits were low. The leading genetic correlation of cassava root yield components was positive and found on plant height where r = 0.054 (Figure5 and Table 34). The direct effect of roots per plant gave the greatest magnitude (0.492). The other positive effect was observed on direct effect of dry matter (0.159) and root size (0.083). Indirect effects of roots per plant were weak and negative with exception of indirect effect via stem girth (0.001), which was weak but positive.



Where:

1 = plant height	2 = branches per plant	3 = root size	4 = stem girth
5 = dry matter	6 = roots per plant	7 = harvest index	8 = yield

X = residual P_{18} = effect of plant height P_{28} = effect of branches per plant
P_{38} = effect of root size P_{48} = effect of stem girth P_{58} = effect of dry matter
P_{68} = effects of roots per plant P_{78} = effect of harvest index P_{x8} = residual effect

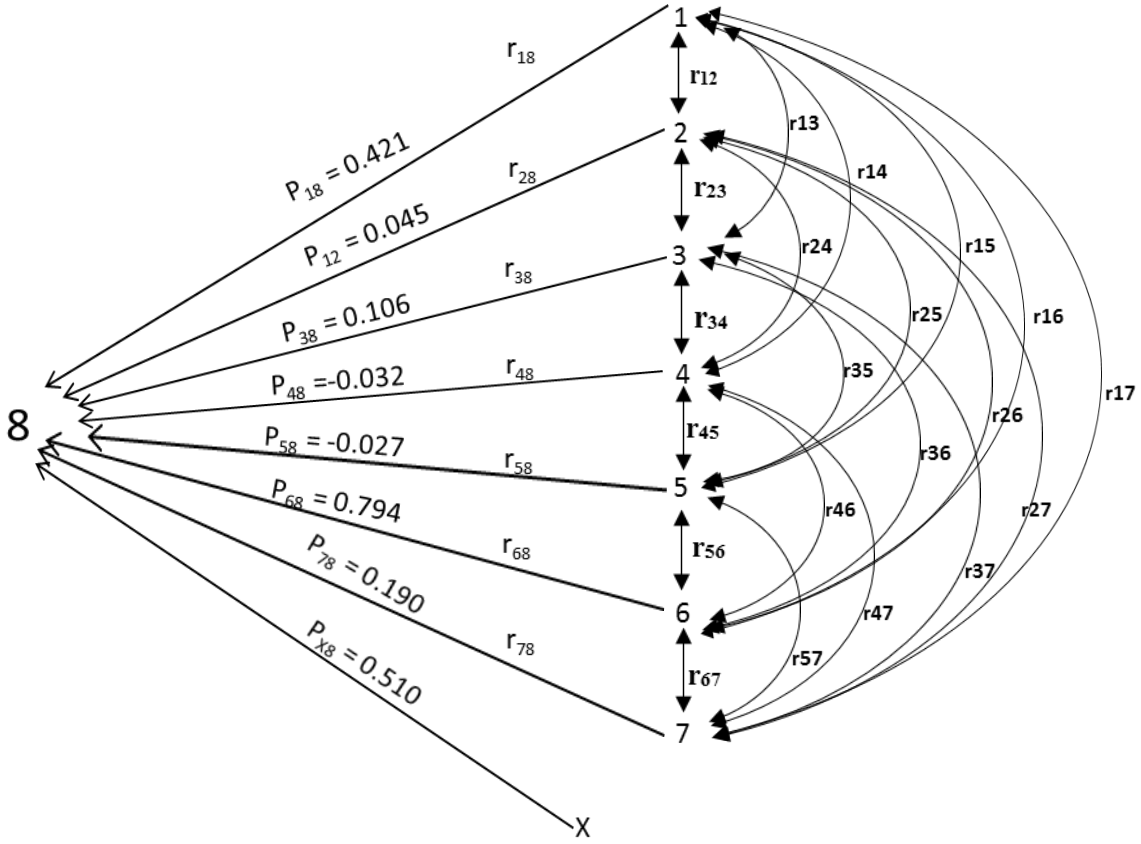
r_{18} = 0.054	r_{12} = -0.192	r_{24} = -0.285	r_{37} = -0.193
r_{28} = 0.046	r_{13} = -0.022	r_{25} = 0.021	r_{45} = -0.221
r_{38} = -0.014	r_{14} = 0.134	r_{26} = 0.153	r_{46} = -0.101
r_{48} = -0.045	r_{15} = -0.24	r_{27} = 0.216	r_{47} = -0.188
r_{58} = 0.010	r_{16} = 0.239	r_{34} = -0.058	r_{56} = -0.009
r_{68} = -0.070	r_{17} = 0.169	r_{35} = 0.118	r_{57} = 0.069
r_{78} = -0.020	r_{23} = -0.071	r_{36} = -0.158	r_{67} = 0.145

P = Direct effect r = Correlation coefficient

Figure 5: Path diagram showing relationships between yield and yield components of cassava at Mtopwa.

4.5.1.3 Asociations at Nachingwea

The path analysis coefficients for Nachingwea are presented in (Figure 6 and Table 34). The highest genetic correlation (0.417) with yield was observed on stem girth, while the highest direct effect on cassava root yield was recorded on roots per plant (0.794), followed by direct effect of plant height (0.421). Stem girth had a direct effect of 0.032, while the weakest indirect effect (-0.027) was given by dry matter. Indirect effects of roots per plant via plant height, branches per plant, root size, stem girth, dry matter and harvest index were - 0.078, 0.017, 0.008, -0.011 and 0.017 respectively.



Where:

1 = plant heigh 2 = branches per plant 3 = root size 4 = stem girth
5 = dry matter 6 = roots per plant 7 = harvest index 8 = yield

X = residual P_{18} = effect of plant height P_{28} = effect of branches per plant
P_{38} = effect of root size P_{48} = effect of stem girth P_{58} = effect of dry matter
P_{68} = effects of roots per plant P_{78} = effect of harvest index P_{x8} = residual effect

$r_{18} = -0.167$	$r_{12} = -0.381$	$r_{24} = -0.032$	$r_{37} = 0.315$
$r_{28} = 0.045$	$r_{13} = 0.030$	$r_{25} = -0.067$	$r_{45} = -0.290$
$r_{38} = -0.158$	$r_{14} = 0.2$	$r_{26} = 0.385$	$r_{46} = 0.343$
$r_{48} = 0.417$	$r_{15} = -0.112$	$r_{27} = 0.111$	$r_{47} = 0.301$
$r_{58} = -0.050$	$r_{16} = -0.185$	$r_{34} = 0.352$	$r_{56} = 0.023$
$r_{68} = -0.047$	$r_{17} = -0.041$	$r_{35} = -0.058$	$r_{57} = -0.17$
$r_{78} = 0.019$	$r_{23} = -0.113$	$r_{36} = 0.077$	$r_{67} = 0.219$
$r_{x8} = 0.510$	P = Direct effect	r = Correlation coefficient	

Figure 6: Path diagram showing relationships between yield and yield components of cassava at Nachingwea

Table 26: Path coefficients for cassava root yield influencing components at Naliendele, Mtopwa and Nachingwea

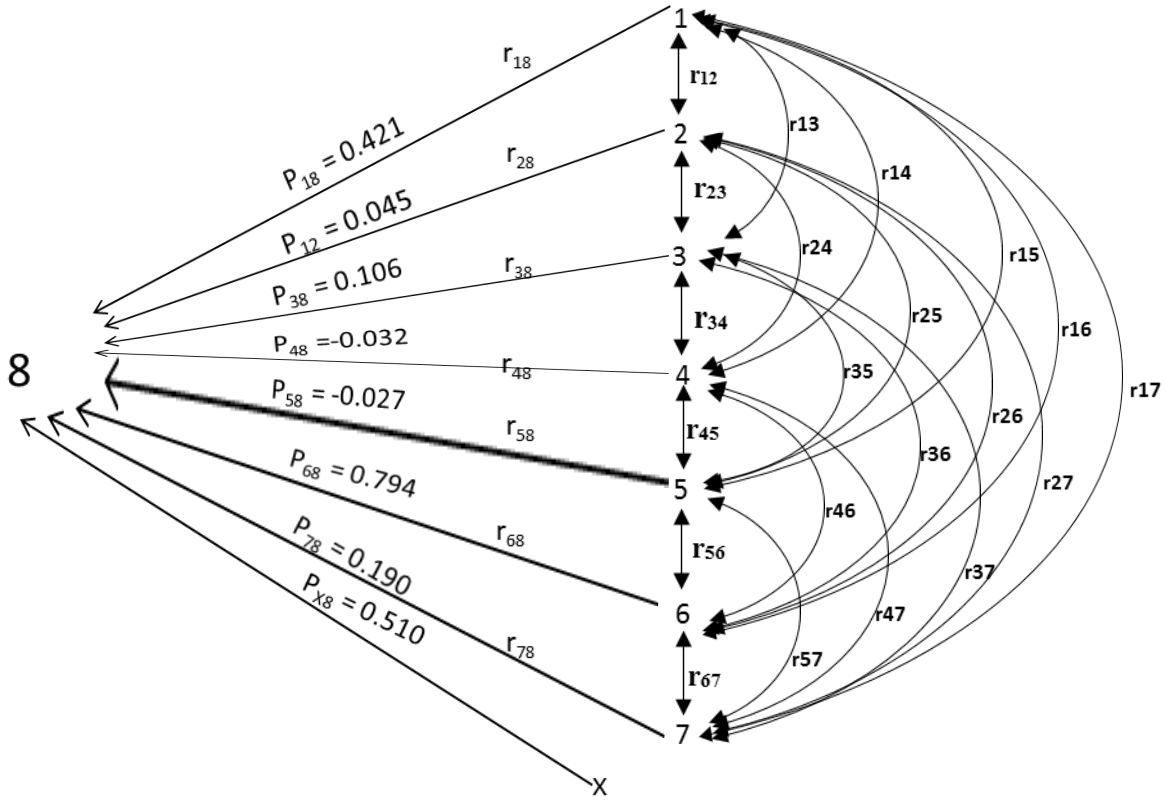
	Effect	Nali	Mtop	Nachi
1	**Plant height on root yield, r_{18}**	**0.573**	**-0.020**	**0.254**
	Direct effect of plant height, P_{18}	0.123	-0.075	0.421
	Indirect effect via branches per plant, $r_{12}P_{28}$	0.032	0.012	-0.017
	Indirect effect via root size, $r_{13}P_{38}$	0.058	-0.002	0.003
	Indirect effect via stem girth, $r_{14}P_{48}$	0.221	-0.001	-0.006
	Indirect effect via dry matter, $r_{15}P_{58}$	0.001	-0.038	0.003
	Indirect effect via roots per plant, $r_{16}P_{68}$	0.14	0.118	-0.147
	Indirect effect via harvest index, $r_{17}P_{78}$	-0.002	-0.034	-0.003
	Total	**0.573**	**-0.020**	**0.254**
2	**Branches per plant on root yield, r_{28}**	**-0.266**	**-0.016**	**0.191**
	Direct effect of branches per plant, P_{28}	-0.19	-0.061	0.045
	Indirect effect via plant height, $r_{21}P_{18}$	-0.021	0.014	-0.16
	Indirect effect via root size, $r_{23}P_{38}$	-0.004	-0.006	-0.012
	Indirect effect via stem girth, $r_{24}P_{48}$	-0.04	0.002	0.001
	Indirect effect via dry matter, $r_{25}P_{58}$	-0.01	0.003	0.002
	Indirect effect via roots per plant, $r_{26}P_{68}$	-0.003	0.075	0.306
	Indirect effect via harvest index, $r_{27}P_{78}$	0.001	-0.043	0.009
	Total	**-0.266**	**0.016**	**0.191**
3	**Root size, r_{38}**	**0.268**	**0.069**	**-0.051**
	Direct effect of root size, P_{38}	0.161	0.083	0.106
	Indirect effect via plant height, $r_{31}P_{18}$	0.044	0.002	-0.16
	Indirect effect via branches per plant, $r_{32}P_{28}$	0.004	0.004	-0.005
	Indirect effect via stem girth, $r_{34}P_{48}$	0.065	0.00	-0.011
	Indirect effect via dry matter, $r_{35}P_{58}$	-0.018	0.019	0.002
	Indirect effect via roots per plant, $r_{36}P_{68}$	0.013	-0.078	0.015
	Indirect effect via harvest index, $r_{37}P_{78}$	-0.001	0.039	0.002
	Total	**0.268**	**0.069**	**-0.051**
4	**Stem girth, r_{48}**	**0.690**	**-0.053**	**0.384**
	Direct effect of stem girth, P_{48}	0.381	-0.008	-0.032
	Indirect effect via plant height, $r_{41}P_{18}$	0.071	-0.01	0.084
	Indirect effect via branches per plant, $r_{42}P_{28}$	0.02	0.017	-0.001
	Indirect effect via root size, $r_{43}P_{38}$	0.028	-0.005	0.037
	Indirect effect via dry matter, $r_{45}P_{58}$	-0.01	-0.035	0.001
	Indirect effect via roots per plant, r_{46P68}	0.2	-0.05	0.272
	Indirect effect via harvest index, $r_{47}P_{78}$	0.00	0.038	0.023
	Total	**0.690**	**-0.053**	**0.384**
5	**Dry matter, r_{58}**	**0.138**	**0.170**	**-0.077**
	Direct effect of dry matter, P_{58}	0.158	0.159	-0.027
	Indirect effect via plant height, $r_{51}P_{18}$	0.001	0.018	-0.047
	Indirect effect via branches per plant, $r_{52}P_{28}$	0.012	-0.001	-0.003
	Indirect effect via root size, $r_{53}P_{38}$	-0.018	0.01	-0.006

	Indirect effect via stem girth, $r_{54}P_{48}$	-0.023	0.002	0.001
	Indirect effect via roots per plant, $r_{56}P_{58}$	0.008	-0.004	0.018
	Indirect effect via harvest index, $r_{57}P_{78}$	0.00	-0.014	-0.013
	Total	**0.138**	**0.170**	**-0.077**
6	**Roots per plant, r_{68}**	**0.624**	**0.423**	**0.746**
	Direct effect of roots per plot, P_{68}	0.31	0.492	0.794
	Indirect effect via plant height, $r_{61}P_{18}$	0.055	-0.018	-0.078
	Indirect effect via branches per plant, $r_{62}P_{28}$	0.002	-0.009	0.017
	Indirect effect via root size, $r_{63}P_{38}$	0.007	-0.013	0.008
	Indirect effect via stem girth, $r_{64}P_{48}$	0.246	0.001	-0.011
	Indirect effect via dry matter, $r_{65}P_{58}$	0.004	-0.001	-0.001
	Indirect effect via harvest index,$r_{67}P_{78}$	0.00	-0.029	0.017
	Total	**0.624**	**0.423**	**0.746**
7	**Harvest index, r78**	**-0.015**	**-0.180**	**0.268**
	Direct effect of harvest index, P_{78}	0.008	-0.2	0.078
	Indirect effect via plant height, $r_{71}P_{18}$	-0.023	-0.013	-0.017
	Indirect effect via branches per plant, $r_{72}P_{28}$	0.022	-0.013	0.005
	Indirect effect via root size, $r_{73}P_{38}$	-0.019	-0.016	0.033
	Indirect effect via stem girth, $r_{74}P_{48}$	-0.004	0.002	-0.01
	Indirect effect via dry matter, $r_{75}p_{58}$	-0.003	-0.011	0.005
	Indirect effect via roots per plant, $r_{76}P_{68}$	0.004	0.071	0.174
	Total	**-0.015**	**-0.180**	**0.268**

Key: Nali = Naliendele, Mtop = Mtopwa and Nachi = Nachingwea

4.5.2 Associations among cassava root yield influencing components in combined analysis

In the combined analysis, roots per plant revealed to have the highest influence on cassava root yield (Figure 7 and Table 35) Roots per plant had the highest direct effect of 0.619 on cassava root yield. The stem girth had the highest correlation coefficient (r = 0.481) with root yield. Roots per plant had both positive and negative indirect effects on other variables. Positive indirect effects were found via plant height (0.129) and harvest index (0.014), while negative indirect effects were found via branches per plant (- 0.011) and stem girth (- 0.047). On the other hand, no influence was revealed in indirect effect of roots per plant via root size (0.000) and dry matter (0.000).



Where:
1 = plant height 2 = branches per plant 3 = root size 4 = stem girth
5 = dry matter 6 = roots per plant 7 = harvest index 8 = yield

X = residual P_{18} = effect of plant height P_{28} = effect of branches per plant
P_{38} = effect of root size P_{48} = effect of stem girth P_{58} = effect of dry matter
P_{68} = effects of roots per plant P_{78} = effect of harvest index P_{x8} = residual effect

r_{18} = 0.253	r_{12} = -0.026	r_{24} = 0.033	r_{37} = 0.083
r_{28} = 0.139	r_{13} = 0.11	r_{25} = -0.041	r_{45} = -0.155
r_{38} = 0.044	r_{14} = 0.59	r_{26} = 0.244	r_{46} = 0.505
r_{48} = 0.481	r_{15} = -0.057	r_{27} = 0.176	r_{47} = 0.093
r_{58} = 0.012	r_{16} = 0.446	r_{34} = -0.006	r_{56} = -0.001
r_{68} = 0.086	r_{17} = 0.301	r_{35} = 0.074	r_{57} = 0.027
r_{78} = 0.248	r_{23} = -0.061	r_{36} = 0.003	r_{67} = 0.265

P = Direct effect r = Correlation coefficient

Figure 7: Path diagram showing relationships between yield and yield components of cassava under combined analysis.

Table 27: Path coefficients for combined analysis of cassava root yield influencing variables

	Effect	Coefficients
1	**Plant height on root yield, r_{18}**	**0.543**
	Direct effect of plant height, P_{18}	0.290
	Indirect effect via branches per plant, $r_{12}P_{28}$	0.001
	Indirect effect via root size, $r_{13}P_{38}$	0.017
	Indirect effect via stem girth, $r_{14}P_{48}$	-0.055
	Indirect effect via dry matter, $r_{15}P_{58}$	-0.002
	Indirect effect via roots per plant, $r_{16}P_{68}$	0.276
	Indirect effect via harvest index, $r_{17}P_{78}$	0.016
	Total	**0.543**
2	**Branches per plant on root yield, r_{28}**	**0.095**
	Direct effect of branches per plant, P_{28}	-0.045
	Indirect effect via plant height, $r_{21}P_{18}$	-0.008
	Indirect effect via root size, $r_{23}P_{38}$	-0.009
	Indirect effect via stem girth, $r_{24}P_{48}$	-0.003
	Indirect effect via dry matter, $r_{25}P_{58}$	-0.001
	Indirect effect via roots per plant, $r_{26}P_{68}$	0.151
	Indirect effect via harvest index, $r_{27}P_{78}$	0.010
	Total	**0.095**
3	**Root size, r_{38}**	**0.198**
	Direct effect of root size, P_{38}	0.153
	Indirect effect via plant height, $r_{31}P_{18}$	0.032
	Indirect effect via branches per plant, $r_{32}P_{28}$	0.003
	Indirect effect via stem girth, $r_{34}P_{48}$	0.001
	Indirect effect via dry matter, $r_{35}P_{58}$	0.003
	Indirect effect via roots per plant, $r_{36}P_{68}$	0.002
	Indirect effect via harvest index, $r_{37}P_{78}$	0.004
	Total	**0.198**
4	**Stem girth, r_{48}**	**0.388**
	Direct effect of stem girth, P_{48}	-0.093
	Indirect effect via plant height, $r_{41}P_{18}$	0.171
	Indirect effect via branches per plant, $r_{42}P_{28}$	-0.001
	Indirect effect via root size, $r_{43}P_{38}$	-0.001
	Indirect effect via dry matter, $r_{45}P_{58}$	-0.006

	Indirect effect via roots per plant, r_{46P68}	0.313
	Indirect effect via harvest index, $r_{47}P_{78}$	0.005
	Total	**0.388**
5	**Dry matter, r_{58}**	**0.046**
	Direct effect of dry matter, P_{58}	0.036
	Indirect effect via plant height, $r_{51}P_{18}$	-0.017
	Indirect effect via branches per plant, $r_{52}P_{28}$	0.002
	Indirect effect via root size, $r_{53}P_{38}$	0.011
	Indirect effect via stem girth, $r_{54}P_{48}$	0.014
	Indirect effect via roots per plant, $r_{56}P_{68}$	-0.001
	Indirect effect via harvest index, $r_{57}P_{78}$	0.001
	Total	**0.046**
6	**Roots per plant, r_{68}**	**0.704**
	Direct effect of roots per plot, P_{68}	0.619
	Indirect effect via plant height, $r_{61}P_{18}$	0.129
	Indirect effect via branches per plant, $r_{62}P_{28}$	-0.011
	Indirect effect via root size, $r_{63}P_{38}$	0.000
	Indirect effect via stem girth, $r_{64}P_{48}$	-0.047
	Indirect effect via dry matter, $r_{65}P_{58}$	0.000
	Indirect effect via harvest index,$r_{67}P_{78}$	0.014
	Total	**0.704**
7	**Harvest index, r_{78}**	**0.302**
	Direct effect of harvest index, P_{78}	0.054
	Indirect effect via plant height, $r_{71}P_{18}$	0.087
	Indirect effect via branches per plant, $r_{72}P_{28}$	-0.008
	Indirect effect via root size, $r_{73}P_{38}$	0.013
	Indirect effect via stem girth, $r_{74}P_{48}$	-0.009
	Indirect effect via dry matter, $r_{75}p_{58}$	0.001
	Indirect effect via roots per plant, $r_{76}P_{68}$	0.164
	Total	**0.302**

4.6 Estimates of Variance Components (σ^2), Coefficient of Variation (%GCV and %PCV), Broad Sense Heritability (h^2_b) and Expected Genetic Advance (%EGA) for the Variables under Study

The magnitude of phenotypic coefficient of variation was consistently higher than the genotypic coefficient of variation in all the characters studied (Table 36). The phenotypic coefficient of variation ranged between 8.48% to 63.55%, cassava root yield showing the highest magnitude followed by root size (61.91%), while the lowest (8.48%) was observed on dry matter. Also the highest genotypic coefficient of variation (45.02%) was observed on root yield and the lowest (1.94%) in dry matter. Broad sense heritability (h^2_b) and genetic gain for different characters varied considerably. Heritability obtained over locations ranged between 5% and 72.9%. Plant height had the highest h^2_b of 72.9% while dry matter had the lowest h^2_b of 5%. Stem girth, root yield, roots per plant, branches per plant, harvest index and root size recorded broad sense heritabilities of 69.4%, 50.19%, 44.88%, 28.52, 25.22% and 11.47% respectively. The expected genetic gain values were moderate ranging between 0.91% to 65.71%, cassava root yield recording the highest while the lowest expected genetic gain was recorded for dry matter. Roots per plant, plant height, stem girth, branches per plant and root size recorded expected genetic gains of 37.05%, 36.67%, 33.63, 17.60 and 14.63 respectively.

Table 28: Estimates of parameters of variability for yield and yield components for cassava in the trial sites

Variable	Mean	δ^2g	δ^2ph	δ^2l	GCV (%)	PCV (%)	h^2b	EGA (%)
Plant height	130.3217	738.3795	1012.8815	274.5019	20.8507	24.4208	0.729	36.6731
Number of branches	2.6506	0.1799	0.6306	0.4507	15.9997	29.9587	0.2852	17.6022
Root size	0.2528	0.0029	0.0249	0.022	20.969	61.9131	0.1147	14.6298
Roots per plant	4.3889	1.3886	3.0938	1.7052	26.8494	40.0767	0.4488	37.0549
Stem girth	4.4354	0.7554	1.0884	0.333	19.596	23.5217	0.6941	33.6305
Dry matter (%)	37.6309	0.5327	10.1789	9.6462	1.9395	8.4782	0.0523	0.914
Harvest index	0.685	0.0028	0.0109	0.0082	7.6693	15.2714	0.252	7.934
Root yield	12.6326	32.3499	64.4545	32.1045	45.0238	63.5525	0.5019	65.7082

Where: δ^2g = variance due genotypic, δ^2ph = variance due to phenotypic, δ^2l = variance due location, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, h2b = broad heritability, EGA (%) = expected genetic advance.

4.7 Stability Parameters for Studied Cassava Yield and Yield Influencing Components

The results for stability parameters for the studied cassava yield and yield influencing components are presented in figures 8 to 23 and Table 37.

4.7.1 Relationships of stability parameters with roots per plant

4.7.1.1 b-value

Genotypes D and F had roots per plant of (5.47 and 4.49 respectively) above the mean. Genotypes G and H had mean roots per plant values (3.67 and 3.46 respectively) below the mean (Table 37), but comparably with b-values above and close to unity (Figure 8). Genotype D had a b-1 value of 0.16 which is closer to zero, however among all the genotypes, genotype G had the lowest b-1 value closest to zero (0.10).

4.7.1.2 S^2d and b- value

Genotypes 11 and 12 comparably showed low variances of deviation (0.46 and 0.37) and regression coefficients (0.80 and 0.81) closer to unit value than other genotypes (Table 37). On the other hand, variety 3 showed low stability (Figure 9) with S^2d value of 5.80, R^2 value of 0.30 and b-1 value of 0.5.

4.7.2 Relationships of stability parameters with stem girth

4.7.2.1 b-value

Genotype C had stem girth mean (4.81 cm) above the mean value, with b-1value of 0.05. (Figure 10). Genotype H had a b-1 value of 0.16, but with the lowest mean stem girth (3.46 cm) and which is also below the mean value (Table 37).

4.7.2.2 S^2d and b- value

Variety, 1 showed the lowest stability among the tested genotypes (Figure 11), while genotypes 7 and 8 showed low variance of deviation (0.0078 and 0.0017 respectively) and regression coefficients (0.95 and 0.96) approaching unit value (Table 37). While variety 8 showed b – value (1.16), very close to unity, variety 1 had a stem girth mean (4.88 cm) below average with the lowest stability (Figure 11). Genotypes 11, 6 and 12 showed b – values of 1.26, 1.25 and 1.24 respectively, above the unit value and variance of deviation values below average variance of deviation, where genotype 11 comparably showed low variance of deviation (0.04) (Figure 11 and Table 37).

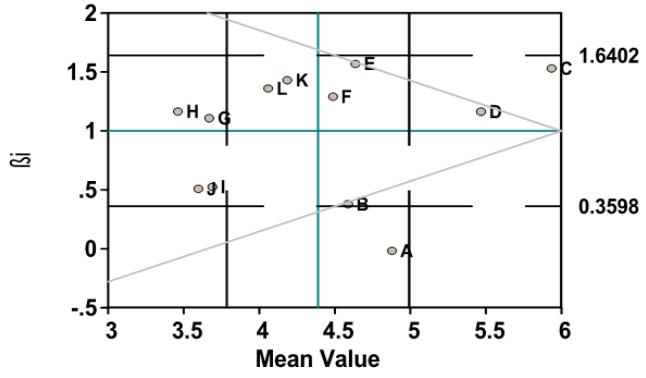


Figure 8: **b – values against roots per plant mean values**

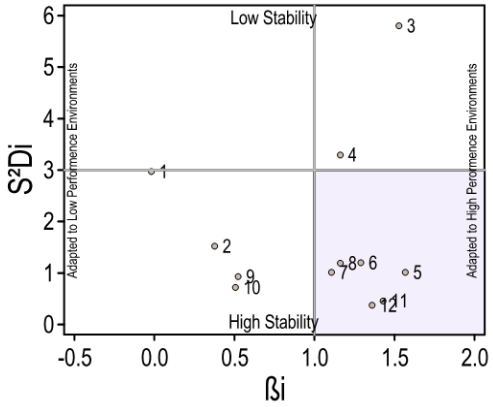


Figure 9: S^2d values against b – values for roots per plant

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

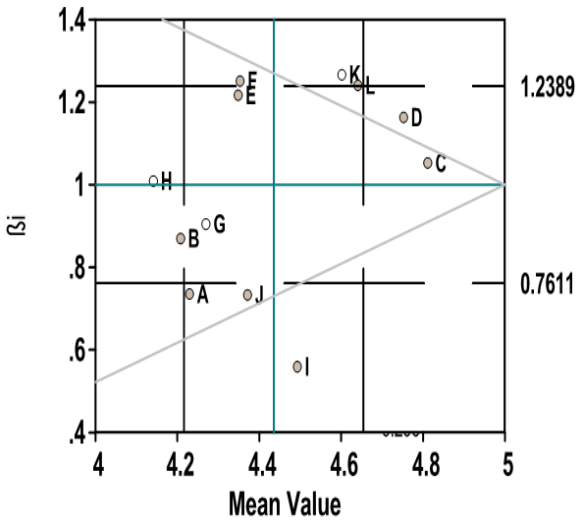


Figure 10: **b – values against stem girth mean values.**

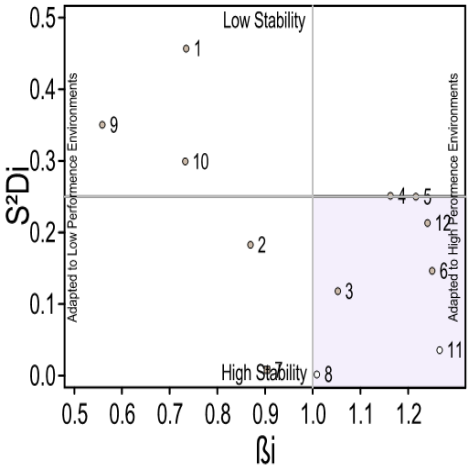


Figure 11: **S^2d values against b – values for stem girth**

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.3 Relationships of stability parameters with plant height

4.7.3.1 b-value

Genotypes I and L had plant height values of 131.7 cm and 138.9 cm respectively, above the mean value, and showed b-1 values of -0.014 and -0.012 respectively. Genotype H showed the lowest plant height mean (116.7 cm), with b-1value of 0.126 (Figure 12 and Table 37).

4.7.3.2 S^2d and b- value

Genotype 12 showed the lowest variance of deviation (8.8), with a regression coefficient (0.95) which was very close to 1 (Table 37). Genotype 9 had b-1 value

of -0.014 very near to zero and S^2d close to average value of variance of deviation (229.9). Variety 1 had low stability in plant height with S^2d value of 442.4 (Figure 13 and Table 37).

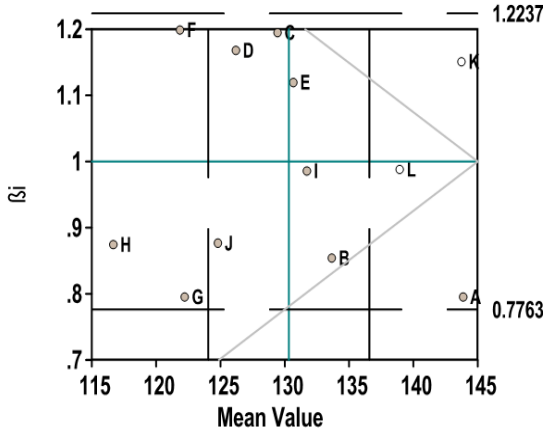


Figure 12: b – values against plant height mean values

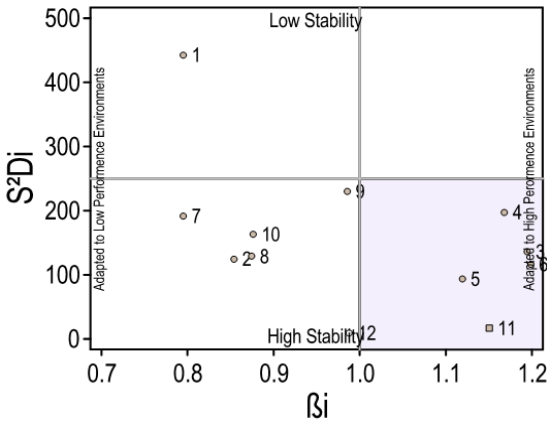


Figure 13: S^2d values against b – values for plant height

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.4 Relationships of stability parameters with number of branches per plant

4.7.4.1 b-value

Variety B, had number of branches per plant (2.68) which is above the average mean value with regression coefficient (0.83) and b-1 value of -0.136. Genotypes I, J and K had number of branches per plant of 2.63, 2.54 and 2.27 respectively, just below the mean value and had regression coefficients of 0.5231, 0.8371 and 0.4057 respectively. (Figure 14 and Table 37).

4.7.4.2 S^2d and b- value

Genotypes 5 and 10 had low variances of deviation (- 0.0064 and - 0.0071) with regression coefficients of 0.60 and 0.84and b-1 values of -0.265 and 0.346 respectively (Table 37). Genotype I had the b -1 equals to 0.439, whereas genotype 5 had the b-1 value of -0.265. Variety 2 with 0.136 (b-1 value), had higher variance of deviation relative to genotype 11, 5 and 10. Variety 3 and genotype 4 showed low stability, b-1 values of 2.159 and 2.037, to the number of branches per plant with S^2d values of 0.52 and 0.46 respectively (Figure 15 and Table 37).

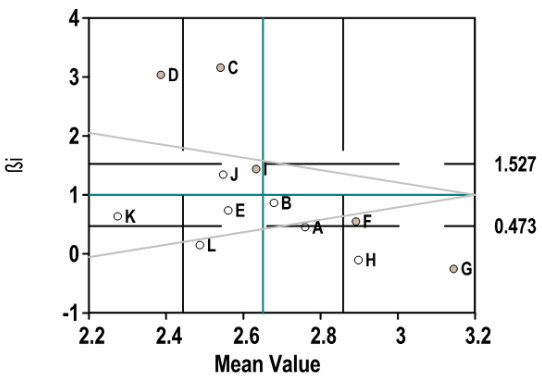


Figure 14: b – values against number of branches per plant mean values

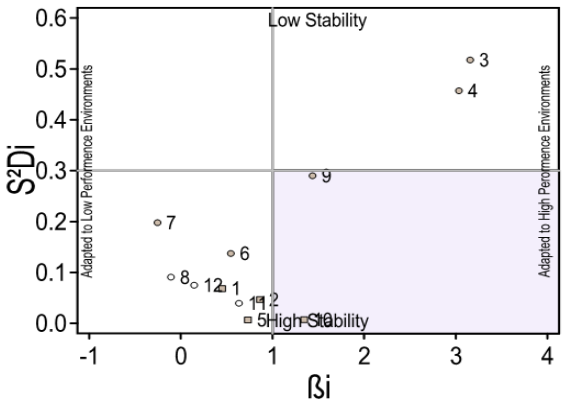


Figure 15: S^2d values against b – values for number of branches per plant

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.5 Relationships of stability parameters with root size

4.7.5.1 b-value

Genotypes K and L had b-1 values (-0.113 and -0.194) with mean root sizes (0.27 and 0.28) above the mean value respectively. Genotype F had a mean root size value below the root size mean value but with b-1 value (0.123) (Table 37).

4.7.5.2 S^2d and b- value

High stability was shown by the genotypes 6, 11 and 12 with S^2d values of 0.002, 0.004 and 0.005 respectively. Genotypes 9 and 10 had very low variances of deviation of 0.0004 and – 0.0001 (Table 37), but had regression coefficients close to one (0.8831 and 0.8963 respectively). The low stability on root size across the locations was shown by the genotype 5 (Figure 17), with S^2d value of 0.04 and b-1 value of 1.342 (Table 37).

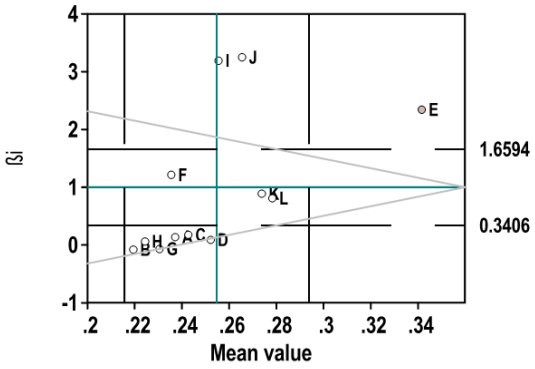


Figure 16: b – values against root size mean values.

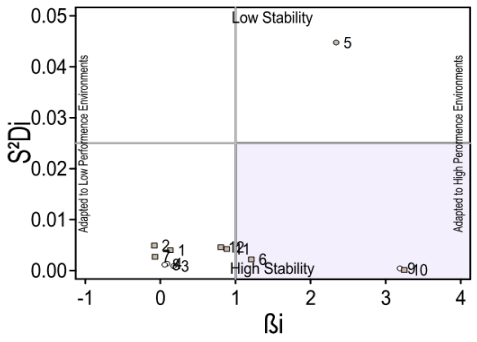


Figure 17: S^2d values against b – values for root size.

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.6 Relationships of stability parameters with root yield

4.7.6.1 b-value

Genotypes E and K had root yield values of 12.89 and 13.07 t ha^{-1} above the mean respectively, with b-1 values (-0.0029 and 0.26 respectively) (Figure 18). Genotypes F and L had root yield values below the mean, but approaching mean value with regression coefficients (0.83 and 0.70) and b-1 values of -0.066 and 0.213 respectively (Table 37).

4.7.6.2 S^2d and b- value

Genotype 9 had the lowest variance of deviation (3.51) followed by genotype 8 (4.73) and both having b-1 values of (-0.5313 and -0.7419) (Figure 19 and Table 37). Genotypes 3 and 4 had low stability on root yield (S^2d =102.93*** and 91.45** respectively). Genotypes 11 and 12 had relatively low variances of deviation (12.00 and 7.77) with b- values of 1.26 and 1.21 respectively above the unit value. Variety 3 and genotype 4 had low stability on yield across the locations (Figure 19).

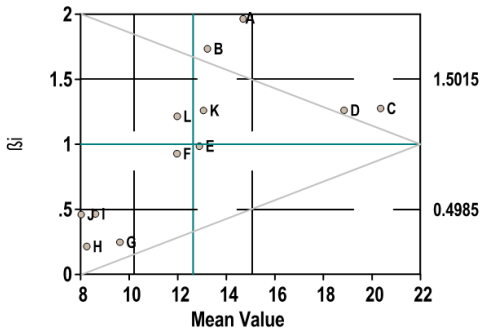


Figure 18: b – values against root yield mean values.

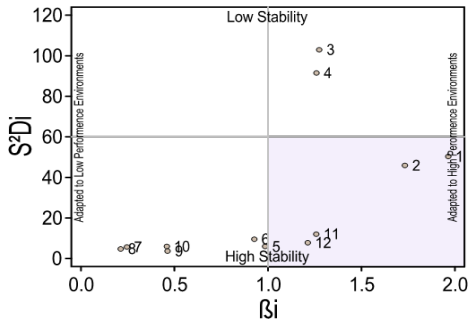


Figure 19: S^2d values against b – values for root yield.

KEY:

1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.7 Relationships of stability parameters with harvest index

4.7.7.1 b-value

Genotype F had the harvest index value (0.69) above the mean value and had b-1 value of 0.12. Genotype K had the harvest index value (0.67) below the mean value, with b-1 value of 0.08 (Table 37).

4.7.7.2 S^2d and b- value

Genotypes 5 and 8 had the lowest same variance of deviation (0.0002), however genotype 5 being more close to unit value as compared to genotype 8(Figure 21). Genotypes 10, 6 and 11 had comparably low variances of variation and b-1 values of 0.118, 0.12 and 0.08 respectively. Among the genotypes, genotype 11 had the lowest b-1 value (0.08) most close to zero. Variety 3 showed the lowest stability (S^2d = 0.011) on harvest index (Table 37).

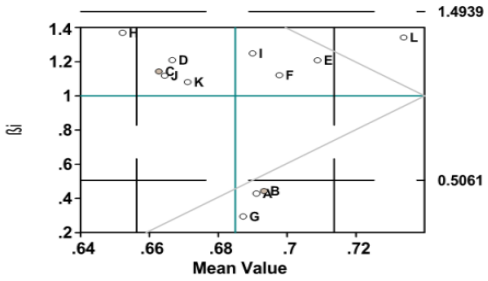


Figure 20: b – values against harvest index mean values

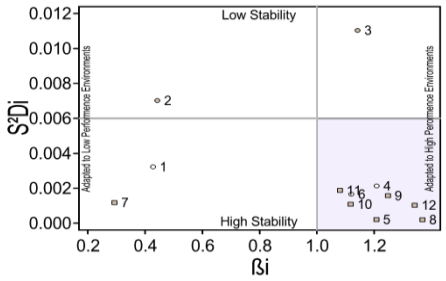


Figure 21: S^2d values against b – values for harvest index

KEY:
1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

4.7.8 Relationships of stability parameters with dry matter

4.7.8.1 b-value

Genotype I had dry matter content (37.89%) above the mean value and b-1 value of 0.13. Genotypes D and G had dry matter values (38.93% and 38.23 respectively) above the mean value (Figure 22) and b – values (1.44 and 1.37) close to unit value. Genotypes F, H and K had dry matter content of 37.46%, 37.22% and 37.01 below the mean value respectively and with b – values of 1.20, 1.37 and 0.74 (Table 37).

4.7.8.2 S^2d and b- value

Variety 2 had the lowest variance of deviation (0.05), with b-1 value (1.786) (Table 37). Variety 3 and genotype 4 showed the lowest variance of deviation (0.39 and 0.52), after variety 2, and were close to unit value (Figure 23). Genotypes 9 and 6 had comparably b-1 values (0.13 and 0.20), with moderately high variance of deviations 2.44 and 1.65 respectively. The low stability (S^2d = 8.51) on dry matter content across the locations was shown by the genotype 11 with b-1 value of 0.256.

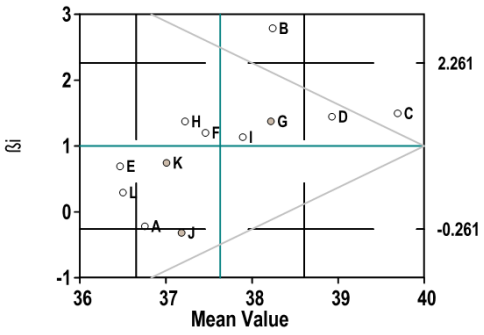


Figure 22: b – values against dry matter mean values.

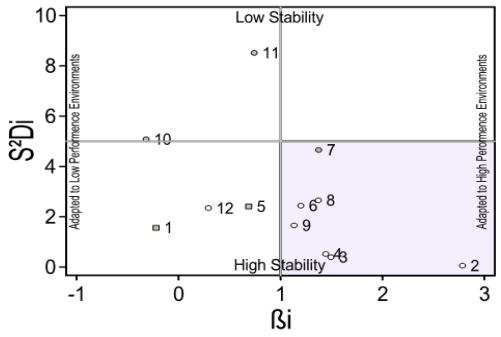


Figure 23: S^2d values against b – values for dry matter.

KEY:

1 = Albert, 2 = Kiroba, 3 = Naliendele, 4 = NDL 2006/030, 5 = NDL 2006/104, 6 =NDL 2006/283, 7 = NDL 2006/438, 8 = NDL 2006/487, 9 = NDL 2006/738, 10 = NDL 2006/741, 11 = NDL 2006/840, 12 = NDL 2006/850.

A = Albert, B = Kiroba, C = Naliendele, D = NDL 2006/030, E = NDL 2006/104, F =NDL 2006/283, G = NDL 2006/438, H = NDL 2006/487, I = NDL 2006/738, J = NDL 2006/741, K = NDL 2006/840, L = NDL 2006/850.

Table 29: Stability parameters for the root yield and yield components

Variable		Code	Genotype	Mean	b -value	b-1	Rank	S^2d	Rank	R^2
Roots per plant	1	A	Albert	4.8794 ± 0.6032	0.018	-0.982	12	2.9678 ***	10	0.0001
	2	B	Kiroba	4.5889 ± 0.6032	0.377	-0.623	11	1.5177 ***	9	0.0882
	3	C	Naliendele	5.9350 ± 0.6032	1.529	0.529	9	5.7994 ***	12	0.3049
	4	D	NDL 2006/030	5.4678 ± 0.6032	1.162	0.162	2	3.2922 ***	11	0.3056
	5	E	NDL 2006/104	4.6378 ± 0.6032	1.569	0.569	10	1.0116 ***	6	0.708
	6	F	NDL 2006/283	4.4889 ± 0.6032	1.290	0.290	4	1.1990 ***	8	0.5846
	7	G	NDL 2006/438	3.6706 ± 0.6032	1.107	0.107	1	1.0104 ***	5	0.5473
	8	H	NDL 2006/487	3.4628 ± 0.6032	1.163	0.163	3	1.1862 ***	7	0.5358
	9	I	NDL 2006/738	3.6911 ± 0.6032	0.524	-0.476	7	0.9309 ***	4	0.226
	10	J	NDL 2006/741	3.5983 ± 0.6032	0.508	-0.492	8	0.7180 ***	3	0.2557
	11	K	NDL 2006/840	4.1861 ± 0.6032	1.429	0.429	6	0.4565 ***	2	0.7989
	12	L	NDL 2006/850	4.0600 ± 0.6032	1.360	0.360	5	0.3718 **	1	0.8085
		$\bar{x}$		**4.3888**	**1.003**	**0.003**	**6.5**	**1.7051**	**6.5**	**0.4303**
Stem girth	1	A	Albert	4.2300 ± 0.2191	0.735	-0.265	9	0.4569 ***	12	0.529
	2	B	Kiroba	4.2083 ± 0.2191	0.869	-0.131	4	0.1828 **	6	0.7745
	3	C	Naliendele	4.8117 ± 0.2191	1.053	0.053	2	0.1180 *	4	0.8749
	4	D	NDL 2006/030	4.7528 ± 0.2191	1.163	0.163	5	0.2512 ***	9	0.826
	5	E	NDL 2006/104	4.3489 ± 0.2191	1.217	0.217	6	0.2498 ***	8	0.839
	6	F	NDL 2006/283	4.3533 ± 0.2191	1.251	0.251	8	0.1462 **	5	0.8941
	7	G	NDL 2006/438	4.2700 ± 0.2191	0.904	-0.096	3	0.0078	2	0.9548
	8	H	NDL 2006/487	4.1417 ± 0.2191	1.009	0.009	1	0.0017	1	0.9552
	9	I	NDL 2006/738	4.4933 ± 0.2191	0.559	-0.441	12	0.3503 ***	11	0.4514
	10	J	NDL 2006/741	4.3717 ± 0.2191	0.733	-0.267	11	0.2989 ***	10	0.6188
	11	K	NDL 2006/840	4.6017 ± 0.2191	1.266	0.266	10	0.0357	3	0.9524
	12	L	NDL 2006/850	4.6411 ± 0.2191	1.241	0.241	7	0.2132 ***	7	0.8607
		$\bar{x}$		**4.435375**	**1.001**	**-0.0053**	**6.5**	**0.0150**	**6.5**	**0.7942**
Plant height	1	A	Albert	143.9 ± 6.3	0.795	-0.205	11	442.4 ***	12	0.5597
	2	B	Kiroba	133.7 ± 6.3	0.854	-0.146	6	124.4 **	5	0.8084
	3	C	Naliendele	129.4 ± 6.3	1.195	0.195	9	135.7 **	7	0.8856
	4	D	NDL 2006/030	126.2 ± 6.3	1.168	0.168	8	197.2 ***	10	0.8466
	5	E	NDL 2006/104	130.7 ± 6.3	1.119	0.119	3	93.3 *	3	0.8988
	6	F	NDL 2006/283	121.9 ± 6.3	1.199	0.199	10	116.3 **	4	0.8973
	7	G	NDL 2006/438	122.2 ± 6.3	0.795	-0.205	12	191.4 ***	9	0.7239
	8	H	NDL 2006/487	116.7 ± 6.3	0.874	-0.126	5	128.8 **	6	0.8118

	9	I	NDL 2006/738	131.7 ± 6.3	0.986	-0.014	2	229.9 ***	11	0.7759
	10	J	NDL 2006/741	124.8 ± 6.3	0.876	-0.124	4	163.1 **	8	0.7835
	11	K	NDL 2006/840	143.7 ± 6.3	1.151	0.151	7	-16.6000	2	0.9787
	12	L	NDL 2006/850	138.9 ± 6.3	0.988	-0.012	1	8.8000	1	0.9468
		$\overline{x}$		**130.3167**	**1**	**0.0913**	**6.5**	**-3.9**	**6.5**	**0.8264**
Branches/plant	1	A	Albert	2.7606 ± 0.2072	0.451*	-0.549	7	-0.0683	5	0.8503
	2	B	Kiroba	2.6794 ± 0.2072	0.864	-0.136	1	-0.0464	4	0.8338
	3	C	Naliendele	2.5411 ± 0.2072	3.159	2.159	12	0.5174 ***	12	0.765
	4	D	NDL 2006/030	2.3867 ± 0.2072	3.037	2.037	11	0.4566 ***	11	0.7702
	5	E	NDL 2006/104	2.5611 ± 0.2072	0.735	-0.265	2	-0.0064	1	0.6025
	6	F	NDL 2006/283	2.8917 ± 0.2072	0.548	-0.452	6	0.1370 *	8	0.215
	7	G	NDL 2006/438	3.1444 ± 0.2072	-0.254	-1.254	10	0.1977 **	9	0.0438
	8	H	NDL 2006/487	2.8983 ± 0.2072	-0.106	-1.106	9	0.0903	7	0.013
	9	I	NDL 2006/738	2.6333 ± 0.2072	1.439	0.439	5	0.2897 **	10	0.5231
	10	J	NDL 2006/741	2.5478 ± 0.2072	1.346	0.346	3	-0.0071	2	0.8371
	11	K	NDL 2006/840	2.275 ± 0.2072	0.635	-0.365	4	0.039	3	0.4057
	12	L	NDL 2006/850	2.4878 ± 0.2072	0.146	-0.854	8	0.0746	6	0.0269
		$\overline{x}$		**13.40917**	**13.4092**	**0.1395**	**6.5**	**13.4091667**	**6.5**	**13.409**
Root size	1	A	Albert	0.2372 ± 0.0391	0.1360*	-0.864	5	-0.004	8	0.0515
	2	B	Kiroba	0.2194 ± 0.0391	0.0790*	-0.921	9	-0.0049	11	0.0462
	3	C	Naliendele	0.2428 ± 0.0391	0.177	-0.823	4	0.0009	3	0.0211
	4	D	NDL 2006/030	0.2522 ± 0.0391	0.088	-0.912	6	0.0014	5	0.005
	5	E	NDL 2006/104	0.3417 ± 0.0391	2.342	1.342	10	0.0447 ***	12	0.3242
	6	F	NDL 2006/283	0.2356 ± 0.0391	1.213	0.213	3	-0.0022	6	0.6617
	7	G	NDL 2006/438	0.2306 ± 0.0391	-0.07	-1.07	8	-0.0027	7	0.0076
	8	H	NDL 2006/487	0.2244 ± 0.0391	0.059	-0.941	7	0.0012	4	0.0023
	9	I	NDL 2006/738	0.2556 ± 0.0391	3.1910*	2.191	11	0.0004	2	0.8831
	10	J	NDL 2006/741	0.2656 ± 0.0391	3.2500*	2.25	12	-0.0001	1	0.8963
	11	K	NDL 2006/840	0.2739 ± 0.0391	0.887	-0.113	1	-0.0042	9	0.7347
	12	L	NDL 2006/850	0.2783 ± 0.0391	0.806	-0.194	2	-0.0046	10	0.7599
		$\overline{x}$		**0.254775**	**0.68775**	**0.0131667**	**6.5**	**-0.0017091**	**6.5**	**0.3661**
Root yield	1	A	Albert	7.32 ± 2.4315	1.962	0.962	12	50.28 ***		0.4827
	2	B	Kiroba	21.72 ± 2.4315	1.7311	0.7311	9	45.86 ***	9	0.3152
	3	C	Naliendele	11.4 ± 2.4315	1.2832	0.2832	6	102.93 ***	12	0.8113
	4	D	NDL 2006/030	8.95 ± 2.4315	1.2612	0.2612	5	91.45 ***	11	0.7105
	5	E	NDL 2006/104	12.89 ± 2.4315	0.9971	-0.0029	1	5.87***	4	0.591

	6	F	NDL 2006/283	10.88 ± 2.4315	0.934	-0.066	2	9.53 ***	7	0.8354
	7	G	NDL 2006/438	20.61 ± 2.4315	0.2581	-0.7419	10	5.68 ***	3	0.3361
	8	H	NDL 2006/487	17.5 ± 2.4315	0.2132	-0.7868	11	4.73 ***	2	0.6896
	9	I	NDL 2006/738	13.47 ± 2.4315	0.4687	-0.5313	7	3.61 ***	1	0.7849
	10	J	NDL 2006/741	8.93 ± 2.4315	0.4553	-0.5447	8	5.88 ***	5	0.2161
	11	K	NDL 2006/840	13.07 ± 2.4315	1.261	0.261	4	12.00 ***	8	0.1957
	12	L	NDL 2006/850	14.17 ± 2.4315	1.2132	0.2132	3	7.77 ***	6	0.6545
		$\overline{x}$		**13.4091**	**1.0031**	**0.003175**	**6.5**	**28.7992**	**6.5**	**0.5519**
Harvest index	1	A	Albert	0.6911 ± 0.0287	0.428	-0.572	11	0.0032	10	0.1168
	2	B	Kiroba	0.6933 ± 0.0287	0.443	-0.557	10	0.0070 **	11	0.0792
	3	C	Naliendele	0.6628 ± 0.0287	1.142	0.142	4	0.0110 ***	12	0.2875
	4	D	NDL 2006/030	0.6667 ± 0.0287	1.209	0.209	6	0.0021	9	0.5646
	5	E	NDL 2006/104	0.7089 ± 0.0287	1.208	0.208	5	-0.0002	2	0.7178
	6	F	NDL 2006/283	0.6978 ± 0.0287	1.12	0.12	3	0.0017	7	0.553
	7	G	NDL 2006/438	0.6872 ± 0.0287	0.293	-0.707	12	-0.0012	5	0.2001
	8	H	NDL 2006/487	0.6522 ± 0.0287	1.369	0.369	9	-0.0002	1	0.7648
	9	I	NDL 2006/738	0.69 ± 0.0287	1.248	0.248	7	-0.0016	6	0.8614
	10	J	NDL 2006/741	0.6644 ± 0.0287	1.118	0.118	2	-0.0011	4	0.7731
	11	K	NDL 2006/840	0.6711 ± 0.0287	1.08	0.08	1	-0.0019	8	0.8675
	12	L	NDL 2006/850	0.7339 ± 0.0287	1.341	0.341	8	-0.001	3	0.8252
		$\overline{x}$		**0.6849**	**0.9999**	**0.0927**	**6.5**	**0.0014**	**6.5**	**0.5509**
Dry matter	1	A	Albert	36.7561 ± 0.9756	-0.219	-1.219	10	-1.561	4	0.0297
	2	B	Kiroba	38.24 ± 0.9756	2.786	1.786	12	0.0522	1	0.6758
	3	C	Naliendele	39.6911 ± 0.9756	1.496	0.496	8	0.3896	2	0.3489
	4	D	NDL 2006/030	38.9283 ± 0.9756	1.444	0.444	7	0.5165	3	0.3242
	5	E	NDL 2006/104	36.4683 ± 0.9756	0.691	-0.309	4	-2.404	7	0.5198
	6	F	NDL 2006/283	37.4595 ± 0.9756	1.2	0.2	2	2.4394	8	0.1725
	7	G	NDL 2006/438	38.2194 ± 0.9756	1.375	0.375	6	4.6501 *	10	0.1608
	8	H	NDL 2006/487	37.2233 ± 0.9756	1.371	0.371	5	2.6494	9	0.2072
	9	I	NDL 2006/738	37.8933 ± 0.9756	1.135	0.135	1	1.6495	5	0.1802
	10	J	NDL 2006/741	37.1828 ± 0.9756	-0.319	-1.319	11	5.0746 *	11	0.0096
	11	K	NDL 2006/840	37.0072 ± 0.9756	0.744	-0.256	3	8.5116 **	12	0.0355
	12	L	NDL 2006/850	36.5017 ± 0.9756	0.293	-0.707	9	2.3355	6	0.0125
		$\overline{x}$		**37.6309**	**0.9998**	**-0.0002**	**6.5**	**0.674122**	**6.5**	**0.223**

CHAPTER FIVE

5.0 DISCUSSION

5.1 Performance of Cassava Genotypes in three locations

5.1.1 Cassava root yield

The results from this study showed variations in cassava root yield among genotypes within and across locations. The mean root yield across locations ranged from 7.32 – 21.72 t ha-1. However the analysis for root yield revealed that, Kiroba and NDL 2006/487 were identified as superior yielding genotypes across the locations (Table 14). NDL 2006/487 showed wider adaptability across the locations, while Kiroba showed instability in root yield performance. This implies that NDL 2006/487 can be grown in any of the three locations, while Kiroba is favourable for Nachingwea site. The superiority for these treatments existed probably because these two varieties had consistently high number of roots per plant across the locations and furthermore the two genotypes were less affected by diseases. These results agree with previous study by Ntuwurunga *et al.,* (2001), who reported that, cassava root yield increases as plant root number increases. Variation among locations on root yield was observed on NDL 2006/850 and NDL 2006/738 and therefore regarded as unstable genotypes. Stable genotypes across the locations were NDL 2006/438 and NDL 2006/741, although the latter recorded lower yields across the locations.

Generally the trend for the root yield (Figure 2) was not consistent with increase in altitude, as the yields were higher at Nachingwea located 465 masl, followed by the yields at Naliendele located at 120 masl and lastly Mtopwa which is located at relatively high altitudes 760 masl. These results are in agreement with observations

by Ntawurunga and Dixon, (2010) that experienced the same trend of root yield at different altitudes. This is because cassava performs better in mid altitudes, as compared to low and high altitudes where temperatures are very high and very low respectively (Ntawurunga, 2000). Therefore the differences in yield among the three locations could be due to differences in temperature; where at Mtopwa site the temperatures are relatively low and therefore the rate of growth and root filling needs longer time for the crop to attain its optimum yield, while at Naliendele the temperatures are very high to an extent that both plant growth and root expansion are retarded. However selecting the best performing genotypes and locating them to the most suitable locations remains a necessary criterion for the best yield results. The variety Kiroba was on average considered as the best for root yield across the three locations and specifically for Nachingwea, while genotype NDL 2006/487 was more suitable for Naliendele and Mtopwa (Table 6). Based on these results therefore, Nachingwea was the most suitable location for cassava root yield production, as this location had suitable conditions for cassava growth and development (Appendix 9). The weather data agrees partially (in this season), with optimum conditions for cassava growth and production as those suggested by (Nassar and Ortiz, 2007).

The performance of yield and yield components at all locations were below the expected ones as most of the newly selected genotypes were expected to yield 18 t ha^{-1} and above. Mkamilo *et al.*, (2010) in unpublished research reports, reported that, these genotypes when tested in Advanced Yield Trials, had root yields ranging between 18 - 25 t ha^{-1}. This low performance may be attributed to the weather

conditions that prevailed during the cropping season 2011/2012 (Appendix 9), which was not optimum. These results do not conform to the optimum conditions for cassava growth and development. According to Nassar and Ortiz, 2007, cassava performs better in low land tropics requiring a warm temperature ($24^{\circ C}$ – $27^{\circ C}$), moist climate and rainfall between 1000mm – 1500mm per annum.

5.1.2 Plant height

At Nachingwea, genotypes had the tallest cassava plants as compared to the two locations. This could be due to the fact that Nachingwea had good rainfall and optimum temperatures (Appendix 9) which had favoured plant growth compared to Naliendele and Mtopwa. Genotype NDL 2006/850 had the highest plant height across the locations and also gave highest plant heights at Nachingwea and Mtopwa. Plants with high heights do not guarantee high yields as plant height is not among the main factors contributing to yield (Ntawurunga *et al.,* 2001). Also this is supported in this experiment whereby Kiroba had low to medium plant heights, but with high to highest root yields. The overall mean number of plant height was 144.9 cm. These results are within the range of cassava plant height of 100 to 400 cm (Ekanayake *et al.*, 1997; Tan and Cock, 1979).

5.1.3 Number of branches per plant

This variable showed significant variations within and across locations. Nachingwea had many plants with many branches per plant compared to other sites. High number of plants with high number of branches at Nachingwea was supported by the good moisture availability (Appendix 9), which favoured both vegetative growth and root

yield. The number of branches per plant varied from 1.15 to 4.17 in the three locations. This differed a little bit from the results obtained by Villamayor, (1983) in research done at Philippines' Root Crop Research and Training Center, where number of branches per plant ranged between 1.6 and 2.0. The overall highest number of branches per plant was recorded on the treatment Kiroba. High number of branches per plant is not an indicator for high root yield, as the correlation between number of branches per plant was positive non – significant (0.0947). To support this, NDL 2006/487 had the lowest number of branches per plant within and across the locations, however it was among the best yielders; whereas NDL 2006/741 had higher numbers of branches per plant, but it was the least yielder, indicating that selection for high yield would require other parameters apart from number of branches per plant.

5.1.4 Stem girth

This parameter showed significant variations within and across locations. Naliendele had many plants with wider stem girths compared to the other two locations. The widest value of plant stem girth was recorded on Naliendele variety at Naliendele site. Higher plant stem girths at Naliendele could be contributed by the moderate moisture content, as compared to Mtopwa and Nachingwea, experienced during plant growth (Appendix 9). The stem girth ranged between 2.79 and 6.17 cm. This agrees with study done by Ikeh *et al.,* (2012), who reported that cassava stem girths ranged between 3.10 and 5.80 cm. Stem girth had positively and highly significant correlation with yield (r = 0.481**) indicating that, improvement of stem girth will also improve root yield. This agrees with findings by Ntawurunga *et al., (*2001), who

reported that, stem girth is among the main yield components contributing to root yield.

5.1.5 Number of roots per plant

Based on this study, it was observed that the mean number of roots per plant varied significantly within and across locations. Nachingwea had plants with many roots compared to other locations. The differences may have been caused by distribution of rainfall and temperature in these locations. Nachingwea received more rainfall as compared to Naliendele and Mtopwa. Furthermore, the temperatures for Nachingwea during the 2011/2012 cropping season (Appendix 9), favoured growth and development of cassava and hence many roots per plant. Number of roots per plant varied from 1.63 to 10.03. These results were below the number of roots per plant obtained by Cock, (1985) at CIAT, which were in the range of 5 to 20 roots per plant. This remarkable difference between these two experiments may be due to different environmental conditions. The sites under this study are in dry environments, and according to Cock, (1979), fewer storage roots are formed in drier environments. Kiroba, NDL 2006/438 and NDL 2006/487 gave better performance at Nachingwea, indicating that, these three genotypes were suitable in that location for good number of roots per plant and ultimately high yields. This variable had a positively and highly significant correlation with yield (0.7053***).

5.1.6 Root size per plant

Mean weight in kilograms of roots revealed significant variations within and across locations. Nachingwea had the highest mean weight of roots per plant compared to

other sites. In this study, across the locations root size ranged between 0.19 kg and 0.38 kg, which agrees with study conducted by Alfredo, (1997), who reported that weight of a single cassava root varied from 0.17 to 2.35 kg. Albert, NDL 2006/283, NDL 2006/438, and NDL 2006/487 appeared to be stable in terms of performance with respect to this character and had average to high values. These genotypes had (b -1) values of 0.213, -1.07 and 0.941 respectively as an indication of their stability. This suggests that, these genotypes had wider adaptability in terms of root size. Genotype NDL 2006/741 appeared to be unstable with inconsistent performance from one location to another with a (b -1) value of 2.25.

5.1.7 Harvest Index

With respect to harvest index, genotypes varied significantly within and across locations. The highest harvest index was obtained from Kiroba at Naliendele, while the overall highest harvest was obtained on NDL 2006/738. This highest value of harvest index at Naliendele, probably may be due to low rainfall (Appendix 9) received in this area, and therefore made the accumulation of water in the shoots to be low; which resulted to low shoot weight, low total weight and hence high harvest index. With respect to Kiroba having the highest harvest index at Naliendele, this may be due to the short and reduced aerial parts of Kiroba, which was 116 cm tall with average of 7 roots per plant as compared to NDL 2006/850 (144 cm tall) with average of 4 roots per plant. The harvest index values ranged between 0.57 and 0.84. This was in contrast with what was observed by Joseph *et al.,* (2011) who reported a range of 42.33 – 54.54 % in hybrids (crosses) and 14.30 – 37.83 % in parents of those crosses. This big difference in harvest index probably has been

contributed by variations in genetical traits, as harvest index in cassava is little affected by the environment and is a good indicator of the potential performance of a genotype across agro-ecological zones (Kawano, 1990).

5.2 Studied Cassava Diseases

5.2.1 Cassava brown streak disease

Significant variations were observed among the treatments at all locations. The highest disease incidence and severity were observed at Nachingwea on the variety Albert. The higher occurrence of the disease in Nachingwea compared to other locations can be due to location specific problem, as Nachingwea is known to be one of the high pressure disease areas in southern Tanzania (Hillocks, 1997). Albert was a stable susceptible variety which consistently recorded the highest disease incidences and severities across the locations. Probably, this is due to the genetical make up of this variety, which is highly susceptible to CBSD, as this disease is also transmitted through dissemination of infected planting materials. Other treatments that showed significant effect on this disease were Naliendele at Nachingwea and NDL 2006/283 at Naliendele sites.

5.2.2 Cassava mosaic disease

Based on the results of this study, it was observed that the mean CMD varied significantly within and across locations. Nachingwea had the highest disease incidence and severity recorded on the genotype NDL 2006/741. The highest incidences and severity at Nachingwea is probably due to location as disease spread between plants is by whitefly and can be rapid in some areas with high occurrence of

this vector (Hillocks and Thresh, 2000). NDL 2006/741 was susceptible across the locations as it was consistently affected by the CMD. Genotypes Naliendele (at Naliendele and Nachingwea), NDL 2006/104 (at Naliendele) and NDL 2006/840 (at Naliendele) also showed significant disease symptoms. The observed differences in CMD incidence and severity among the genotypes could be due to genetic differences. This is because according to Hillocks and Thresh (2000), the variations between cassava lines/genotypes diseases are inherited from planting materials and hence, genetically controlled. This suggests that, for the tolerant newly developed genotypes, there is a room for using them both directly for cassava root production and or using them in breeding programs as parents.

5.3 Genetic Correlations

In this study the significant positive genotypic correlations were observed between plant height and stem girth (r = 0.5900***), plant height and roots per plant (r = 0.4463***) and stem girth and roots per plant (r = 0.5046***) (Table 32). These results are in accordance with the report of Aina *et al.,* (2009) who reported that plant height, stem girth, and number of roots per plant are positively correlated. Furthermore, the above highly correlated traits had positive correlations with root yield. This suggests that, improvement of root yield can therefore be achieved through selection of these highly correlated characters, as increase in mean value of any one of these characters would significantly increase the means of others (Mahungu, 1983). Insignificant association between both dry matter and root size with all variables indicated that, yield improvement through direct selection of dry matter or root size as a single character would be impractical. This agrees with previous report by Akinwale *et al.,* (2009), who reported the same.

5.4 Associations among Cassava Root Yield and its Components

Generally the nature of inter trait correlations may enhance or retard the selection progress. A positive relationship indicates that selection for improvement would result in concomitant increase in one or more of the other components. This type of relationship was recorded in most of the studied traits. Positive and high correlations among roots per plant (r = 0.619), plant height (r = 0.290), root size (r = 0.153) and root yield (Table 35) suggest that root yield can be improved through selection of these yield components. Negative direct effects of branches per plant (r = -0.045) and stem girth (r = -0.093) suggests that favouring one of these traits alone and in absence of other traits, will automatically reduce cassava root yield.

5.5 Estimates of Parameters of Variability for Yield and Yield Components for Cassava in the Trial Sites

The results of this study revealed that, phenotypic estimates were higher than genotypic estimates an indication that, the apparent variations in the genotypes were not only genotypic but also due to environmental influence (Table 36). This observation agrees with the earlier findings by CIAT, (1984), Cock, (1985) and IITA, (1990). The extent of the environmental influence on any character is indicated by the magnitude of the difference between phenotypic coefficient of variation and genotypic coefficient of variation. Large differences reflect high environment influence, while small difference reveals high genetic influence. Plant height, stem girth and roots per plant had high to medium heritabilities, (0.729, 0.694 and 0.449 respectively) (Table 36), meaning that these are primarily under genetic control and reliable selection for them can be achieved through their

phenotypic performance (Makame, 1995). Also high heritability in the broad sense observed for plant height and stem girth suggests the presence of large components of cassava heritable portion of variation, which is the portion exploited by plant breeders (Aina *et al*., 2009). With high h^2b rapid progress in selection would be achieved, even with simple selection procedures, as recurrent phenotypic selection would be effective. This has also been observed from the findings of Naskar *et al.*, (1991). As shown in (Table 36), the low heritability in the broad sense recorded for dry matter (0.052) and root size (0.114) indicate that these characters are greatly influenced by the environment and direct selection of these characters will be ineffective (CIAT, 1995). Significant variations ($P < 0.05$) on dry matter content were observed among treatments and across locations. Although locations gave highly significant ($P < 0.001$) differences in root dry matter content, its contribution to the variation was only 3.92% while genotypes contributed 24.33% (Appendix 10). The contribution of variation of the locations coupled with insignificant G x E interaction, and the main effects of the replicates suggests that, dry matter content is not much influenced by the environment as by genetic differences. These results agree with other studies of Perez *et al.,* (2001), who reported that dry matter content in cassava roots is likely to be controlled by one or a few major genes. Dry matter content had both low heritability estimate and low genetic gain; this may be attributed to non-additive gene action.

5.6 Stability Parameters on Yield and Yield Components for the Studied Genotypes

The observations from this study (Figure 8 to 23 and Table 37) revealed that, most of the studied genotypes were unstable in most of the important parameters and also location specific. The stability analysis of genotypes on roots per plant revealed that, four genotypes showed adaptation to low performing environments ($b < 1$), eight genotypes were responsive to environmental improvement ($b > 1$), with G having b-1 value of 0.1070 (Figures 8 and 9 and Table 37). No genotype showed value of b-1equals to zero, hence limited number of the genotypes was considered to be stable in this aspect. Furthermore, all these genotypes had a low number of mean roots per plant and all of the mean square deviations were significant ($P < 0.01$, $P < 0.001$) (Table 37). Most of genotypes showed low R^2 values. This shows that, they were not close to the desired value (zero), thus depending on other characteristics of interest there was a narrow array of stable genotypes to be selected for further testing.

For results of stability for stem girth, genotypes G had a low regression coefficient closer to unity ($0.904 < 1$) (Table 37), with non-significant variance of deviation, and is adapted to low performance environments (Figure 10). Genotypes H and K are suitable for high performance environments with b-1 values above and closer to zero (0.009 and 0.266 respectively). All three genotypes were not significantly ($P < 0.05$) different from the mean square deviation and hence are stable genotypes in terms of stem girth, and can be used for further breeding programs. Basing on the coefficients of determination (R^2) (Table 37), they were high, which implies that there was room for selection of more ideal or with b values close to 1 genotypes.

With respect to plant height, genotypes K and L had high and low mean values respectively, with regression coefficients close to unit value and non-significant mean square deviation (Table 37). Genotype, K performed better under favorable environments, while genotype L performed better under unfavourable environments (Figure 12). These two genotypes are stable with respect to plant height. K and L have b-1 values of 0.15 and -0.012 and S^2d of -16.6 and 8.8 respectively with coefficients of regression 0.9787 and 0.9468 respectively. This suggests that, the genotypes can be used to cross with short genotypes for yield improvement, as plant height is highly correlated (0.5436***) to root yield. R^2 values were moderately high implying that selection of genotypes basing on plant height was possible.

Results from stability analysis for branches per plant revealed that, eight genotypes showed adaptation to low performing environments (b < 1) and four were responsive to environmental improvement. Among these genotypes, variety C, genotypes D, F, G and I showed significant effects on mean square deviation (Table 37), which also regressions show significant difference from unit value. Varieties, A and B and genotypes E, H, J, K and L showed b – values close to unit value and non-significant effects on mean square deviation were observed within them. This suggests that, these genotypes are stable.

With respect to root size, genotypes K, H, J, I, A, C and B showed adaptation to low performing environments (b < 1) while four genotypes D, E, F, K and L were responsive to environment improvement (b > 1) (Figures 16 and 17). Variety E was among the eight varieties with adaptation to low performing environments but was

the only one which had a high value b-1 (1.342). Most of the genotypes were considered to be stable since they had regression coefficients close or equal to one and also had high R^2 values. Furthermore, all these varieties had relatively high root size and minimum deviations from regression. The mean square deviations were not significant ($P < 0.05$) (Table 37). This shows that they were close to zero which is desired value. Thus depending on other traits of interest, there was a wide array of stable genotypes to select from for breeding purposes.

Results on stability analysis for root yield revealed that, six genotypes showed adaptation to poor performing environments ($b < 1$) and six genotypes showed adaptation to high performing environments ($b > 1$). Genotypes E and F were the only ones with non-significant regression coefficients less than 1 ($P <0.05$) (Figures 18, 19 and Table 37) while genotype L was the only one with non-significant regression coefficient among the genotypes adapted to high performing environments. On top of that, all these genotypes had relatively medium yield and high deviations from regression. The mean square deviations were significant ($P < 0.05$) and coefficients of determination (R^2) were found to range between low and medium. This suggests that, most of the tested genotypes (NDL 2006/438, NDL 2006/487, NDL 2006/738, NDL 2006/741, Kiroba and Albert with b-1 values of -0.7419, -0.7868, -0.5313, -0.5447, 0.7311 and 0.9620 respectively) were unstable and therefore selection from them will be impractical.

With respect to harvest index, results revealed that, genotypes B, C and G showed adaptation to poor performing environments ($b < 1$) while nine genotypes showed

adaptation to high performing environments (b > 1). Genotypes B, C and Naliendele variety were the only ones with significant regression coefficients less than 1 (P <0.05) (Figures 20, 21 and Table 37) while the remained genotypes had non-significant regression coefficient. Genotype NDL 2006/840 had the b- value approaching to unity. This suggests that, NDL 2006/840 is stable and suitable for all the locations basing on harvest index. On the other hand, B and C are adapted to low performing environments.

In the case of dry matter content, seven genotypes were adapted to high performing environments, while five genotypes were adapted to low performing environments. Among those adapted to high performance environments, genotype I had b-value closest to 1 (b < 1.135) (Figures 22, 23 and Table 37), due to its closeness to unity value, with non-significant mean deviation, it was considered to be ideal stable genotype with respect to dry matter content. On the other hand, genotypes G, J were significant at (P < 0.05), and K was significant at (P < 0.01) respectively and had very low R^2 values (Table 37), although they had high mean dry matter content. This suggests that, these genotypes are not stable, G registered for specific favorable environments, whereas genotypes K and J were specific for low performing environments.

5.7 Farmers' Criteria for Genotype/Variety Selection

5.7.1 Cassava root yield

Root yield ranked first both at Naliendele and Nachingwea (Table 26), while at Mtopwa yield criterion ranked the third. At Naliendele and Nachingwea locations

farmers gave root yield great importance as cassava crop comparatively performs better in these areas. Furthermore, in these two sites farmers depend very much on cassava as source of food (Naliendele site) and as a source of income (Nachingwea) by selling of "Makopa" (dried peeled cassava roots). At Mtopwa yield ranked third after taste and diseases. This is because the weather conditions at Mtopwa are not in favour of cassava crop.

5.7.2 Planting material

At Mtopwa cassava planting material is not a big deal (Table 26) since the weather condition at this site provides high viability of the planting materials without special care. On the other hand at Naliendele and Nachingwea where the temperatures are high during harvesting of the crop, planting material was given moderate importance. Planting materials has been valued because there is a time lag (dry spell) between harvesting time and the next season planting time in these two locations, hence most of the planting materials do lose their viability. Therefore, genotypes/varieties with large amount of planting materials are preferred as not all can be lost due to dry weather with good conservation of the planting materials.

5.7.3 Plant architecture

At Naliendele and Nachingwea plant architecture is of less importance (Table 26) criterion as farmers in these sites used to grow sole crops because of the nature of soils in the area (poor sand soils). At Mtopwa archtexrture was given moderate importance as farmers do intercrop cassava with other crops.

5.7.4 Root flesh colour

This criterion has neither been mentioned at Mtopwa nor at Nachingwea (Table 26). This is not by chance but it is because farmers in this location are used only to one root flesh colour (white) varieties. Contrary to farmers at Naliendele, as they are nearby to NARI, they had come across with "Yellow Fleshed Varieties" which are tested at NARI. Farmers do not prefer yellow fleshed varieties, as the ones at Naliendele have bitter taste.

5.7.5 Diseases

Criterion diseases at Mtopwa, ranked the first (Table 26), as most of farmers in this location do leave cassava crop in the field for two or more cropping seasons before harvesting in order for the crop to attain optimum growth and/or yield. For such extended period to maturity, if a variety is diseased, then at the end of growing season farmers will harvest nothing. For Naliendele and Nachingwea, diseases are of importance but because of short growing period (6 – 12 months) these sites are advantaged as compared to Mtopwa.

5.8 Nutritional Quality Characteristics of the Studied Cassava Genotypes

Significant variations ($P < 0.05$) among genotypes were observed for protein, dry matter, starch and root taste. Across locations, genotype NDL 2006/487 outperformed all of the tested genotypes for all of the nutritional traits studied, viz; dry matter percentage content, starch percentage content, protein percentage content and the highest root taste score (Table 23). This indicates that, the genotype has an added advantage for high nutritional quality characteristics. Furthermore, the

genotype can be grown in variable locations because of being stable for these characters.

5.8.1 Dry matter percentage

Based on the results of this study, it was observed that the mean dry matter percentage varied significantly within and across locations. Percentage dry matter content in genotypes ranged from 33.54 to 41.78 % (Table 20). This is in range with the results from the experiment done by Perez, *et al.,* (2001) where the dry matter content ranged between 10.72 and 57.23%. Nachingwea had relatively higher dry matter percentage means compared to other sites. However, all treatments were observed to have consistent dry matter percentage across the locations (Table 23). This suggests that, dry matter in cassava roots is not much influenced by environment as by genetic differences, this is revealed in its contribution to the environment variation which was only 3.92% while genotypes contributed 24.33% (Appendix 10) (Perez *et al.,* 2001). The highest values of dry matter percentage at Nachingwea could be contributed by the amount of rainfall received in that location during 2011 – 2012 cropping season (Appendix 9). This suggests that the root dry matter yield decreases under low water conditions. This is in agreement with Schulthess *et al., (*1991) who observed that the effect of drought caused the breaking of apical dominance, leading to lateral shoot formation which use reserves from roots and stems.

5.8.2 Starch percentage

This variable showed significant variations within and across locations. Nachingwea had significantly different highest values of starch percentage compared to the other two locations. Genotype, NDL 2006/487 recorded highest starch percentage content both at Nachingwea and Naliendele. The differences observed so far from one location to another could be due to the differences in rainfall distribution between those locations. There was more rainfall at Nachingwea and thus gave enough time for good starch accumulation. Genotype, NDL 2006/487 showed consistent accumulation of starch percentages across the locations. This suggests that, this genotype is suitable for those three locations, when the intention is starch production. Starch percentage values ranged between 18.14 and 23.99 %.

5.8.3 Protein percentage

Significant variations were observed within and across locations among the studied genotypes. In this study, percentage protein content in genotypes varied significantly, ranged from 0.08 to 1.39%. This differed to some extent with results from the experiment done by Ceballos *et al.,* (2006) at CIAT, where the crude protein ranged between 0.95 to 6.42%, and also FAO, (2004) reported protein in cassava roots ranging from 1 – 2%. Genotype NDL 2006/487 had the highest protein percentage means across the locations. However, the genotype had a bitter taste and hence high amount of hydrogen cyanide (Nassar and Dorea, 1982). Therefore highest values of protein percent in NDL 2006/487 may be contributed by presence of non-protein hydrogen compounds since this genotype contains high content of hydrogen cyanide. Almost all the genotypes showed wider adaptability

for protein percentage mean content as performed consistently (Table 23) across the locations.

5.8.4 Root taste

Root taste was based on scale of 1 – 2, where 1 represents sweet genotypes while 2 represents bitter genotypes. Across the locations, genotype NDL 2006/487 was found to be the most bitter, while genotype NDL 2006/741 was the sweetest. Genotype NDL 2006/283 was the most bitter at Mtopwa and Nachingwea, while at Naliendele genotype NDL 2006/487 was the most bitter. At Naliendele and Nachingwea genotype NDL 2006/741 was recorded as the sweetest (Table 25). It was generally observed that, in bitter varieties the content of protein is higher compared to sweet genotypes. This may be contributed by presence of glycosides that are present in bitter varieties, as they contain non protein nitrogen (Nassar and Dorea, 1982). In sweet genotypes the protein content was relatively low.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

In conclusion, this study showed the presence of and type of G x E interactions among the 9 genotypes and their yield components. High yielding genotypes with broad adaptation and some with specific adaptation were identified. Kiroba, Naliendele and genotypes NDL 2006/487, NDL 2006/438 and NDL 2006/283 were adapted to varying environments. On contrary, NDL 2006/850 and NDL 2006/738 were more suitable for Nachingwea. Naliendele variety and NDL 2006/030 had high yields at Naliendele site, hence regarded as more suitable for Naliendele.

Significant and positive correlations were observed between growth characters and root yield of cassava. When correlation coefficients were partitioned into direct and indirect effects, plant height had the highest contribution followed by roots per plant and stem girth, while harvest index contributed the lowest. These three characters therefore, should serve as basis for selection in cassava improvement.

Among the genotypes used in this study, variety Kiroba and genotype NDL 2006/487, showed high mean root yield, and were not significantly affected by diseases. Furthermore, variety Naliendele and genotype NDL 2006/438, although significantly affected by diseases, had high mean root yields at Naliendele and Nachingwea respectively. This showed that these varieties are tolerant to diseases. Furthermore Kiroba, Naliendele, NDL 2006/487 and NDL 2006/438 were stable

over the environments and therefore can be used in the breeding programs for the development of high yielding stable genotypes over different environments for future use.

Famers, criteria for variety/genotype selection were not so different from those of researchers. This is because the best four criteria for farmers in all locations included root yield and diseases, which are the characters that researchers are trying to work on. Furthermore, farmers' genotype/variety selection is very good and can be employed in genotype selection where scientific methods are not available. This is justified by the results obtained from researcher and during harvesting. Farmers observed that, genotypes NDL 2006/487, NDL 2006/438, Kiroba, and Naliendele were good root yielders at one or more locations; the same as results from the researcher. On the other hand, farmers assessed treatments Albert, NDL 2006/741 and NDL 2006/840 as poorer yielders, the same as recorded in researcher's results.

For all nutritional quality characteristics (starch percentage, percentage dry matter, protein content) of the genotypes tested, NDL 2006/487 showed superiority over the other genotypes. This indicates that, the genotype has an added advantage for high nutritional quality characteristics. Furthermore, the genotype can be grown in variable locations because of being stable for these characters over the experimental locations.

6.2 Recommendations

For cassava root yield production, it is recommended to grow Kiroba at Nachingwea and genotype NDL 2006/487 to be grown at Naliendele and Mtopwa sites where it performed best. However, for nutritional characteristics, (starch percentage, dry matter percentage, protein content) genotype NDL 2006/487 is recommended for all sites.

From the results, it showed that, number of branches per plant has negative effect on cassava root yield, due this therefore, care must be taken by plant breeders when breeding for cassava plants with high number of branches per plant.

For future G x E experiments, it is recommended to employ the aspect of seasons or years in order to have reliable and precise information on given varieties or genotypes. Also, further investigations on G x E interactions at important crop growth stages for yield, yield components and biochemical profiles would help to develop strategies that integrate traditional plant breeding with modern molecular marker based selection for tailoring cassava genotypes/cultivars for higher yield and target environments.

It is urged that, identified genotypes with desirable traits be used as parents in future breeding programs, so as to incorporate the desirable traits to the new progenies. For the genotypes and varieties that showed high susceptibility to the studied disease(s), exploitation has to be done through crosses in order to capture those positive traits they possess e.g. NDL 2006/438 and Naliendele variety which had many positive

attributes that can be incorporated to other genotypes for future improvement of cassava in breeding programs. Both genotypes, Naliendele and NDL 2006/438 are sweet, have high content of starch/dry matter, mature earlier and also are high yielders.

It is important that, in any research or project/experiment planned for improvement of crops, farmers have to be involved from the start as the target group is farmers; and also, the end products of most of agricultural researches are utilized by farmers.

As it has been revealed that, NDL 2006/487 is the best genotype in nutritional qualities, improved cassava processing technologies must be in place, so as it can used for food regardless of its bitterness (which is associated with the poisonous compound, hydrogen cyanide).

REFERENCES

A.O.A.C. (1990). Statistical Manual of the Association of Official Analytical Chemists.Official Methods of Analysis. Association of Official Analytical Chemistry, 88pp.

Aina, O.O., Dixon, A.G.O., Paul, I. and Ankirinde, E.A. (2009). G x E interacttion effects on yield and yield components of cassava (landraces and improved genotypes in the savanna regions of Nigeria. *African Journal of Biotechnology,* 8(19), 4833 – 4945.

Akinwale, M.G., Akinyele, B.O., Dixon, A.G.O. and Odiyi, A.C. (2009). Genetic variability among cassava genotypes in three agro ecology zones of Nigeria. In: *African Crop Science Conference Proceedings, Uganda,* 9, 541 – 546.

Akinwale, M.G., Akinyele, B.O., Dixon, A.G.O. and Odiyi, A.C. (2010). Genetic variability among forty-three cassava genotypes in three agro-ecological zonesof Nigeria. *Journal of Plant Breeding Crop Science,* 2(5): 104 – 109.

Akinyele, B.O. and Osekita, O.S. (2011). Genotype x Environment interaction in NH47 – 4 variety of Okra – *Abelmoschus esculentus* (Linn.) Moench. *Internatioanl Journal of . Geneics and Mollecular Biology*, 3(4), 55 – 59.

Alfredo, A.C.A. (1997). Cassava Botany and Physiology. Embrapa Cassava and Fruits. Bahia, Brazil, 23pp.

Alicai, T., Omongo, C. A. and Maruthi, M. N. (2007) "Re-emergence of cassava brown streak disease in Uganda," *Plant Diseases*, 91(1), 24–29.

Al-jibouri, H.L., Miller, P.A., and Robinsion, H.F. (1958). Genotypic and Environment variances and covariances in upland cotton cross of interspecific origin. *Agronomy Journal* 50: 633 – 636.

Alves, A.C. (2002). Cassava botany and physiology. *In:* R.J. Hillocks, J.M. Thresh, and A. Bellotti (ed.) Cassava: Biology, production, and utilization. CAB International, Oxfordshire, UK. 67 – 89 pp.

Baidu – Forson, J. (1997). On-station farmers' participatory varietal evaluation: A strategy for client-oriented breeding. *Experimental Agriculture* 33: 43 – 50.

Banziger, M. and Cooper, M. (2001). Breeding for low input conditions and consequences for participatory plant breeding: Examples from tropical maize and wheat. *Euphytica* 122: 503 – 519.

Bokanga, M. (2001). Cassava: Post-harvest operations. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, 220pp.

Bolhuis, G.G., (1954). The toxicitty of cassava roots. *Netherlands Journal of Agriculture Science,* 2: 176 – 185 .

Calle, F., Perez, J.C., Ceballos, H., Morante, N., Gaitan, W., Liano, G. and Alvarez, E. (2005). Within-Family genetic variation and epistasis in Cassava (*Manihot esculenta,* Cranz) adapted to acid soil environment. *Ephytica*, 145 (1-2): 77 – 85.

Carter, S.E., Fresco, L.O., Jones, P.G. and Fairbairn, J.N. (1992). An Atlas of Cassava in Africa: *Historical, Agroecological and Demographic Aspects of Crop Distribution*. CIAT, Cali, Colombia. 128pp.

Ceballos, H., Sanchez, T., Morante, N., Fregene, M., Dufour, D., Smith, A., Denyer, K., Perez, J., Calle, F., and Mestres, C. (2006). Discovery of an Amylose –free starch mutant cassava (*Manihot esculenta* Crantz). *Journal of Agriculture and Food Chemistry*. 55: 7469 – 7476.

Ceccarelli, S., Grando, S., Singh, M., Michael, M., Shikho, A., Al Issa, M., Al Saleh, A., Kaleonjy, G., Al Ghanem, S.M., Al Hassan, A.L., Dalla, H., Basha, S. and Basha, T. (2003). A Methodological Study on Participatory barley breeding. II. Response to Selection. *Euphytica* 133: 185 – 200.

CIAT (1984). Selection and preparation of cassava cuttings for planting. Study Guide 1984, 28pp.

CIAT (1995). Cassava Breeding, Agronomy Research and Technology Transfer in Asia. Howeler, R.H. (ed.). *Proceedings of Fourth Regional Workshop held in Trivandrum, India*. 2–6 Nov. 1993. CIAT, Cali, Colombia, 464pp.

CIAT, (1995). Annual Report. International Center of Tropical Agriculture, Cali, Colombia, 85 – 103pp.

Cock, J.H. (1979). Cassava research. *Field Crops Research* 2: 185-191.

Cock, J.H. (1985). Cassava: physiological basis. In: *Cassava Research, Production and Utilization.* CIAT, Cali, Colombia, 33-62.

Cock, J.H. (1985). New Potential for the neglected crop. West view press Incoorporation. Boulder Fredrick Apraeger. Common Wheat in Italy Plant Breeding, 113, 197 – 205.

COSCA Tanzania, (1996). Production prospects for Cassava in Tanzania (draft). *COSCA Working paper No. 16.* Collaborative Study of Cassava in Africa, International Institute of Tropical Agriculture (IITA) and Ministry of Agriculture, Tanzania. In: Agricultural technology development through participatory research: *Proceedings of the third collaborative research workshop* : held in Morogoro, 24-26 May 2004, 317pp.

COSCA, (1996). Processing potential for cassava production growth in Africa. *COSCA Working paper No. 11*. Collaborative Study of cassava in Africa. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.47 pp.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path coefficient analysis of component of crested wheatgrass seed production. *Agronomy Journal* 51: 515-518.

Diasolua, N. D., Kuo Y.H. and Lambein, F. (2002). Food safety and amino acid balance in processed cassava "Cossettes".*J ournal of Agricriculture and Food Chemistry.* 50: 3042-3049.

Diasolua, N.D., Kuo, Y.H. and Lambein, F. (2003). Amino acid profiles and protein quality of cooked cassava leaves or 'saka-saka'. *Journal of Food Science and Agricriculture.* 83: 529-534.

Dixon, A.G.O., Asiedu, R. and Hahn, S.K. (1994). Genotype stability and adaptation: Analytical methods and implications for Cassava Breeding for low input agriculture. In: Ofori, F., Hahn, S.K. (Eds.) Tropical Root Crops in a Developing Economy*: Proceedings of the 19th Symposium of the International Society for Tropical Root Crops held in Accra,* Ghana. 225 – 232 pp.

Eberhart, S.A. and Russel, W. A. (1966). Stability Parameters for comparing varieties. *Crop Science Journal,* 6: 36- 40.

Eeuwijk van, F.A and Elgersma, A. (2008). Incorporating environmental information in an analysis of genotype by environment interaction for seed yield in perennial ryegrass. [http://www.nature.com/hdy/journal/v70/n5/abs/hdy199366a.html] site visited on 09/04/2012.

Ekanayake, I.J, Osiru D.S.O., Porto M.C.M., (1997). Agronomy of cassava. IITA Research Guide 60. Training Program, IITA, Ibadan, Nigeria. 30pp.

FAO (2004). The Global Cassava Development. Agriculture and Consumer Protection [http://www.fao.org/docrep/007j1255e00htm] site visited on 17/10/2012.

FAO (2005). FAOSTAT [http://www.faostat.fao.org] site visited on 20/09/2011.

FAO (Food and Agriculture Organization of the United Nations) (2002). *Proceedings of the Validation Forum on the Global Cassava Development Strategy*, Rome, Italy, 26 – 28 April 2000, 1-62.

FAOSTAT (2008). Statistical database of the Food and Agriculture Organization of the United Nations FAOSTAT http://faostat.fao.org site visited on 10/08/ 2011.

Gilbert, R.A., Shine, J.M., Miller, J.D., Rice, R.W., and Rainbolt, C.R. (2007). The effect of genotype, emvironment and time of harvest on sugarcane yields in Florida USA. [http://cat.inist.fr/?aModele=afficheN&cpsidt=17403817] site visited on 12/06/2012.

Goncalves, P.S., Bortoletto, N., Martins, A.L.M., Costa, R.B. and Gallo, P.B. (2003). Genotype x environment interaction and phenotypicstability for girth growth and rubber yield for hevea clones in Sao Paulo State, Brazil. [htt://www. br/scielo.php?script=sci_arttext&pid=S1415 4757200300040000&LNG=nrm=isso] site visited on 05/04/2012.

Hahn, S.K. and Keyer, J. (1985). Cassava: A basic food of Africa. *Out look on Agriculture* 14(2): 95 – 100.

Halima, M.K. (2005). Evaluation on Farmer knowledge on Cassava Brown Streak Disease (CBSD) in the Roman Catholic Church Diocess of Tunduru – Masasi in South Eastern Tanzania. *MSc. Dissertation. Southern New Hampshire Open Universty of Tanzania.* 83pp.

Hanson, H.L., Robinson, H.F and Comstock, R.E. (1956). Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy journal* 48: 268 – 272.

Harrison, B.D., Zhou, X., Otim-Nape, G.W., Liu, Y. and Robinson, .D.J. (1997). Role of a novel type of infection in the geminivirus-induced epidemic of severe cassava mosaic in Uganda. *Annals of Applied Biology,* 131, 437 – 448.

Haugerud, A. and Collinson, M.P. (1990). Plants genes and people: Improving the relevance of plant breeding in Africa. *Experimental Agriculture* 26: 341 – 362.

Hillocks, R.J. (1997). Cassava virus diseases and their control with special reference to southern Tanzania. *Integrated Pest Management Reviews,* 2, 125–138.

Hillocks, R.J. and Thresh, J.M. (2000). Cassava mosaic and cassava brown streak virus diseases in Africa. A comparative guide to symptoms and aetiologies. *Roots.* 7(1), 4 -12.

IFAD (International Fund for Agricultural Development) and FAO (Food and Agriculture Organization of the United Nations) (2000). The world cassava economy: Facts and outlook. Rome. 31pp.

IITA (1990). International Institute of Tropical Agriculture (IITA). Cassava in Tropical Africa Reference Manual, 176pp.

IITA (2010). Cassava Disease Surveillance Surveys 2009, Lake zone of Tanzania Mapping Report, Great Lakes Cassava Initiative, 44pp.

IITA (1990). Cassava in tropical Africa. Reference manual, IITA. 176 pp.

Ikeh, A. O., Ndaeyo, N. U., Udoh, E. I., Iboko, K. O. and Udounang, P. I. (2012). Growth and Yield of Cassava (*Manihot esculenta* Crantz) as Influenced by the Number of Shoots Retained per Stand on an Ultisol. *Nature and Science,* 10(8), 16 - 20

Jennings, D.L. (1994). Breeding for resistance to African cassava mosaic geminivirus in East Africa. *Tropical Science* 34, 110 – 122.

Joseph, K., Rob M., Mark L., John, D., Paul, S., and Eliud, C. K. N. (2011). Farmers' participatory selection for early bulking cassava genotypes in semi-arid Eastern Kenya. *Journal of Plant Breeding and Crop Science,* 3(3), 44–52.

Kang, M.S. (1998). Using genotype by environment interaction for crop cultivar development. *Advanced Agronomy,* 35: 1999 – 240.

Kapinga, R., Bart de Steenhuijsen, P, Kajiru, S., Chirimi J., Rugutu C., Mahungu, N.M. (1997). Selection of cassava varieties by farmers in the lake zone of Tanzania. *African Journal of Root Tuber Crops,* 2: 248-253.

Kavishe, F.P. (1993). Nutrition relevant action in Tanzania. *Monograph Series No. 1.* Tanzania Food and Nutrition Center, Tanzania. 49pp.

Kawano, K. (1990). Harvest index and evolution of major food crop cultivars in the tropics. *Euphytica*, 46: 195-202.

Kawano, K. (1998). Socio Economic Contribution of cassava varietal improvement to the small farmer community in Asia. *In:* Cassava Breeding, Agronomy and Farmer Participatory Research in Asia. *Proceedings, 5th Regional Workshop, held in Danzhou, Hainan, China*. Nov. 3 – 8, 1996. 170 – 190.

Kawano, K., Goncalvez, F.W.M. and Cenpukdee, U. (1987). Genetic And environmental effects on dry matter content of cassava root. *Crop Science Journal*, 27: 69 – 74.

Kilic, H., Sagir, A. and Bayram, Y. (2009). Estiamtes of Genotype x environment interactions and heritability of Black Point in Durum Wheat. *Journal of Biolology Science,* 1(1), 92 – 96.

Lema, N. and Heemskerk (1996). The Lake Zone Research Planning Workshop Ukiriguru. Mwanza 3 - 4th October 1996. 58p.

Magoon, M.L., Krishman, R. and Lakshmi, K.E. (1970). Association of plant and tuber characteristics with yield of cassava. *Tropical Root and Tuber Crop Newsletter*, 5:29 – 30.

Mahungu, N.M. (1983). Relationship among selected agronomic characters and their effects on tuberous root yield of cassava (*Manihot esculenta* Cratz). *PhD Thesis*, University of Ibadan. 193pp.

Makame, M. (1995). Genetic variation stability of performance of cassava clones and their responses to intercropping with sweet potato in Zanzibar. PhD. Thesis, University of Ibadan, Ibadan, Nigeria. 248pp.

Masumba, E.A. (2006). Genetic diversity and field performance of cassava (*Manihot esculenta* Crutz) landraces commonly grown in eastern, southern, and lake zones. Masters of Science in Crop Science Dissertation, Sokoine University of Agriculture, Morogoro, Tanzania. 89pp.

Mirzawan, P.D.N., Cooper, M. and Horgath, D.M. (1993). The impactt of genotype multiply environmemnt interactions for sugar yield on the use of indirect selection in southern Queensland.
[http//www.publish.csiro.au/paper/EA9930629.com.html] site visited on 06/02/2012.

Mkamilo, G., Njapuka, A. and Kundy, A.C. (2010). Roots and Tuber Progrmme Technical Report. Naliendele Agricultural Resarch Institute, Southern Zone, Mtwara, Tanzania. 23pp.

Mkamilo, G.S. and Jeremiah, S.C. (2005). Current status of cassava improvement prgramme in Tanzania. In: African Crop Science Conference Proceedings, Volume 7. *African Crop Science Society, Uganda,* pp1311 – 1314.

Mkumbira, J., Mahungu, N.M. and Gullberg, U. (2003). Grouping locations for Efficient Cassava Evaluation in Malawi. *Experimental Agriculture*, 39, 167 – 179.

Morris, M.L. and Bellon, M.R. (2004). Participatory Plant Breeding Research: Opportunities and challenges for the international crop improvement system. *Euphytica* 136: 21 – 35.

Msabaha M.A.M., Ndibaza, R.E., and Nyango, A.K.. (1988). Cassava research advances in Tanzania for the period 1930-1988. Tanzania Agricultural Research Organisation, Ministry of Agriculture and Livestock Development, Tanzania. 25pp.

Msabaha, M.A.M. (1990). Sweet Potato. Subject matter specialist paper presented for Tanzania Agricultural Research Masterplan. Ministry of Agriculture and Livestock Development Tanzania. 30pp.

Mtunda K.J., Muhanna M., Raya M.D. and Kanju E.E. (2002). Current status of cassava brown streak virus disease in Tanzania. In: J.P. Legg and R.J. Hillocks 2002. Cassava brown streak virus disease: past present and future. *Proceedings of an international workshop, Kenya,* 7-11.

Muhanna, M. and Mtunda, K.J. (2002). A report on the study of cassava root rot problem in Muheza District, Tanga Region Tanzania. Submitted to the District Director. 34pp.

Naskar, S.K., Singh, D.P. and Lakshimi, K.R. (1991). Variability and Correlations in F1 population of cassava genotypes. *Journal of Root Crops,* 15, 29 – 31.

Nassar, N. M. A. and Dorea, J. G. (1982). Protein contents of cassava cultivars and its hybrid with *Manihot* species. *Turrialba* 32: 429-432.

Nassar, N.M.A. and Ortiz, R. (2007). Cassava Improvement: Challenges and Impacts. Cambridge University Press. United Kingdom, *Journal of Agricultural Science.* 145, 163 – 171.

Ngeve, J.M., Dixon, A.G.O. and Nukinine, E.N. (2005). The Influence of Host Genotype x Environment Interactions on the Response of Cassava Anthracnose Disease in Diverse Agro-ecologies in Nigeria. *African Crop Science Journal,* 13(1), 1 – 11.

Nichols R.F.W. (1950). The brown streak disease of cassava. Distribution, climatic effects and diagnostic symptoms. *East African Agriculture Journal,* 15: 154-160.

Ntawuruhunga, P., Ojulong, H. and Dixon, A.G.O. (1998). Genetic variability among cassava genotypes and its growth performance overtime. In: *Proceedings of the 6th Symposium of International Tropical Root Crops, Africa – Branch* , 22 – 28 Oct. 1995, Lilongwe, Malawi. 242 – 248.

Ntawuruhungu, P., Rubayihayo, P., Whyte, J.B.A., Dixon, A.G.O. and Osiru, D.S.O. (2001). A Search for storage root yield indicators. *African Crop Science Journal*, 9 (4): 599 – 606.

Ntawurunga, P. (2000). Evaluation of cassava (*Manihot esculenta* Cratz) genotypes for adaptation to different altitudes. PhD Thesis, Makerere University, Uganda, 156pp.

Ntawurunga, P. And Dixon, A.G.O. (2010). Qualitative variation and interrelationship between factors influencing cassava yield. *Journal of Applied Biosciences*. 26: 1594 – 1602.

Nuwamanya, E., Baguma , Y., Kawuki, R.S. and Rubaihayo, P.R. (2009). Quantification of starch physiochemica lcharacteristics in a cassava segregating population. *African Crop Science Journal*, 16: 192 – 202.

Nyango, A. (1980). Cassava Bacterial Blight in four regions of the United Republic of Tanzania; A Preliminary Survey Report- Roots and Tuber Crops, ARI, Ukiriguru. 30pp.

Ogbe, F.O., Songa, W. And Kamau, J.W. (1996). Survey of the incidence of African cassava mosaic and East African mosaic viruses in Kenya and Uganda using a monoclonal antibody based diagnostic test. *Roots* 3: 10 – 13.

Olsen, K.M. and Schaal, B.A. (2001). Micrfosatellite variation in cassava (*Manihot esculenta*, Euphobeaceae) and its wild relatives: further evidence for a southern Amanzonian origin of domestication. *American Journal of Botany* 88:131 – 142.

Padi, F.K. (2007). Euphitica: Spinger Netherlands. Genotype x environment interaction and yield stability in a cow-pea based cropping. [http://www. springerlink.com/content/65877j2280805616/] site visted on 07/02/2012.

Perez, J.C., Morante, N.L.J., Lenis, J.I., Jaramillo. G., Ceballos, H. And Calle, F. (2001). Advantages of New Cassava Breeding Scheme at CIAT. *In*: Taylor, N.J., Ogbe, F. and Fauquet, C.M. (eds). *Abstract book for the Fifth International Scientific Meeting of the Cassava Biotechnology Network,* 4 – 9 November 2001. Donald Danforth plant Science Center, St. Louis, Missouri, USA, pp 271 – 301.

Planning Commission Dar es Salaam and Regional Commissioner's Office Mtwara (2008). Mtwara Region Socio-economic Profile. Planning Commission Dar es Salaam and Regional Commissioner's Office Mtwara. 233pp.

Raya, M.D., Jeremiah, S.C. and Legg, J. (1993). African Cassava Mosaic Virus (ACMV) and Brown Streak survey in Tanzania. 64pp.

Reuben, S.O.W.N., Mulungu, L.S., Nchimbi-Msolla, S., Misangu, R.N., Mbilinyi, L.B. and Macha, M. (1998). Performance of nine exotic and local onion (*Allium cepa* L.) genotypes grown under dry season tropical condition at Morogoro, Tanzania: 2. Path coefficient analysis. *South African Journal of Science*, 94, 454 – 455.

Roots and Tubers (1994). Roots and Tuber Annual Report 1994. Naliendele Agricultural Research Institute, Mtwara. Tanzania. 27pp.

Sakin, M.A., Akincl, C., Duzmer, O. and Donmez, E. (2011). Assessment of Genotype x Environment interactionon Yield and Yield Components of Durum wheat Genotypes by Multivariate Analysis. *African Journal of Biotechnology*, 10(15), 2875 – 2885.

Schulthess, F., Baumgärter, J.U., Delucchi, V., and Gutierrez, A.P. (1991). The influence of the cassava mealybug, *Phenacoccus manihoti* Mat.-Ferr. (Hom., Pseudococcidae) on yield formation, *Manihot esculenta* Crantz. *Journal of Applied Entomology*, 111: 155-165.

Shukla, P.T. (1976). Preliminary report on the green mite (Mononychellus tanojoa Bondar) in Tanzania local cassava varieties. *East African Agricultural Journal,* (42): 55 – 59.

Singh, K., Foley, R. and Onate-Sanches, L. (2002) Transcription factors in plant defense and stress responses. *Brazilian Journal of Plant Physiology,* 5**:**430.

Singh, K.B and Chaudhary, B.D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyan Publishers. New Delhi-India. 318pp.

Ssemakula, G. and Dixon, A. (2007). Genotype x Environment Interaction, Stability and Agronomic Performance of Caretenoid-rich cassava clones. *Science and Research Essay,* 2(9), 390 – 399.

Storey, H. H. (1936). "Virus diseases on East African plants - VII. A progress report on studies of diseases of cassava," *East African Journal,* 2, 34–39.

Tai, G.C.C. (1975). Analysis of genotype x environment interactions based on the method of Path Coefficient analysis. *Canadian Journal of Genetics and Cytology,* 17: 141 – 149.

Tan, S.L, Cock, J.H. (1979). Branching habit as a yield determinant in cassava. *Field Crops Research* 2: 281-289.

TARO. (1983). Root Crops Research Highlights. Tanzania Agricultural Research Organization, Dar-es-Salaam, Tanzania. 25pp.

Trouche, G. (2004). The participatory breeding using population improvement in rice: A new methodology adapted to the needs of small farmers in Central America and the Caribbean. *In: "Population improvement, an alternative to explore the genetic resources of rice in Latin America"* Editor: Guimarães, E. CIAT-CIRAD-Fundación DANAC 12pp.

Villamayor, F.G.J. (1983). Root and Stake Production of Cassava at Different Populations and Subsequent Yield Evaluation of Stakes. Phillipine *Journal of Crop Science*, 8(1): 23 – 25.

Wamatu, J.M. and Thomas, E. (2002). The influence of Genotype x Environment Interaction on the Grain Yields of 10 Pigeon Pea Cultivars Grown in Kenya. [http://www.ingentaconnect.com/content/bsc/jac/2002/00000188/00000001/art00005?crawler=true] site visited on 12/06/2012.

Warburg, O. (1894). Die kulturpfflanzen Usambaras. Mitt. Dtsch. Schutzgeb 7, 131pp.

Welch, R.M. and Graham, R.D. (2004). Breeding for micronutrients staple foods crops from a human nutrition perspective. *Journal of Experimental Biotechnology*, 55: 353 – 364.

Witcombe, J.R. (1996). Participatory approaches to plant breeding and selection. *Biotechnology and Development Monitor,* FAO. 2008. 29: 2 – 6.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research,* 20: 557 – 585.

Yan, W. and Hunt, L.A. (2002). Interpretation of Genotype x Environment Interaction for Winter Wheat Yield in Ontario [http://crop.scijournals.org/cgi/content/full/41/1/19] site visted on 17/08/2012.

APPENDICES

Appendix 1. Analysis of variance for variables studied at Naliendele

S.V	DF	CBSDI	CBSDS	CMDI	CMDS	NECROSIS	DM	STARCH	PROTEIN	TASTE	HARDNESS
	2	52.9	0.02361	243.8	0.0182	0.3229	5.681	1.502	0.009372	0.0556	0.1599
WEED	1	85.22	0.04205	660.1	0.1503	0.0313	2.566*	2.585	0.001901	0.0556	0.0746
Error (A)	2	17.86	0.00572	56.3	0.1857	0.2812	0.094	0.164	0.002239	0.0556	0.5765
GENO	11	3773.02***	1.77591***	2169.1***	1.179***	3.2737***	18.953*	8.793*	1.270001***	0.798***	0.4183
WEED*GENO	11	58.96	0.02472	231.1	0.0709	0.0767	2.153	0.615	0.013114	0.1465	0.6518
Erro(B)	44	67.7	0.03302	177.3	0.1544	0.2188	8.044	3.66	0.006733	0.1616	0.536
Total	71										

Key: REP = Replicates, Geno = Genotype, WEED = Weeding regime, S.V = Source of variation, DF = Degrees of freedom, CBSDI = Cassava brown streak disease incidence (%), CBSDS = Cassava brown streak disease severity, CMDI = Cassava mosaic disease incidence (%), CMDS = Cassava mosaic disease severity, DM = Dry matter (%).

Appendix 2. Analysis of variance for variables at Naliendele

S.V	DF	PLHT	BRCH	GIRT	RTSZ	RPLT	PLHI	RYLD
REP	2	1374.9	0.2826	0.2668	0.0014226	0.6335	0.0396	5.266
WEEDING	1	251.9	0.0387	0.1644	0.0003833	1.7569	0.0004	22.411
Error (A)	2	561.1	0.1001	0.0348	0.0002614	0.6253	0.0291	5.051
GENO	11	1080***	3.1943***	2.7513***	0.0101541***	7.9095***	0.015386*	104.67***
WEEDI*GENO	11	86.7	0.1021	0.0682	0.0006679	0.2018	0.0085	0.972
Error(B)	44	103	0.1774	0.134	0.000943	0.262	0.0064	1.746
Total	71							

Key: REP = Replicates, Geno = Genotype, WEED = Weeding regime, S.V = Source of variation, DF = Degrees of freedom, PLHT = Plant height (cm),
PLBR = Number of branches per plant, GIRT =Plant girth, RPLT = Number of roots per plant, PLHI = Plant harvest index, RYLD = Root yield.

Appendix 3. Analysis of variance for variables studied at Mtopwa

S.V	DF	CBSDI	CBSDS	CMDI	CMDS	NECROSIS	DM	STARCH	PROTEIN	TASTE
REP	2	31.6	0.0001	129.6	0.0347	0.0556	4.389	0.02605	3.254	0.2222
WEED	1	450	0.1387	0.8	0.0098	0.125	11.777*	0.00451	2.301	0.0139
Error (A)	2	788.5	0.2805	134.7	0.04783	0	0.45	0.0072	0.455	0.2222
GENO	11	1501.8**	0.6007**	578.4	0.1824	2.2563***	22.503**	1.95222***	12.865**	1.0745***
WEED*GENO	11	794.7	0.3839	363.9	0.07618	0.0644	7.444	0.03129	3.552	0.0442
Error (B)	44	510.4	0.1991	322.2	0.09572	0.1793	8.116	0.02411	4.292	0.101
Total	71									

Key: S.V = Source of variation, DF = Degrees of freedom, CBSDI = Cassava brown streak disease incidence(%), CBSDS = Cassava brown streak disease severity, CMDI = Cassava mosaic disease incidence(%), CMDS = Cassava mosaic disease severity, DM = Dry matter(%).

Appendix 4. Analysis of variance for variables studied at Mtopwa

S.V	DF	PLHT	BRCH	GIRT	RTSZ	RPLT	PLHI	RYLD
REP	2	79.27	0.1921	0.5912	0.03948	0.0585	0.0284	3.0042
WEED	1	880.11***	0.2323	0.252	0.03533	0.3416	0.0002	14.1069*
Error (A)	2	1.23	0.2883	0.1841	0.05944	0.2964	0.0014	0.6712
GENO	11	1186.62***	2.1548***	0.5521***	0.05465	10.4429***	0.021968*	59.3506***
WEED*GENO	11	52.93	0.3041	0.0423	0.04471	0.2363	0.008	0.9452
Error (B)	44	46.17	0.3808	0.128	0.04611	0.15	0.0088	0.958
Total	71							

Key: REP = Replicates, Geno = Gentype, WEED = Weeding regime, S.V = Source of variation, DF = Degrees of freedom, PLHT = Plant height(cm), PLBR = Number of branches per plant, GIRT =Plant girth, RPLT = Number of roots per plant, Plant harvest index, Root yield.

Appendix 5. Analysis of variance for variables studied at Nachingwea

S.V	DF	CBSDI	CMDI	CMDS	NECROSIS	DM	STARCH	TASTE	HARDNESS
REP	2	92.49	116.1	0.16	0.43	7.41	3.73	0.18	0.26
GENO	11	4949.21***	4602.2***	2.36***	3.51***	28.15*	14.17*	0.80*	0.68*
Error (A)	22	50.11	93	0.06	0.39	9.88	4.98	0.26	0.23
WEED	1	125.98	0	0.01	0.5	8.37	4.21	0.5*	0.13
GENO*WEED	11	57.43	107	0.04	0.14	7.11	3.58	0.05	0.16
ErroR (B)	24	47.02	123.1	0.07	0.33	9.02	4.54	0.08	0.24
Total	71								

Key: REP = Replicates, Geno = Genotype, WEED = Weeding regime, S.V = Source of variation, DF = Degrees of freedom, CBSDI = Cassava brown streak disease incidence (%), CBSDS = Cassava brown streak disease severity, CMDI = Cassava mosaic disease incidence

(%), CMDS = Cassava mosaic disease severity, DM = Dry matter(%),

Appendix 6.Analysis of variance for variables studied at Nachingwea

S.V	DF	PLHT	BRCH	GRTH	RTSZ	RPLT	PLHI	RYLD
REP	2	487	0.11	0.69	0.01	0.21	0.03	3.12
GENO	11	1751.5***	2.99***	1.82***	0.11***	19.08***	0.01*	644.45***
Error (A)	22	228.1	0.15	0.11	0	0.78	0.01	7.08
WEED	1	1464.7**	0.11	0.26	0	0.84	0	38.62***
GENO*WEED	11	80.3	0.17	0.1	0	0.38	0.01	1.44
ErroR (B)	24	116	0.11	0.14	0	0.43	0	0.84
Total	71							

Key: REP = Replicates, Geno = Genotype, WEED = Weeding regime S.V = Source of variation, DF = Degrees of freedom,
PLHT = Plant height , PLBR = Number of branches per plant, GIRT =Plant girth , RPLT = Number of roots per plant, PLHI = Plant harvest index, RYLD =Root yield.

Appendix 7. Combined analysis of variance for variables studied across locations

S.V	DF	CBSDI	CBSDS	CMDI	CMDS	NECR	DM	PRO	SCH	TTE	HDS
REP	2	60.3	0.02	78.7	0.05	0.27	0.61	0.04	0.79	0.28	0.13
SITE	2	31.9	0.02	1561.5*	0.84*	1.01	43.91	0.77***	24.01	0.34	9.18***
Error (A)	4	58.3	0.02	205.4	0.08	0.27	8.44	0	3.85	0.09	0.15
WEED	1	179.5	0.05	205.2	0.11	0.09	0.38	0	1.53	0.12	0.01
SITE*WEED	2	240.8	0.09	227.8	0.03	0.28	11.17	0	3.78	0.23	0.1
Error (B)	6	289.7	0.11	134.2	0.1	0.39	4.37	0	2.31	0.13	0.31
GENO	11	8704.6***	3.48***	4696.6***	2.44***	6.85***	49.57***	4.77***	25.65***	1.66***	0.51*
SITE*GENO	22	759.7***	0.44***	1326.6***	0.64***	1.09***	10.02	0.07***	5.09	0.50***	0.32
WEED*GENO	11	196.3	0.1	169.4	0.06	0.09	6.54	0.02	3.15	0.06	0.33
SITE*WEED*GENO	22	357.4*	0.16645*	266.3	0.06	0.09	5.08	0.01	2.3	0.09	0.25
Error (C)	132	208.7	0.09	201.2	0.1	0.24	8.48	0.02	4.21	0.14	0.27
Total	215										

Key: REP = Replicates, Geno = Genotype, WEED = Weeding regime S.V = Source of variation, DF = Degrees of freedom, CBSDI = Cassava brown streak disease incidence (%), CBSDS = Cassava brown streak disease severity, CMDI = Cassava mosaic disease incidence, CMDS = Cassava mosaic disease severity, DM = Dry matter, TTE = Taste, PRO = Protein, SCH = Starch

Appendix 8. Combined analysis of variance for variables studied across locations

S.V	DF	PLHT	PLBR	GIRT	RTSZ	RPLT	PLHI	RYLD
REP	2	629.6	0.01	0.96	0.01	0.49	0.09	5.09
SITE	2	69071.2***	1.5	72.04***	0.18388*	77.56***	0.28***	1884.41***
Error (A)	4	655.8	0.28	0.3	0.02	0.2	0	3.15
WEED	1	2341.3*	0	0.12	0.02	2.66*	0	72.074***
SITE*WEED	2	127.7	0.19	0.28	0.01	0.14	0	1.53
Error (B)	6	219.8	0.14	0.12	0.02	0.31	0.01	1.98
GENO	11	1799.4***	6.76***	1.27***	0.05881***	21.79***	0.02***	442.64***
SITE*GENO	22	1109.4***	0.7825***	1.92***	0.05876***	7.81***	0.01**	182.91***
WEED*GENO	11	31.8	0.29	0.07	0.02	0.38	0.01	1.31
SITE*WEED*GENO	22	94	0.15	0.07	0.01	0.22	0.01	1.03
Error (C)	132	107.4	0.23	0.13	0.02	0.35	0.01	2.23
Total	215							

Key: S.V = Source of variation, DF = Degrees of freedom, PLHT = Plant heigh t(cm), PLBR = Number of branches per plant, GIRT =Plant girth, RPLT = Number of roots per plant, PLHI = Plant harvest index, RYLD = Root yield.

Appendix 9: Rainfall and temperature data recorded at different locations of the study from January 2012 to August 2012

Month	Rainfall (mm)			Mean monthly temperature (°C)		
	Naliendele	Mtopwa	Nachingwea	Naliendele	Mtopwa	Nachingwea
January	216.3	257.5	240.9	28.2	22	24.84
February	81.4	136.5	113.5	29.9	23.3	25.52
March	260.3	347.3	297.8	28.8	21.7	24.9
April	84.4	98.4	108.5	28.7	20	24.8
May	63.3	7.5	98.10	29	19.4	24.1
June	3.9	0	11	28.3	18.9	25.4
July	13.5	3	0	28.5	20	25.6
August	6.3	12.5	1.2	28.7	22	24.9
Total	**729.4**	**862.7**	**870.0**			

Appendix 10. Dry Matter Analysis of variance

S.V	DF	SS	% SS CONTR	M.S	v.r.	F pr.
REP stratum	2	1.214		0.607	0.07	
SITE	2	87.812	3.92	43.906	5.21	0.077
Residual	4	33.738		8.435	1.93	
WEEDING	1	0.377		0.377	0.09	0.779
SITE.WEEDING	2	22.338		11.169	2.56	0.157
Residual	6	26.2		4.367	0.51	
GENOTYPE	11	545.31	24.33	49.574	5.84	<.001
SITE.GENOTYPE	22	220.37		10.017	1.18	0.276
WEEDING.GENOTYPE	11	71.928		6.539	0.77	0.669
SITE.WEEDING.GENOTYPE	22	111.817		5.083	0.6	0.918
Residual	132	1119.822		8.483		
Total	215	2240.925				

Where; S.V = Source of variation, DF = Degrees of freedom, SS = Sum of squares
%SS CONTR = Sum of squares contribution (%) M.S = Mean squares