Breeding, Evaluation and Selection of Cassava for High Starch Content and Yield in Tanzania

By

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Thesis abstract

High starch content is an important component of root quantity and quality for almost all uses of cassava (flour, chips, and industrial raw material). However, there is scanty information on genetic variability for dry matter and starch contents and relatively little attention has been paid to genetic improvement of root dry matter content and starch content in Tanzania. The major objective of this research was to develop improved cassava varieties that are high yielding, with high dry matter and starch content for Tanzania and specifically to: i) identify farmers' preferences and selection criteria for cassava storage root quality characteristics and other traits of agronomic relevance for research intervention through a participatory rural appraisal; ii) determine the genotypic variability for starch quantity and dry matter content evaluated for three harvesting times in four sites; iii) determine the inheritance of dry matter and starch content in cassava genotypes; and iv) develop and evaluate clones for high storage root yield, high dry matter content and starch. Attributes desired by farmers were yield, earliness, tolerance to pests and diseases. The complementing attributes associated with culinary qualities were sweetness, good cookability, high dry matter content or mealyness and marketability. The preliminary study conducted to evaluate the variability in root dry matter content (RDMC) and starch quantity and yield of ten cassava cultivars indicated that RDMC ranged from 29 to 40% with the mean of 34.3%. The RDMC at 7 months after planting (MAP) was higher than at 11 and 14 MAP. Starch content (StC) ranged from 20.3% to 24.9% with the mean of 22.8%. The StC differed significantly between cultivars, harvesting time and sites. An increase in StC was observed between 0 and 7 MAP, followed by a decline between 7 and 11 MAP, and finally an increase again noted between 11 and 14 MAP. However, for most of the cultivars at Kibaha an increase in StC between 11 and 14 MAP could not surpass values recorded at 7 MAP. At Kizimbani, cultivar Kalolo and Vumbi could not increase in StC after 11 MAP. At Chambezi and Hombolo, a dramatic gain in StC was observed for most of the cultivars between 11 and 14 MAP. Starch yield ranged from 0.54 to 4.09 t ha^{-1}. Both StC and fresh storage root yield are important traits when selecting for commercial cultivars for starch production. Generation of the F_1 population was done using a 10 x 10 half diallel design, followed by evaluation of genotypes using a 4 x 10 α-lattice. Results from the diallel analysis indicated that significant differences in fresh storage root yield (FSRY), fresh biomass (FBM), storage root number (SRN), RDMC, starch content (StC), and starch yield (StY), and cassava brown streak disease root necrosis (CBSRN) were observed between families and

progeny. The FSRY for the families ranged from 15.0 to 36.3 t ha^{-1}; StC ranged from 23.0 to 29.9%; RDMC ranged from 31.4 to 40.1%; and StY ranged from 3.3 to 8.3 t ha^{-1}. The cassava mosaic disease (CMD) severity ranged from 1.7 to 2.7, while cassava brown streak disease (CBSD) severity for above ground symptoms ranged from 1.0 to 1.9. Additive genetic effects were predominant over non-additive genetic effects for RDMC, StC, and CBSRN, while for FSRY, FBM, SRN, and StY non-additive genetic effects predominated. Negative and non-significant correlation between RDMC and FSRY was observed at the seedling stage (r=-0.018), while at clonal stage the correlation was positive but not significant (0.01). The RDMC and StC were positive and significantly correlated (r=0.55***) at clonal stage. However, the StC negatively and non-significantly correlated with FSRY (r=-0.01). High, positive and significant correlation (r=0.94; p≤0.001) was observed between the StY and FSRY at clonal stage. High, positive and significant correlations between the seedling and clonal stage in FSRM (r=0.50; p≤0.01), RDMC (r=0.67; p≤0.001), HI (r=0.69; p≤0.001), and SRN (r=0.52; p≤0.01) were observed, suggesting that indirect selection could start at seedling stage for FSRM, RDMC, HI, and SRN. The best overall genotype for StC was 6256 (40.9%) from family Kiroba x Namikonga followed by genotype 6731 (40.6%; Vumbi x Namikonga). Among the parents, Kiroba and Namikonga were identified as the best combiners in terms of GCA effects for StC. Genotype 6879 from family Vumbi x AR 42-3 had the highest StY value of 34.8 t ha^{-1} followed by genotype 6086 (30.4 t ha^{-1}; Kalolo x AR 40-6). Among the parents, Kalolo and AR 42-3 were identified as good combiners for the trait. Mid-parent heterosis for StC ranged from 41.6 to 134.1%, while best parent heterosis ranged from 30.4 to 119.6%. Genotype KBH/08/6807 from family Vumbi x TMS 30001 had the highest mid-and best parent heterosis percentage for StC. For StY, mid-parent and best parent heterosis ranged from 168.0 to 1391.0%, and from 140.4 to 1079.0%, respectively, with the genotype 6879 (Vumbi x AR 42-3) exhibiting the highest mid- and best parent heterosis percentage for StY. Improvement for StC, RDMC, and CBSRN may be realized by selecting parents with the highest GCA effects for the traits and hybridize with those that combine well to maximize the positive SCA effects for the StC, RDMC and CBSRN. Selected genotypes from the clonal stage will be evaluated in preliminary yield trial and advanced further to multi-locational trials while implementing participatory approaches involving farmers and processors in selection. New promising lines should be tested at different sites and the best harvesting dates should be established.

Declaration

I**, Kiddo Julius Mtunda,** declare that

1.   The research report in this thesis, except where otherwise indicated, is my original research.
2.   The thesis has not been submitted for any degree or examination at any other university.
3.   This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.
4.   This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. When other written sources have been quoted, then:
     a.   Their words have been re-written but the general information attributed to them has been referenced;
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Signed…………………………………Date…………………………….

Kiddo Julius Mtunda (Student)

As research supervisors, we agree to the submission of this dissertation for examination:

Signed…………………………………..Date………………………………

Prof Rob. Melis (Principal supervisor)

Signed…………………………………..Date………………………………

Dr Paul Shanahan (Co-supervisor)

Acknowledgements

Dedication

To Julius, Nesaa and Yona

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Introduction to Thesis

1.   Importance of cassava

Cassava (*Manihot esculenta* Crantz) is a tropical root crop consumed by over 600 million people in Africa, Asia and Latin America. It is the third most important source of calories in the tropics after rice and maize (Fauquet and Tohme, 2008). The crop is vital for both food security and income generation. In Asia and Latin America, cassava serves as livestock feed, an industrial raw material, and a source of food. In Africa, it serves as the second most important source of calories, an inexpensive food, and emerging cash crop (Fauquet and Tohme, 2008). It is known to have the highest carbohydrates contents among the staple crops (Coursey, 1973). In sub-Saharan Africa, cassava is mainly a subsistence crop grown by small-scale farmers and it feeds over 200 million people daily (Madeley, 1993).

World production of fresh cassava roots was 172 million metric tons in 2000, an increase of almost 75% since 1970. In 2007, world production had reached 228 million metric tons, with Africa accounting for more than 53%, Asia for 30% and Latin America and the Caribbean for 17% of the total (FAOSTAT, 2007). According to Scott et al. (2000), the production of cassava is expected to increase to 290 million metric tons by 2020. The annual per capita consumption of cassava in sub-Saharan Africa is estimated at 106 kg and is reported to have increased by 2.1% annually between 1983 and 1996 (Scott et al., 2000). However, in some sub-Saharan African countries, consumption exceeds 300 kg per person per annum (Fregene et al., 2003). The demand for cassava in developing countries is estimated to grow at 2% annually for food purposes and 1.6% for feed (Scott et al., 2000). This escalating demand calls for improved varieties that are high yielding to satisfy current food and feed requirements.

Cassava plays a number of different but equally important roles in African development, including: a rural food staple, an urban food staple, an industrial raw material and as livestock feed. However, the bulk of cassava production is consumed as food (Nweke et al., 2002). Described as a 'classic food security crop' (DeVries and Toenniessen, 2001), cassava offers several advantages: it grows well under marginal conditions where few other crops could survive, it provides a decent harvest under erratic rainfall conditions and degraded soils, and

it provides a flexible harvesting date or extended harvesting period, allowing farmers to keep the roots stored in the ground until needed (El-Sharkawy, 1993; Cock, 1979). Therefore, there is a need to increase cassava production through improving the yield and adoption of the improved varieties, in order to satisfy the increasing population in developing countries, especially in sub-Saharan Africa.

Table 1 Cassava production, area harvested and yield in the world, including selected major producer countries

Country	Area harvested (Ha)	Production (MT)	Yield (kg ha^{-1})
World	18,664,658	228,138,068	12,223
Africa	11,904,448	117,887,743	9,903
Angola	575,000	5,400,000	9,391
Brazil	1,687,272	23,108,076	13,695
Colombia	208,377	2,214,990	10,629
Congo, D.R.	1,839,962	14,929,410	8,114
Ghana	794,440	9,731,040	12,248
India	270,000	6,900,000	25,555
Indonesia	1,290,000	16,723,257	13,963
Nigeria	3,455,000	34,476,000	9,978
Tanzania	660,000	6,888,000	10,422
Thailand	1,030,000	16,870,000	16,378

Source, FAOSTAT 2007

2. Cassava production in Tanzania

Native to tropical America, cassava was introduced to Africa by the Portuguese in the 16th Century (Cock, 1985). The crop was first recorded in Zanzibar in 1799 (Jennings, 1970; Purseglove, 1968). The cultivation of cassava increased gradually until the mid 19th Century, when its ability to withstand a locust attack and to tolerate drought, low soil fertility and poor husbandry made it a valuable famine reserve crop. Tanzania is the sixth largest producer of cassava in Africa – after Nigeria, the Democratic Republic of Congo, Ghana, Angola and Mozambique – producing almost 7 million tons of fresh cassava roots annually (Table 1), with an average yield of 10 t ha^{-1}, ranging from 1.5 to 35 t ha^{-1} (FAOSTAT, 2007;Temu et al., 2002). The average yield has been stagnant around 10 t ha^{-1} for more than two decades due to many factors, including important abiotic and biotic stresses that occurred in the country. However, a doubling of production from 3.5 to 7.8 million tons per year was noted in the 1970s, with the yield increasing from 5 to 13 t ha^{-1}. This increase was due to factors

such as the growth in the export market of dry cassava to Europe for the animal feed industry (FAOSTAT, 2005) and increased land area under cassava production (Figure. 1).
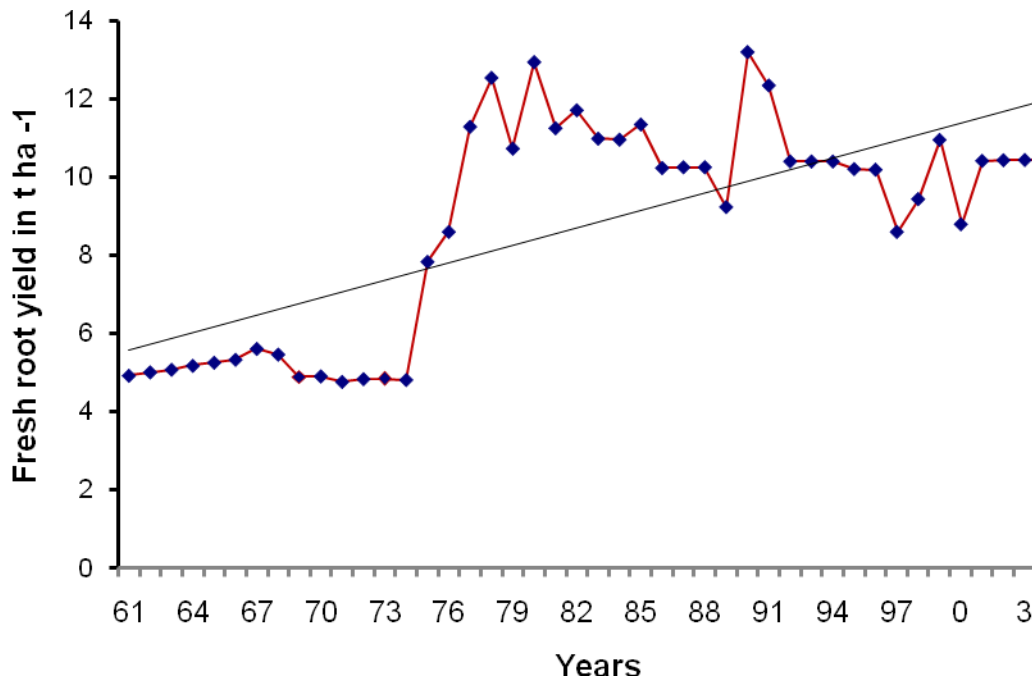
Figure 1: Fresh root yield in tons per hectare in Tanzania from 1961 to 2006 (FAOSTAT, 2007)

In Tanzania, the crop is produced in greatly varying environments. The main producing areas are the coastal belt on the Indian Ocean (humid and sub-humid lowland agro-ecology), the southern zone, the Lake Victoria basin (mid altitude tropical agro-ecologies) and on the shores of lakes Nyasa and Tanganyika (mid to high altitude tropical agro-ecologies). The production of cassava in the southern zone accounts for 32% of the total cassava production in the country, the eastern coastal zone accounts for 18%, the Lake Victoria zone accounts for 13% and the southern highlands for 9%. The central and western zones account for the rest (Herzeberg et al., 2004). Usually, cassava is intercropped with legumes and cereals such as maize and sorghum. The estimated productivity of cassava crops suggests that there is room for improvement since a yield ranging from 1.5 to 35 t ha^{-1} has been reported in different parts and ecologies of the country.

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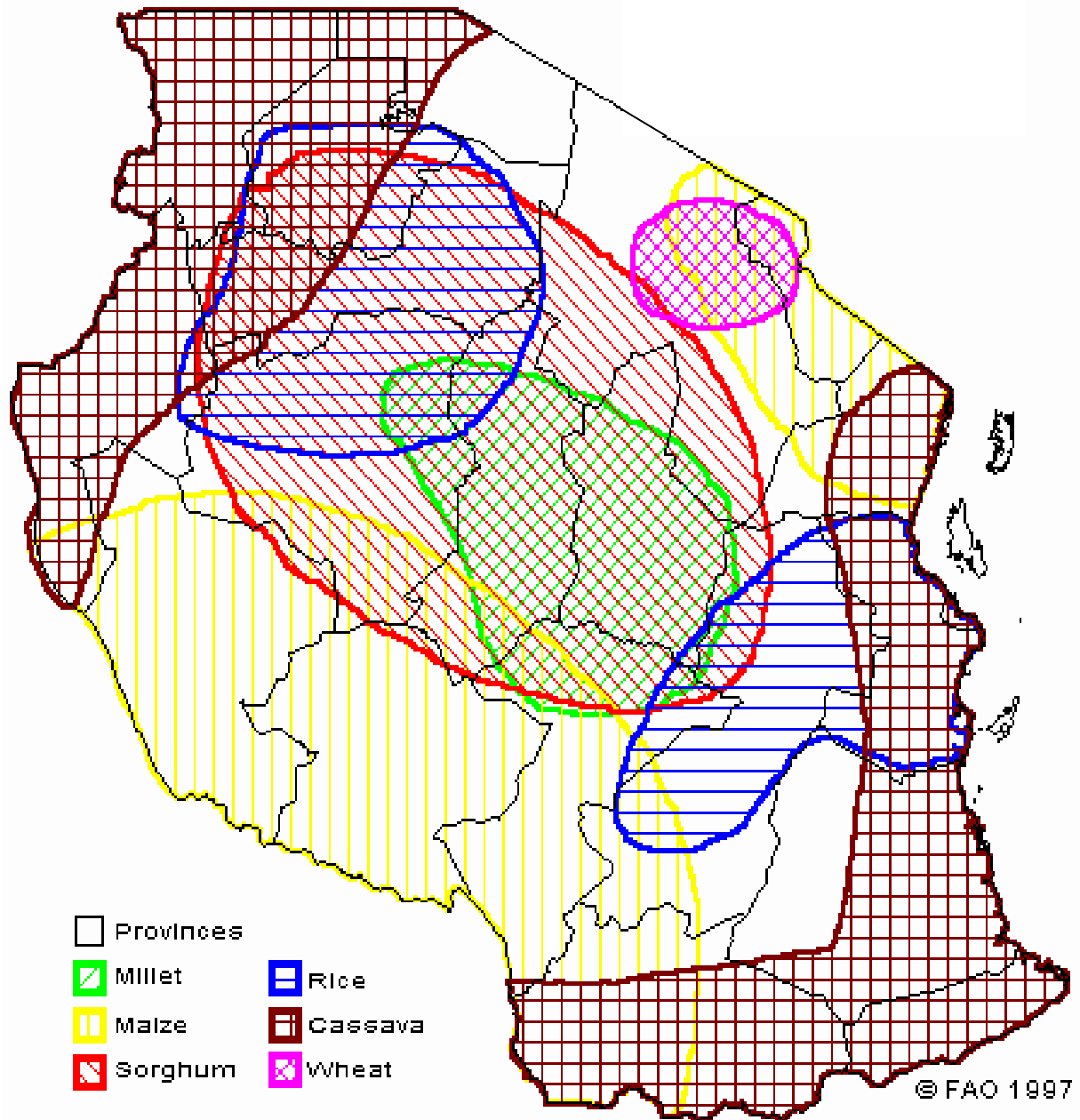
Figure 2 Main crop zones of Tanzania (source FAOSTAT, 1997)

In Tanzania, cassava is a primary or secondary staple food in most households in the four main agro-ecological zones (FAOSTAT, 2005) and is consumed in different ways according to local customs and resources (Table 2). Cassava can be blended with cereals such as maize, sorghum and millet to improve the texture of the stiff porridge 'Ugali'. Reports

indicate that in the 1970s, cassava contributed 12% of the average daily dietary intake per person in Tanzania (Nweke et al., 1998), while in the 1980s, the contribution increased to 24% (Cock, 1985). However, Westby (2002) indicated that in the 1990s the contribution of cassava was 21.6% of the total energy intake of the principal consuming regions. It is estimated that the annual growth of cassava consumption for the period between 1980 and 2000 was 3.4%, which is similar to the estimate for maize (NALRP, 1991). The increased demand for cassava in Tanzania provides justification for the development of improved cassava varieties.

Table 2 Production of starchy staple food in Tanzania in metric tons

Crop	2003	2004
Maize	2,430,000	2,400,000
Cassava (dry weight)	2,067,000	2,067,000
Sorghum	630,000	630,000
Paddy rice	640,159	647,000
Millet	270,000	270,000
Wheat	71,000	71,000
Other root crops (sweet potato, yam, potato)	1,200,000	1,200,000

Source: FAOSTAT 2005.

3.   Cassava production constraints

The major factors limiting cassava production and productivity include the use of genotypes with low root yielding potential, pests and diseases, poor crop management practices, declining soil fertility, inadequate use of inputs, erratic weather conditions, limited access to quality planting material, low adoption rate of improved varieties, poor farm implements and lack of incentives for increased production. However, compared to other crops, cassava excels under sub-optimal conditions, offering the possibility of using marginal land to increase total agricultural production (Cock, 1985).

Different fungal, bacterial, viral and mycoplasma diseases infecting cassava have been reported (IITA, 1990). Of these diseases, cassava mosaic disease (CMD), cassava bacterial blight (CBB), cassava brown steak disease (CBSD) and cassava anthracnose (CAD) are of major economic importance. Important pests are cassava green mites (CGM), cassava

mealybug, and whiteflies. Other pests include; termites, root scales and elegant grasshopper. Whitefly incidence is harmful to cassava only as a vector to CMD and CBSD (Hillocks et al., 2001; Hahn et al., 1979). Cassava mealybugs damage cassava by sucking the sap and hence shoot stunting. Green shoots die due to severe incidence, though die back may or may not occur. Drought stress favours pest incidence and build up (Leuschner, 1976). Green mites feed on young leaves and tender shoots. Usually a 'candle stick' appearance is observed in severe attacks. Economic loss results from the damage to fresh leaves and quality and quantity of tuber production. Cassava productivity could be sustained by using resistant varieties, pests-free and disease-free planting materials, and appropriate crop management practices.

4.   Cassava processing and utilization

Two clusters of cassava, bitter and sweet are of economic importance, as they signify the absence or presence of toxic levels of cyanogenic potential (CNP) (O'Hair, 1990). However, sweetness is not absolutely correlated with low CNP producing ability (Bokanga, 1994). Cases of cyanide exposure and acute intoxication have been reported in Tanzania, Mozambique and elsewhere, but such cases are rare. Cyanide exposure is due to the consumption of insufficiently processed cassava, and occurs mostly during food shortage periods (Mlingi, 1995).

The highly perishable nature of harvested cassava roots and the presence of cyanogenic potential require immediate processing of the storage roots into more stable and safer products (Hillocks, 2002; Westby, 2002). Cassava processing methods involve different combinations of drying, grating, soaking, boiling and fermentation of whole or fragmented roots. The processed products include a wide variety of granules, paste, flours, or starch. Nweke et al. (1998) showed that flour and chips were the most common intermediate products in 90% of the villages in Tanzania. However, cassava roots that are sweet and low in CNP are normally used in fresh form as boiled, roasted, or eaten raw. High levels of CNP observed in some cassava genotypes can be reduced effectively to safe levels by using improved processing technologies for grating, dewatering, and drying. A safe level of cyanogens in cassava flour has been set by the World Health Organization (WHO) as 10 ppm or 100 mg/kg HCN_{eq} (FAO/WHO, 1991).

There is considerable variation in the cassava utilization patterns in different parts of the world. In Africa, the majority of cassava produced is used as human food (88%), with over 50% used as processed products (Nweke et al., 1998). Starch and animal feed are minor uses of the crop in Africa (Westby, 2002). However, attempts were made in several African countries to promote cassava utilization as a commercial feedstuff, with limited success as low international prices for feed grains and overvalued domestic currencies made cassava chips and pellets uncompetitive relative to imported feedstuffs (FAO, 2000). For example, in Tanzania, cassava was utilized in the making of poultry and pig feeds by the Tanzania Feeds Company in the mid 1980s, a practise that was later discontinued as cassava prices were high compared with grains. In contrast, the by-products of cassava processing in Nigeria are gaining popularity among commercial livestock producers (FAO, 2000).

Several large-scale cassava starch factories were installed in the 1970s and 1980s in eastern and southern African countries (in Lira, Uganda; Mwanza, Tanzania; Kitwe, Zambia and in Mombasa, Kenya). However, most of the factories did not operate for long due to a variety of reasons, such as destruction by war and lack of local markets (textile mills and paper industries), shortage of raw materials and low world market prices (SARRNET, 2002; Henry et al., 1998). The Tanzania starch manufacturing company located in Mwanza had the capacity to process 40 t of fresh cassava or 15 t of dry cassava per day (MALD, 1987). A lack of raw material of appropriate varieties was the major bottleneck, which led to the closure of the factory in mid 1980s. Currently, Mohamed Enterprise Company Limited is exploring the possibility of setting up a large-scale starch factory near Tanga town (north-east coast). Several small-scale extraction plants have been established around the coast of Tanzania. It is expected that the demand for varieties with high dry matter content and starch will increase due to the establishment of several processing sites already operating in Tanzania.

Cassava starch is used for the production of starch derivatives, food products; for sizing paper and textiles; and in the manufacture of adhesives (Rickard et al., 1991). Other potential uses include a raw material for ethanol, a binding agent in the timber industry, and in the production of sodium monoglutamate (MSG) (Balagopalan, 2002). Cassava leaves are rich in minerals, protein and vitamins and are consumed in countries such as Tanzania, the Democratic Republic of Congo and Mozambique (Westby, 2002). Expansion of the utilization base of cassava as food and feed, and for new industrial uses, requires the urgent

development of cassava varieties with high root quality, in terms of high dry matter content and starch, as well as high root yields for specific market end-users.

5.   Cassava variety selection by farmers

Nearly all cassava in Tanzania is presently grown by small-scale farmers for use as food and a cash crop. Storage root requirements for the fresh market include taste, the size of the root and low levels of cyanogenic potential in roots (Kawano et al., 1998). For the processing market, cultivars with higher root yield and high starch and dry matter content are required (Kawano et al., 1998). The Collaborative Study of Cassava in Africa (COSCA) conducted in several countries provided much valuable information on the characteristics of improved varieties most sought after by farmers. Prominent among the characteristics are high yield, early bulking and high dry matter content (Nweke et al., 1998). Similarly, Temu et al. (2002) in a study of cassava markets in Tanzania revealed three key attributes that lead to variety acceptance by consumers: high dry matter content, low fibre content and sweetness. Farmers normally select for the desired characteristics over a period of time and cultivars with undesirable characteristics are abandoned. The most frequent reason given by farmers for discarding varieties was late bulking (Hillocks, 2002).

Root dry matter content is believed to be positively correlated with the eating quality especially when the root is consumed after boiling (Kawano et al., 1987). Safo-Kantanka and Owusu-Nipah (1992) studied the cooking qualities of cassava and reported that mealier varieties had a higher content of dry matter and starch. Kapinga et al. (1997) tested cassava varieties on-farm in the Lake Victoria area of Tanzania and reported that improved varieties with relatively low dry matter content were hardly adopted by farmers. Similarly, in the Lake Victoria area, a high yielding improved cassava variety was rejected simply because when processed into flour and cooked into stiff porridge (Ugali) it became watery (or weeping). Therefore, there is a need to include root quality aspects such as starch characteristics in the breeding programme to enhance the adoption of improved varieties.

Cassava storage roots essentially contain large carbohydrate reserves, mainly of starch; therefore, cultivars with high dry matter content are important (Tan and Mak, 1995). In addition, high root dry matter content is important because it ensures a high recovery rate of dried roots (Byrne, 1984). Graham et al. (1999) commented that for the vast majority of

uses, cultivars of high dry matter content are mostly preferred. Participatory plant breeding is important to capture and include desired characteristics by farmers in the breeding programme.

In Tanzania, human food will continue to be the main cassava market. However, animal feed and starch are the principal growth markets in the medium term future. Starch content is the key to nearly every use of cassava. Improved root quality will have the highest overall positive impact on processing and utilization innovations. Breeding offers the possibility of adding value to the products that growers move to the marketplace and therefore, improving starch content by breeding is feasible. The development of high starch varieties that are tolerant to major diseases is of prime importance for cassava development in Tanzania.

6. Research focus

The potential role of cassava in alleviating hunger and generating income through its utilization in the food and industrial sectors (animal feed, food, power alcohol, fermented products and non-starch uses) provides the justification for improving traits such as root yield, dry matter and starch content. In the past, efforts were devoted to improving cassava as a staple food, with an emphasis on generating, adapting and disseminating genotypes with high fresh root yield, resistance to pests and diseases, low CNP and early bulking. These efforts led to the release of varieties for the humid and sub-humid lowlands and for semi-arid areas in Tanzania. However, many of the improved varieties and those clones in the advanced stages of evaluation have been rejected mainly due to a lack of important attributes such as high dry matter content and starch quantity and quality (Kapinga et al*.,* 1997). For cassava to become competitive in the industrial sector, it is imperative to develop varieties that are high yielding, high in dry matter and starch content. However, the genetic variability of cassava for dry matter and starch content has not been fully determined. In other words, there is scanty information on genetic variability for dry matter and starch content. Researchers have given various reasons for the lack of information. Iglesias et al. (1994) and Kawano et al. (1987) suggested that intensive selection for disease resistance and root yield potential in the early stages of the breeding scheme restricted and reduced the availability of genetic variation for dry matter content. In other words, relatively little attention has been paid to the genetic improvement of root dry matter content for an

increased yield. Thus, there is a need to screen the available germplasm to determine its variability for root yield potential, dry matter content and starch content.

7.   Research objectives

The major objective of this research was to develop improved cassava varieties that are high yielding, with high dry matter and starch content; which can be adopted by farmers and different market end-users in Tanzania.

The specific objectives of the research were as follows:

1. Review relevant literature on dry matter content, starch content, yield and yield components;
2. identify farmers' perceptions and preferences for cassava storage root yield, dry matter, root quality characteristics and other traits of agronomic relevance;
3. evaluate and determine variability in root dry matter content, starch, and yield of cassava cultivars in Tanzania
4. develop and evaluate clones for high storage root yield, high dry matter content and starch;
5. determine the inheritance and genotypic variability of dry matter and starch contents in cassava genotypes; and
6. provide a review and conclude the completed research

The content and references of the chapters in this thesis may overlap.

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Chapter 1

Literature Review

1.1   Introduction

A number of studies have been undertaken in the last decade on cassava storage root quality and related agronomic traits relevant to breeders. The objective of this chapter is to critically review current knowledge of cassava breeding for root quality traits (dry matter content and starch) and physiological processes related to its breeding. The review focuses on the cassava plant and its flowering habits, cassava genetic improvement, hybridization in cassava and its techniques, breeding procedures commonly used in cassava, breeding for high dry matter content and starch and the physiological aspects of dry matter accumulation, estimation of dry matter content and starch, starch properties and its challenges. Finally, it highlights correlation between traits in cassava. This chapter forms a framework for reference in this study.

1.2   The cassava plant

1.2.1   Classification of cassava

Cassava is a member of the genus *Manihot*, family *Euphorbiaceae*. The genus has two sections, the *Arborae*, containing tree species, and the *Fructicosae*, containing low-growing shrubs adapted to savannah grassland or desert conditions (Jennings and Iglesias, 2002; Otim-Nape et al., 2001). According to Rogers and Appan (1973), as many as 98 *Manihot* species, all confined to the tropical Americas, have been distinguished. Cultivated cassava belongs to the *Fructicosae* and is regarded as a cultigen unknown in the wild (Rogers and Appan, 1973). All species of *Manihot* have 2n=36 chromosomes, and can be regarded as polyploids (n=18), although the species studied have regular bivalent pairing and behave as diploids (Jennings, 1976). The regular diploid behaviour during meiosis is one of the assumptions for the diallel mating design, hence it is justified to determine the inheritance of cassava root yield, dry matter and starch content using the diallel analysis in this study.

1.2.2   Flowering habit in cassava

Cassava is monoecious, producing both male (pistillate) and female (staminate) flowers on the same plant (Jennings and Hershey, 1985). The female flowers are normally located on the lower part of the inflorescence and are fewer in number than the male flowers, which are numerous on the upper part of the inflorescence (Alves, 2002; Kawano, 1980). On the same inflorescence, the female flowers open one to two weeks before the male flowers (protogyny). Male and female flowers on different branches of the same plant can open at the same time. Usually, cassava is cross–pollinated, thus it is a highly heterozygous plant (Alves, 2002; Jennings and Iglesias, 2002). Sporadic, self-pollination has been reported (Jennings and Iglesias, 2002; Nassar, 2002) but the proportions of self and cross–pollinated seed produced depends on the genotype, plant design and the type of pollinating insect present. Some inbreeding exists in cassava (Nassar, 2002), resulting in high inbreeding depression (Kawano, 2003; Kawano, 1980; CIAT, 1974). Due to its predominantly cross pollinating nature, there is need to control pollination so that only the desired pollinations occur during breeding.

Information about flowering in cassava is scarce (Davies et al., 2005), and some genotypes have never been known to flower (Jennings and Iglesias, 2002). However, flowering is controlled by the complex interaction of a range of genetic and environmental factors (Alves, 2002). A wide variety of flowering types in cassava has been reported (Byrne, 1984), ranging from those with frequent flowering to types that do not flower even after 24 or more months of growth. Flowering may begin very early from six weeks after planting, depending on the cultivar and the environment (Jennings and Iglesias, 2002). Forking or reproductive branching is related to the onset of flowering, depending on the genotype and agro-ecological conditions. Optimum flowering occurs at moderate temperatures of approximately 24℃ (Alves, 2002). According to Kawano (1980), cas sava cannot flower during a long dry season; therefore irrigation of the pollination field during the dry season is important. Knowledge of the optimum flowering period is important so that nurseries can be planted such that crosses will be formed during the period with the best temperatures.

The control of flowering and flowering itself are major challenges in cassava breeding. A valuable genotype may not be used in breeding due to its shyness and non-synchronized flowering (Davies et al., 2005). This is a dilemma for breeders, who must produce shy

flowering types for high yield but require profuse early flowering types for making crosses (Davies et al., 2005; Kawano et al., 1978). Matching the flowering dates of genotypes to be hybridized may present a problem. However, flowering on a single plant usually lasts for more than 2 months (Jennings and Iglesias, 2002). Since male flowers are usually more numerous than female flowers, the number of female flowers available for pollination is a limiting factor for the mass production of hybrid seeds (Alves, 2002; Kawano, 1980). In practice, genotypes to be used as female parents should be planted in larger numbers and staggered in planting dates (Kawano, 1980). Genotypes differ significantly in their ability as female parents in terms of number of seeds set per female flower. The selection of highly fertile genotypes as female parents is a critical factor.

1.2.3   Fruits and seed germination

Cassava fruit generally matures between 75 to 90 days after pollination (Alves, 2002). Rajendran et al. (2005) recorded seed output ranging from 306 to 332 seeds plant^{-1} in one of the improved cassava varieties in India. Seed weight ranging from 95 to135 mg seed^{-1} has been reported elsewhere (Rajendran et al., 2005; Alves, 2002). Cassava seeds usually germinate soon after collection, taking about 16 days on average (Ghosh et al., 1988). However, a lack of quick and uniform seed germination in cassava has been reported (Nassar and O'Hair, 1985), thus presenting a challenge to breeders.

The physiological dormancy of both wild and domesticated cassava seed has been reported (Pujol et al., 2002; Nassar and O'Hair, 1985). Ellis et al. (1981) reported that cassava seeds (*Manihot esculenta* Crantz) are recalcitrant due to the fact that after six months of storage at laboratory temperature and between 5.9% and 1.9% moisture content germination was reduced from 80% to 28%. Rajendran et al. (2005), on the other hand, observed that sexual seeds can be stored under ambient conditions up to 6 months without any appreciable loss of viability, and a gradual loss of viability observed during 6-8 months and after 8 months of storage, which is a sharp decline in germination percentage. However, Kawano (1980) commented that cassava seeds can be stored for about a year under ambient conditions without any serious decline in viability, and much longer at lower temperature and relative humidity. The selection of cassava clones with early germinating seed would permit the use of plant breeding techniques such as mass selection to gradually modify cassava population characteristics.

1.3   Cassava pests and diseases

Although robust in nature, cassava suffers from a number of stresses that must be addressed before it can show its true potential, both as a subsistence crop and an industrial crop. Biotic stresses primarily comprise a range of pests and diseases. African farmers recognize pests and diseases as important production constraints (Ndunguru et al., 2005). Arthropod pests including the cassava green mite (*Mononychellus tanajoa* Bonder), cassava mealybug (*Phenaccocus manihoti* Matile-Ferrero), and whitefly (*Bemisia tabaci* Gennadius) and (*Bemisia afer* Priesner and Hosny) which pose serious damage to the crop, affect the final yield (IITA, 2000). The *M. tanajoa* and *P. manihoti* mainly cause direct physical damage whilst *B. tabaci* is primarily important as a virus vector. Cassava mealybug and cassava green mite are both under effective classical biological control.

One of the major diseases of economic importance is cassava bacterial blight (CBB) (*Xanthomonas axonopodis* f.sp. manihoti) which is the most important non-virus disease (Lozano, 1975). Cassava mosaic disease (CMD) caused by cassava mosaic geminiviruses (CMGs) (Geminiviridae; Begomovirus) and cassava brown streak disease (CBSD) caused by cassava brown streak virus (CBSV) (Potyviridae; Ipomovirus) (Hillocks and Jennings, 2003; Nichols, 1950). Yield losses on susceptible varieties due to CMD have been reported to range from 20 to 95% (Hahn et al., 1979). Unlike CMD, symptoms of CBSD may be found on the roots as brown/yellow, corky necrosis in the starch-bearing tissue, making the severely affected roots unfit for consumption (Hillocks et al., 2001). Cassava brown streak disease can decrease the root weight of the susceptible cultivars by up to 70% (Hillocks et al., 2001). Mtunda et al. (2003) recorded yield losses due to CBSD of up to 64% in Muheza district, Tanzania. These diseases are the biggest threats to the crop's health and productivity.

Recent studies (Ndunguru et al., 2005) have uncovered the presence of six distinct cassava mosaic geminiviruses (CMG) species found to infect cassava in Africa: African cassava mosaic virus (ACMV), East African cassava mosaic virus (EACMV), East African cassava mosaic Cameroon virus (EACMCV), East African cassava mosaic Malawi virus (EACMMV), East African cassava mosaic Zanzibar virus (EACMZV) and South African cassava mosaic virus (SACMV). The report indicate that much variation exists in the CMGs including the evidence that certain CMGs when present in mixtures, employ

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pseudo-recombination or re-assortment strategies and recombination at certain hot spots such as the origin of replication resulting in the emergence of new viruses with altered virulence (Ndunguru et al., 2005). For example, the severe CMD designated East African cassava mosaic virus-Ugandan variant (EACMV-Ug) currently devastating cassava in east and central Africa is a recombination between ACMV and EACMV. Additionally, small satellite DNA molecules (satDNA II and III), which seem to spread with CGMs and have shown to increase disease severity and break resistance in some of the most CMD-resistant varieties, have been discovered (Ndunguru et al., 2005). These emerging CMGs and satellite DNA molecules pose the greatest threat to cassava production and productivity in Tanzania.

The extent of the yield reduction caused by these pests and diseases depends on the variety, soil and climatic conditions, cultural practices and the severity of the pest and disease incidences (Hahn et al., 1979). However, effective control measures include using resistant varieties, pest- and disease-free planting materials, and appropriate crop management systems. Cassava breeders have devoted great efforts to breeding and developing new varieties with moderate levels of resistance to many pests and diseases. However, the consequences of cassava virus infections are not limited to a reduction in crop yield; they include undermining the ongoing efforts in genetic improvement for yield, and quality aspects such as starch and dry matter content.

1.4   Genetic improvement in cassava

In cassava, genetic improvement begins with the assembly and evaluation of broad based germplasm (Ceballos et al., 2004; Poehlman and Sleper, 1995; Hahn et al. 1979). The source populations with high frequencies of genes associated with desirable characters are acquired, followed by the production of new recombinant genotypes derived from selected elite clones (Ceballos et al., 2004; Hahn et al., 1979). Selected genotypes from the initial germplasm evaluation normally enter the hybridization scheme, followed by selection of superior clones in the segregating population (Kawano, 2003; Poehlman, 1987).

1.4.1 Hybridization and selection in cassava

Hybridization in crops is important for evolving new varieties and is achieved by the transfer of genes across different plants, through the exploitation of heterosis and recombination of the desirable traits from different plants (Simmonds and Smartt, 1999; Wricke and Weber, 1986). The recombination of genes occurs only as a result of sexual reproduction (Poehlman, 1987). Since the cassava parent genotypes are highly heterozygous, the selection of suitable parents for hybridization is one of the most important steps in a hybridization programme. Parents are generally selected on the basis of their known performance as varieties and as parents in hybridization programmes. However, selection based on phenotypic performance alone is not a sound procedure (Hallauer and Miranda, 1988), since phenotypically superior lines may yield poor recombinants in the segregating population. Hence, it is necessary that the parents are chosen on the basis of genetic value (Singh, 2003).

The performance of a genotype in hybridization programmes depends on its effectiveness in transmitting heredity characteristics to its offsprings and combining ability (Falconer and Mackay, 1996). If general combing ability (GCA) is more important, a small number of parents with good GCA should be used in hybridization programmes. On the other hand, when specific combining ability (SCA) is important, a large number of parents should be used to produce a large number of the F_1 families (Singh, 2003; Poehlman, 1987). Knowledge of the clones to be used as parents is very important to enhance effective hybridization.

Improvement through hybridization comprises 1) selection of parents; 2) production of F_1 progeny; and 3) selection of superior clones (Singh, 2003). Crossing in cassava is relatively easy (Kawano, 1980; Kawano et al., 1978). Clonally propagated crops are generally improved by crossing two or more desirable clones, followed by selection in the F_1 progeny. Crossing can occur by controlled pollination, carried out manually to produce full-sib families, or in polycross nurseries where open pollination results, in half-sib families (Ceballos et al., 2004). The breeding procedure, then, is essentially the clonal selection (Poehlman, 1987).

1.4.2 Breeding procedures

The major objective of breeding is to improve the characteristic of plants so that they become more desirable agronomically and economically (Singh, 2003; Chahal and Gosal, 2002). However, improvement in some specific traits of certain crops may become a priority objective for various agronomic and economic reasons. The common breeding methods in cassava include: clonal selection, recurrent selection and backcross breeding. Backcross breeding has been used to incorporate genes for disease resistance (Ceballos et al., 2004; Hahn et al., 1979).

1.4.3 Clonal selection

A clone is a group of genetically identical vegetatively propagated from a single plant (Simmonds and Smartt, 1999; Poehlman and Sleper, 1995). Clones are obtained by sexual reproduction, which is necessary to create genetic variability through gene recombination. By crossing clones with superior characters, a source population is created that may be utilized for the selection of new clones (Poehlman and Sleper, 1995). Seeds obtained from the cross are grown into seedlings. Seedlings are exposed to major diseases and pests such as CMD, CBSD, and bacterial blight (CBB). Susceptible seedlings are eliminated (Hahn et al., 1979).

From a mixed variable population, a few hundred to a few thousand desirable plants are selected. Clones from the selected plants are grown separately, without replications (Ceballos et al., 2004; Hahn et al., 1979). The selection is based on visual observations and on breeders' judgement of the value of the clone (Singh, 2003). The replicated preliminary yield trial should be conducted with a suitable standard check. A few superior performing clones with desirable characteristics are selected for the next yield trials. Replicated trials are conducted in several locations along with a suitable standard check. The yielding ability, quality (dry matter) and disease resistance are evaluated. The best clones are then multiplied and released as a new variety (Poehlman, 1987; Hahn et al., 1979).

Alternatively, superior clones may be isolated and propagated as a variety from a genetically mixed population of an asexually propagated species. The progress is limited to the isolation of the best genotype present (Poehlman, 1987). The phenotypic value of a clone is due to

the effects of its genotype, the environment and the genotype x environment interactions (Dhabolkar, 1992). In the early stages of clonal selection, single plants or single plots are considered. The emphasis is to eliminate weak and undesirable plants (Hahn et al., 1979). In later stages, i.e. in replicated yield trials yield and yield components are the basis of selection, and the emphasis is to identify and select superior clones (Jennings and Hershey, 1985; Byrne, 1984). At the clonal stage, starch content has seldom been considered as a trait for selection, hence the loss of genetic variability for starch content.

1.4.4   Recurrent selection

Recurrent selection involves: 1) selecting a number of plants with desirable phenotype, 2) growing, evaluating and selecting the seedling-derived clones grown from seeds produced in the first step, and 3) intercrossing the progenies in all possible combinations (Singh, 2003; Poehlman and Sleper, 1995). At IITA, a recurrent selection system has been used to improve populations for CMD resistance and other agronomic characters, while maintaining a large genetic variation (Hahn et al., 1980). Resistance alone was improved in one cycle, taking 1-2 years; however, it took 4-5 years to combine resistance with high yield potential. Introgression of exotic sources from other continents, especially Latin America, into IITA breeding populations was done after achieving adequate resistance to CMD (Hahn et al., 1980).

1.4.5   Backcross breeding

In the backcross method of breeding, the hybrid and the progenies in subsequent generations are repeatedly backcrossed to one of the parents (Poehlman, 1987). As a result, the progeny becomes increasingly similar to the recurrent parent. Nichols (1947) achieved interspecific hybridisation between cultivated cassava (*M. esculenta*) and other related *Manihot* species, particularly *M. glaziovii*. This was followed by backcrossing to cultivated cassava to recover positive agronomic characters of cassava as well as resistance to CMD. The results from the first backcross were variable. However, an improvement in fertility was noted in the second backcross generation. The production of the F_3 generation by controlled back-crossing to cassava using cassava as the female parent was successful (Jennings, 1976; Nichols, 1947).

In an attempt to transfer the high protein content of the tuberous roots from wild species, hybrids between cassava and M. *tristis* subsp. *saxiola* were used (Bolhuis, 1967; Nichols, 1947). However, efforts to increase the protein content in cassava roots were unsuccessful as the high levels in the initial hybrids were not maintained in the backcross progenies (Asiedu et al., 1994). Although incompatibility systems that prevent crossing among species in genus *Manihot* have not been reported so far, differences among genotypes in their performance as female parents in crossing schemes do exist (Kawano, 1980).

1.4.6 Inbreeding in cassava

Inbreeding raises the frequency of desirable genes by reducing the genetic load of deleterious genes (Ceballos et al., 2004) and improves selection efficiency (Easwari-Amma et al., 1995). In sweet potato for example, it has been observed that inbreeding depression occurs for total storage root yield and to a lesser extent for total storage root number and vine length, yet it does not occur for dry matter content (Komaki et al., 1998). They suggested that for the best method to develop new cultivars with high dry matter content and high storage root yield, the development of high dry matter inbred lines was necessary. These inbred lines can be crossed among themselves or with superior cultivars. The concentration of genes controlling the starch content in a cultivar is essential for the development of the cultivar with high starch content (Komaki et al., 1998). However, inbreeding in cassava has seldom been pursued, particularly due to the time required to obtain high levels of inbreeding (9-10 years) and the high level of inbreeding depression (Ceballos et al., 2004). Tolerance to inbreeding depression can be bred into crops. Fifth generation inbred lines of cassava have been developed at IITA (DeVries and Toenniessen, 2001). In addition, successive generations of inbred lines of cassava that are reasonably homozygous have been reported in four generations in India (Easwari-Amma et al., 1995). The breeding programme in Tanzania may explore inbreeding procedures to concentrate the genes controlling starch content.

1.4.7   Selection and evaluation in cassava

Any breeding programme should have priority research themes and objectives that are clearly established on the basis of the production constraints to be resolved (Hahn et al., 1979) and/or on the ultimate use of the crop (Ceballos et al., 2004). Most of the efforts in the early days of the International Centres (CIAT, IITA) and the national programmes were devoted to improving cassava as a human staple food (Jennings and Iglesias, 2002). The general breeding objectives were: a high yield, resistance to major insect pests and diseases, adaptability to a wide range of environmental conditions, root characteristics and early maturity (Ceballos et al., 2004; Hahn et al., 1979). Relatively little attention was given to the genetic improvement of root dry matter content and starch. Intensive selection for disease resistance and root yield potential have restricted the availability of genetic variability for dry matter content and starch (Iglesias and Hershey, 1994).

Early generation testing is used in self- and cross-pollinated species to estimate the genetic potential of an individual (Fehr, 1987). The early selection in cassava includes seedling and clonal (single row) stages which are based on high heritability traits such as plant type, branching habits and reaction to certain diseases (Iglesias et al., 1994; Hershey, 1988; Hahn et al., 1980) and harvest index (Kawano, 1990). In addition, selection has been based on single plant performance (Ceballos et al., 2004). Seedlings are normally exposed to important diseases such as CMD, CBSD and CBB using spreader varieties, and susceptible seedlings are selected out. This method was implemented in Africa, where CMD is endemic (Hahn et al., 1979) (Appendix 1).

Plants that are low branching (branching height of about 50-100 cm) are discarded because they are associated with heavy branching that tends to lead to a low harvest index and yield (Kawano, 2003; Kawano et al., 1998; Hahn et al., 1979; Tan and Cock, 1979). Seedlings with a short neck (1–3 cm) and fat roots that are uniform, short, and compact are selected. Seedlings from low cyanide populations are selected (Iglesias and Hershey, 1994; Sadik et al., 1974). The selected seedlings are uprooted after 12 months and screened for conformation and root characteristics. Kawano and Thung (1982) suggested that it is important to establish seedling populations at low planting densities to give all plants an opportunity to express their genetic capacity and to minimise the effects of intergenotypic competition. When seedlings are planted at very high densities, it is possible for plants in the population not to express their genotypic ability properly. Competition between neighbouring

genotypes in the clonal evaluation trial may favour more vigorous plant architectures (Kempton, 1997; Kawano and Thung, 1982).

In order to handle a large number of materials at lower costs visual evaluation with few data recording has been a common feature in the first stages of selection (Ceballos et al., 2004). Selection relied heavily on highly heritable traits such as harvest index (Kawano, 2003; Kawano et al., 1998), plant type, and sometime root dry matter and cyanogenic potential (Iglesias and Hershey, 1994). In cassava, the harvest index represents the efficiency of storage root production and is usually determined by the ratio of storage root weight to the total plant weight. However, significant differences in harvest index have been reported among cultivars (Kawano et al., 1978), indicating that it can be used in cassava as a selection criterion for higher yield potential in cassava. However, care should be taken in using the harvest index as a selection criterion due to the differential response of plants to soil fertility and water stress (Cock and El-Sharkawy, 1988)

The clones that perform poorly in terms of establishment, growth and resistance to diseases, and insect pests are discarded (Hahn et al., 1979). Only the selected clones are evaluated for dry matter, yield potential and cyanogenic potential (Iglesias and Hershey, 1994; Hahn et al., 1979). However, it has become apparent that cassava genotypes perform differently at different stages of evaluation and selection (Kawano and Thung, 1982). Byrne (1984) observed that there were significant correlations (r=0.48**) between dry matter content in seedling and single row trials, and suggested that evaluation for dry matter content was feasible at the F_1 stage.

At a later stage, the emphasis of selection shift from highly heritable traits to those of low heritability such as yield. Trials that are considered include preliminary yield trial (PYT), advanced yield trial (AYT) and regional trial (RT). Each plot is replicated twice or more (Ceballos et al., 2004). At this stage, selection is based on yield per plot, dry matter, CNP levels, consumer acceptance, and adaptation of the crop (Hahn et al., 1979). The trials are conducted in several locations covering a wide range of environments. Stability across location is given greater weight. Elite clones are evaluated on-farm for farm level testing and farmer evaluation. The clones that are the most popular with farmers are multiplied and distributed.

1.5   Breeding designs

1.5.1   Gene action and inheritance

The gene, the basic unit of inheritance, is responsible for the transmission of characteristics from one generation to the next (Chahal and Gosal, 2002). Crop improvement involves both gene actions and gene inheritance. The action of genes determines the expression of every characteristic of a plant, such as its morphology, response to environmental conditions, and yielding ability. Physiologically, gene action reflects gene differences that provide the basis for the selection of desirable genotypes in plant breeding (Sleper and Poehlman, 2006; Rasmusson and Gengenbach, 1983). Gene inheritance is the transmission of genetic information to succeeding generations (Falconer, 1989). Inheritance, as explained by the classical Mendelian genetic pattern (Klug and Cummings, 1999; Poehlman and Sleper, 1995), indicates the expression of one dominant, when two contrasting characters are brought together in a cross and the other one is recessive (latent) in F_1 and in F_2 the two characters segregate and express themselves phenotypically. The efficient recovery and maintenance of desirable genes transmitted from selected parents to their progeny requires knowledge about gene inheritance (Falconer and Mackay, 1996).

Multiple genes affect the phenotypic expression of a quantitative trait in any of the following four gene actions: additive, dominance, epistatic and overdominance. Additive genes act cumulatively or additively to a quantitative character, while dominance gene effects are deviations from additive effects (Bernado, 2002; Falconer, 1989). Epistatic effects are a result of non-allelic gene interactions, while over-dominance effects occur when each allele contributes a separate effect, and the combined alleles contribute an effect greater than either allele separately (Falconer and Mackay, 1996; Sharma, 1995; Hayman, 1958).

The majority of physiological characters i.e. dry matter content, yield and disease resistance are inherited quantitatively (Poehlman and Sleper, 1995). The varied expression of the character is continuous and can be measured (Rasmusson and Gengenbach, 1983). The quantitatively inherited characters are conditioned by polygenes with small individual effects and often there is a sizeable environmental effect (Falconer, 1989; Rasmusson and Gengenbach, 1983).

Different mating designs e.g. diallel or North Carolina II, allow for the estimation of two important genetic parameters for the set of genotypes involved: (a) the average performance of parents in crosses, which estimates the breeding value of a given genotype due to additive gene effects, known as GCA, and (b) the deviation of individuals crosses from the average performance of parents, due to specific allelic combinations or dominance effects, or SCA (Falconer, 1989).

1.5.2 Estimation of genetic variances

Phenotype is a joint expression of genotypic and environmental effects. The main interest of a breeder is to determine what proportion of the phenotypic expression is due to genotypic and environmental effects (Hallauer and Miranda, 1988). The genotypic effect for a particular genotype is the difference between the mean of all the phenotypes with that genotype and the mean of all the phenotypes in the population (Falconer, 1989; Cockerham, 1956). In predicting what improvement can be expected from inbreeding and crossing, the variance between crosses is important. Therefore, mating designs that develop progenies for evaluation should be considered for the estimation of components of variance (Falconer, 1989; Hallauer and Miranda, 1988).

The purpose of using the mating designs is: firstly to furnish the breeder with information on the genetic control of the character under investigation. Secondly, it is to generate a breeding population that can be used as a basis for the selection and development of potential varieties (Sharma, 1995; Dabholkar, 1992). This in turn will enable the breeder to choose an appropriate breeding strategy and so assess the progress that can be expected for a given selection intensity (Hill et al., 1998). Dabholkar (1992) and Cockerham (1963) classified mating designs as one, two, three and four factor designs, depending upon the number of ancestors per progeny over which control is exercised.

A number of mating designs have been described (Kearsey and Pooni, 1996; Hallauer and Miranda, 1988; Mather and Jinks, 1982). These include: biparental progenies (BIP), North Carolina I (NCI) (Nested design), North Carolina II (NCII), North Carolina III (NCIII) and Diallels. In all mating designs, the individuals are taken randomly and crossed to produce progenies which are related to each other as half-sibs or full-sibs. A form of multivariate analysis or the analysis of variance can be adopted to estimate the components of variance

(Bernado, 2002; Chahal and Gosal, 2002). The expected values of these variances in terms of different components of genetic variance i.e. additive, dominance, and epistasis are determined by equating with the observed values to estimate the components of genetic variation. Common mating designs such as diallel cross, North Carolina designs (I, II and III), line x tester and partial diallel are two factor designs. The triallel and quadriallel crosses are three and four factor mating designs, respectively (Bernado, 2002; Hill et al., 1998; Hallauer and Miranda, 1988). A set of half-sib families or polycross progenies constitute on one factor design (Hill et al., 1998; Dabholkar, 1992). The choice of the mating design depends primarily on simplicity of the information provided by the design and its interpretation.

However, at the early stages of a breeding programme, additive genetic variation is more important (Sprague and Tatum, 1942). Non-additive effects become more important when selection proceeds because the selected material has greater similarity, thereby largely eliminating additive effects. The particular mating design chosen should reflect these processes.

1.5.3   Polycross design

The polycross is a mating arrangement for intercrossing a group of cultivars or clones using natural hybridisation in an isolated crossing block (Stuber, 1980). A polycross design is frequently used for forage grasses and legumes, sweetpotato, cassava and sugarcane (Poehlman and Sleper, 1995). The purpose of the polycross is to provide an equal opportunity for each entry to be crossed with every other entry; the field layout is the critical feature of the design (Wright, 1965). Progeny from each entry have a common parent in the polycross (Stuber, 1980). Polycross design in cassava does not prevent self-pollination, but it produces considerably more cross-bred seeds than controlled pollination methods (Jennings and Iglesias, 2002).

A minimum effort for intermating a group of entries is required in the polycross. Deviations from random mating may occur unless all entries flower simultaneously (Stuber, 1980). Early flowering cultivars may be delayed to synchronise mating. Emasculation of plants located near an intercrossing population may be applied (Jennings and Iglesias, 2002; Byrne, 1984). The use of male sterile genotypes is another alternative to minimise self-pollination. Male

sterility could be due to either male flowers dropping before they reach maturity or a male flower fully develops, but the anthers do not contain any pollen (Kawano, 1980). In polycross design, half-sib families are generated which are frequently used for evaluating general combining ability (GCA). In addition, the design is often used for generating synthetic cultivars and may be used for recombining selected entries or families in recurrent selection programmes (Stuber, 1980)

The variation measured in a progeny test can be partitioned into within and between maternal groups. Like the paired cross (biparental) design the polycross generates insufficient statistics to estimate all the parameters. Nevertheless, an estimate of the additive genetic component can be calculated from between maternal groups if dominance is assumed to be absent (Hill et al., 1998). In a polycross, the breeder has no control over the pollen source (Kawano, 1980). Therefore, doubt arises about the actual relationship among the offspring of a particular mother. A polycross can only yield a pure half-sib family if every pollen grain involved in the pollination of a maternal plant comes from a different male; this is an unrealistic assumption (Hill et al., 1998). In practise, therefore, maternal progenies will be a mixture of full- and half-sibs. Consequently, the variance between maternal groups will overestimate the additive genetic component, even if dominance is assumed to be absent.

The polycross design is ideally suited for identifying those mother plants with superior genotypes, as judged by the performance of their progeny in out-breeding species (Hill et al., 1998; Hallauer and Miranda, 1988). The estimation of GCA for a particular line depends upon the mating design (Sharma and Sain, 2004). The GCA is essentially the departure of its progeny mean from the mean of all lines included in the trial. In theory, therefore, it is the difference between maternal groups that measures variation in their GCA. Improvement in cross-fertilized crops, such as legumes, maize, rye requires genotypes with high GCA (Hill et al., 1998). The cassava improvement programme in Tanzania has been implementing a polycross design, and therefore information on variance components for Tanzanian germplasm is lacking.

1.5.4   The North Carolina II mating design

The North Carolina II (NC II) mating design is a factorial design that has been modified from North Carolina I (NC I) by Comstock and Robinson (1948). It is used to estimate genetic

variances and to evaluate inbred lines for combining ability (Stuber, 1980). It involves different sets of parents used as males and females. In NCII, an equal number of males and females is randomly selected from an F_2 population; each male is crossed with each female creating female half-sib (HS) groups as well as male HS groups (Kearsey and Pooni, 1996; Dabholkar, 1992). This is accomplished by a systematic crossing programme in which males and females are mated in all possible combinations to give progeny families. Reciprocal crosses may be carried out to analyse maternal effects (Hill et al., 1998; Hallauer and Miranda, 1988). The mean squares for males and females supply separate and independent estimates of the additive component of variation, viz- 1) variance due to males, and 2) variance due to females. Similarly, the interaction mean squares between males and females yield an estimate of the non-additive genetic variance (dominance variance).

The difference between the mean performance of the progeny of a given male and the mean of the progeny from all the males is the GCA. It reflects how well the genes combine, on average, to produce the best progeny when crossed to a random sample of females in the population. Hence, the mean square (MS) between HS family groups is often referred to as the GCA MS. Any significant deviation from the mean performance of the progeny must be due to dominance or epistatic effects. These deviations, specific to individual crosses, are measured by the 'male x females' MS in the ANOVA of the NCII (Kearsey and Pooni, 1996)

The NCII enables the inclusion of a large number of parents in the experiment (Hallauer and Miranda, 1988). The expectation of males and females for design II are equivalent to GCA, and the male x female source of variation is equivalent to the SCA variation of the diallel analysis. Since there are two sets of parents in design II, there are two independent estimates of GCA. Provided the number of males and female parents are the same (i.e. $n_1=n_2=n$) then the extent of the maternal effects is determined from the variance ratio MS_F/MS_M (Kearsey and Pooni, 1996). The design provides a test of significance and estimates of additive and dominance variances (V_A and V_D), hence heritability estimates can be calculated (Kearsey and Pooni, 1996).

1.5.5   Diallel design

The diallel cross is a set of all possible matings between several genotypes (Stuber 1980; Griffing, 1956a; Hayman, 1954). Diallel crossing schemes and analyses have been

developed for parents that range from inbred lines, clones or individuals. The mating design permits an estimation of the magnitude of additive and non-additive components of heritable variance. Hallauer and Miranda (1988) commented that although extensive theoretical research and discussion have been presented, the main problem arises from the interpretations and inference that can be made about estimates obtained from analysis of the diallel crosses. Diallel analysis is based on the following assumptions (Dabholkar, 1992; Hayman, 1954): 1) normal diploid segregation, 2) lack of maternal effects, 3) absence of multiple alleles, 4) homozygosity of parents, 5) absence of linkage among genes affecting the character, 6) lack of epistasis and 7) random mating.

Most diallel experiments are restricted to the estimation of GCA and SCA mean squares and effects (Sharma, 1995; Dabholkar, 1992; Baker, 1978). The diallel analysis, although effective and widely used, does not provide estimates of non-allelic interactions (Sharma and Sain, 2004; Hill et al., 1998). Significant epistatic variation clearly indicates the role of epistatic gene actions besides additive and dominance gene actions, which play a major role in the expression of heterotic potential (Stuber and Moll, 1974; Brim and Cockerham, 1961; Hayman, 1958). Perez et al. (2005) reported significant epistatic effects in fresh root yield of cassava combined with a large dominance variance. A major disadvantage of the diallel is the large number of crosses generated in the mating scheme. Thus, requirements for space, seed, and labour involved in the crossing block and in the experimental evaluations usually limit the number of parents to no more than eight to ten (Stuber, 1980).

Diallel methods proposed by Griffing (1956b) determine the combining ability of lines and characterises the nature and extent of gene action in plants and animals (Christie and Shattuck, 1992). Griffing's analysis allows the option to test for fixed (Model 1) or random (Model 2) effects. Four methods of diallel crossing includes: 1) method 1 (full diallel), the parents, F_1 and reciprocals included; 2) method 2 (half diallel), parents and F_1's included, but no reciprocals; 3) method 3, F_1's and reciprocals included, but no parents and 4) method 4, F1's included, but no reciprocals or parents. No genetic assumptions on combining ability are required in Griffing's analysis. In addition, reliable information on the combining potential of parents is indicated. The best parental combiners can be crossed to identify the optimal hybrid combinations or hybridised with the intention of selecting promising genotypes within the segregating generation (Christie and Shattuck, 1992).

General combining ability measures the average performance of a parent in hybrid combination. When the performance of a hybrid is relatively better or worse than would be expected on the basis of the average performance of the parents involved is the SCA (Falconer and Mackay, 1996). A relatively large GCA/SCA variance ratio suggests the importance of additive gene action effects, and a low ratio implies the presence of dominant and/or epistatic gene effects (Kearsey and Pooni, 1996; Christie and Shattuck, 1992; Dabholkar, 1992). Where the SCA is small relative to the GCA, the performance of the single cross progeny can be predicted on the basis of the GCA of the parents. However, the choice of Griffing's methods depends on: 1) researcher preferences; 2) the characteristic of the crop; and 3) the trait under evaluation (Christie and Shattuck, 1992).

The controversy over diallel crosses is centered on three issues: 1) The choice of design; 2) the nature of the population under test (ancestral or descendant); and 3) the type of analysis and the assumptions required (Christie and Shattuck, 1992; Wright 1985). To avoid much of the controversy and criticism, breeders need to consider carefully the goals of their research or the level of analysis required. Wright (1985) and Bray (1971) suggested three possible levels of analysis: 1) estimation of general and specific combining ability; 2) estimation of genetic variance components; and 3) complete genetic analysis.

According to Christie and Shattuck (1992), the GCA effects for each parent and the SCA effects for each cross may be estimated, and no assumptions are necessary with regard to a reference population. Comparison can be made based on the best parents or parental combinations selected. The parents may be a selected or fixed group or a random sample from an ancestral reference population, in which case the variance of GCA and SCA can be estimated as well. Baker (1978) suggested that diallel analyses should be used only to estimate combining ability and to attempt to do anything more would involve assumptions which would be difficult to meet.

To estimate variance components, a reference population is required which is in the Hardy-Weinberg equilibrium (Bernado, 2002; Christie and Shattuck, 1992). Authors (Christie and Shattuck, 1992; Wright, 1985; Griffing, 1956a) have suggested two possibilities for generating a reference population, i.e. ancestral or descendant. The ancestral population is one from which the diallel parents can be considered a sample or from which they were derived by inbreeding without selection. Unbiased estimates of V_A and V_D will be obtained

from such a population only if the parents are excluded in the analysis (Dabholkar, 1992). If the ancestral reference population is used, the assumptions are that of no epistasis and no reciprocal effects (Christie and Shattuck, 1992). The F_1s are assumed to be a sample of crosses from the population, but parents and especially their S_1 (one generation of self-pollinated) offspring should not be considered as a part of the ancestral population. Therefore, data from F_1s should be used to estimate variance components such as in method 3 or 4 of Griffing (1956b) (Christie and Shattuck, 1992). A descendant reference population is the equilibrium population generated by repeated cycles of random mating among the diallel parents. This population relates to the genetic properties of the parents (Wright, 1985). It is this population which is defined when assuming a random distribution of genes among parents. The complete diallel set should be included; hence method 1 is appropriate (Christie and Shattuck, 1992). This is the full genetic analysis, devised by Jinks and Hayman (1953), for which parents are required and for which the assumptions can be used. According to Griffing (1956a), it is often advisable to include parents and use methods 1 or 2, especially for inbreeding species. It is impossible to estimate the genetic components of variance if parents are not included.

1.5.6 Partial diallel

As the number of parents increases, diallel crosses become unmanageable in terms of time, labour and physical resources. A sample of crosses can be grown and analysed to obtain reasonable estimates of variance genetic components (Christie and Shattuck, 1992). In a partial diallel, the relative proportion of the degree of freedom attributable to GCA effects increases, while the precision is reduced by the decrease in the expected value of the GCA mean square (Kempthorne and Curnow, 1961). Partial diallels are constructed so that each parent is represented in the same number of crosses. Kempthorne and Curnow (1961) mentioned three advantages for the partial diallel cross: 1) selection can be among crosses from many parents; 2) the GCA of the parents will be estimated with less precision, but larger gains may result from intense selection among a larger number of parents; and 3) where the parents represent a population, the variance for general combining ability can be estimated more accurately. Moreover, a partial diallel has an advantage over the complete diallel where an incomplete and irregular series of crosses have been made which must be evaluated (Hill et al., 1998; Tai, 1976). However, the usefulness of a partial diallel depends

on its size, because of its statistical estimates based on only a small number of crosses may be far removed from the actual values for the population of parents (Hill et al., 1998).

In a partial diallel, high SCA variances can lead to inconsistencies in the ranking of parents for combining ability (Hill et al., 1998; Bray, 1971). Characters for which the parents exhibit SCA are particularly prone to misinterpretation. Therefore, partial diallels should be confined to those characters which exhibit a greater proportion of additive rather than non-additive variation (Hill et al., 1998). Because of these limitations the partial diallel is not commonly used. The analysis of variance of a partial diallel is similar to that presented by Griffing (1956a) for the four experimental methods (Hill et al., 1998).

To summarise, polycross design has been used extensively in cassava breeding. However, polycross design does not generate sufficient statistics to estimate all the parameters. In addition, in polycross the maternal variance (σ^2_{BM}) provides an overestimated additive genetic component (Hill et al., 1998). The North Carolina II and diallel designs provide the same type of information and similar tests of the hypothesis. In this research, the diallel design will be implemented based on the amount of information which the design supplies, the characteristic of the crop and the traits under evaluation. In order to capture information, all possible crosses will be made with the parental lines. An attempt to determine the GCA and SCA will be made. This information has been lacking for the Tanzanian cassava germplasm.

1.6 Breeding for high dry matter and starch content

1.6.1 Cassava root yield

Fresh root yield multiplied by the root dry matter percentage constitute the dry matter yield of cassava (Kawano et al., 1987). Traditionally, cassava root yield is expressed in fresh root weight. However, there are significant varietal differences for root dry matter content (CIAT, 1976). The total photosynthesis of the crop sets the ceiling for the dry biomass, which is to be shared among fresh root yield and dry matter content (Kawano et al., 1998). When the genetic variation in the dry biomass is ample, fresh root yield and dry matter content can be handled largely as independent characters. As breeding advances, the capacity of the breeding population may approach the physiological ceiling of photosynthetic assimilation.

Then, fresh root yield and dry matter content become components competing for the same resources at a given harvest index (Kawano and Takahashi, 1968). Kawano et al. (1987) commented that there was no indication of a negative correlation between fresh yield and dry matter content, which suggest that the plateau has not yet reached. Consequently, selection for either fresh yield or dry matter can be done independently. Studies at CIAT and IITA have established that dry matter content and starch content are closely correlated traits (r=0.81) (IITA, 1974; CIAT, 1975), suggesting that indirect selection can be applied to improve starch content.

1.6.2 Dry matter content

The concentration of dry matter in cassava roots can vary from 15 to 45% depending on the age of the crop plus the genotype and environmental conditions (Babayoko et al., 2009; Okechukwu and Dixon, 2009; Ojulong et al., 2008; Graham et al., 1999) thus providing the potential for selection. On average, about 90% of root dry matter is carbohydrate, with 4% crude fibre, 3% ash, 2% crude protein and 1% fat (Kawano et al., 1987; Lim, 1968). This makes dry matter an important trait for cassava producers since it is a crop grown largely for its carbohydrate content (Byrne, 1984). High root dry matter content is important especially when roots are used as food, feed and industrial raw materials (Tan and Mak, 1995). Iglesias et al. (1994) reported that root dry matter content segregated either independently or was positively correlated with root yield, indicating that both traits could be improved simultaneously. However, dry matter content is not associated with fresh root yield, although it is still uncertain whether a high level can be maintained when yields are high and that progress in one may require sacrifice in the other. Heritability of dry matter content has been observed to be intermediate to high (Kawano et al., 1987), and the trait can be improved by simple breeding techniques such as phenotypic mass selection to exploit the additive variations.

1.6.3 Partitioning of dry matter into cassava storage root

In cassava, the partitioning of dry matter into different parts of the plant varies during the growth cycle (Figure 1.1). The allocation of dry matter to the storage roots varies from almost zero during the early growth stages to nearly 80% of the daily dry matter production during the late growth stages (Ekanayake et al., 1997). Between 60-75 days after planting

(DAP), cassava accumulates dry matter more in the leaves than in the stems and storage roots (Alves, 2002). Then accumulation in the storage roots increases rapidly, reaching 50–60% of the total dry matter around 120 DAP (Howeler and Cadavid, 1983). Thus selection for dry matter content should not be performed before 120 DAP.
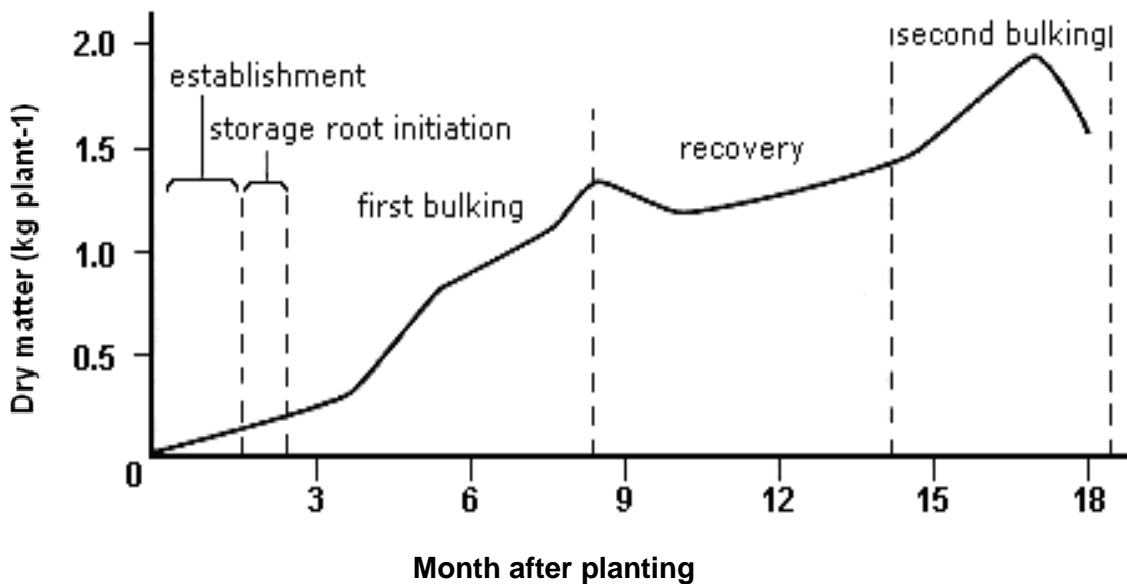
Figure 1.1 Dry matter accumulations in cassava storage roots (source: www.iita.org)

Genotypes differ in the duration of the maximum rates for dry matter accumulation, depending on growing conditions (Alves, 2002). Suggesting that breeders can select for different number of days to maximum dry matter accumulation, depending on the environment in which varieties would be deployed. A maximum rate of dry matter accumulation attained at 3-5 months after planting (MAP) has been reported under tropical conditions where the growth rate is fastest (Howeler and Cadavid, 1983). Similarly, Oelsligle (1975) observed a maximum rate of dry matter accumulation at 7 MAP at high altitude. Kawano and other workers (1987) reported that root dry matter content tended to be higher at 8 MAP rather than 12 MAP, and higher at the beginning of the dry season than at the beginning of the wet season, because during this period starch material is hydrolysed as a source of energy for the growing leaves, leaving roots with less starch. The importance of

growing conditions in determining the maximum rates for dry matter accumulation suggests that the germplasm should be evaluated under different environments to estimate the possible problem of G x E during selection.

The dry matter accumulation depends on the availability of photo-assimilates and the sink capacity of the storage roots (Alves, 2002). Cock et al. (1979) assumed that the storage roots received only those assimilate remaining after the requirements for shoot growth had been satisfied. It is suggested that vigorous genotypes produce large amounts of stems and leaves while root production is slow, and less vigorous genotypes produce relatively few stems and leaves but translocate most of their dry matter to the roots, which become the dominant sink after the third month (Howeler and Cadavid, 1983). Varieties that branch six to eight weeks after planting and six to eight times a year with four branches formed on each occasion, allocate too little of their resources to the roots (Cock et al., 1979), suggesting that they are low yielding.

1.6.4 Estimation of dry matter content

There are essentially two methods for determining the dry matter content in cassava. Specific gravity method is a quick method for determining root dry matter content. The other method is the forced oven dry method (Jennings and Iglesias, 2002; Kawano et al., 1987; Wholey and Booth, 1979). Usually unpeeled fresh roots are weighed in air and then in water or by passing samples through a series of sodium chloride solutions of increasing specific gravity to find the one with the lowest specific gravity in which samples will float (Jennings and Iglesias, 2002). Keating et al. (1981) observed a linear relationship between specific gravity and dry matter content by calculating a regression model. Similar relationships have been reported by several researchers working in different countries (Kawano et al., 1987; Wholey and Booth, 1979; CIAT, 1976) (Table 1.1). However, root dry matter content (as a percentage of fresh storage root yield; RDMC) has been reported to vary depending on genotypes and the environment (Nassar, 2002; Kawano et al., 1987; Wholey and Booth, 1979). The RDMC regressed on storage root specific gravity provides a linear regression model that determines estimates of RDMC and starch content (Bainbridge et al., 1996). The formula calibrated at CIAT is commonly used in Africa. However, there is a limitation that calibration of the method should be done for fresh cassava grown under diverse conditions of environment, soil type, age at harvest etc.

Table 1.1 Linear regression equations developed by different researchers for determining dry matter percentage

Linear regression	R^2	Country of Origin	Reference
Y= 199.1x - 189.1	0.95	Australia	Keating et al. (1981)
Y= 142.3x - 124.9	n/a	Malaysia	Wholey and Booth (1979)
Y= 158.3x - 142.0	0.84	Colombia	CIAT (1976)
Y= 159.1x - 147.0	n/a	Virgin Islands	Krochmal and Kilbride (1966)
Y= 239.2x - 244.8	n/a	Madagascar	Cours G. (1951)
Y= 271.7x - 287.6	n/a	Madagascar	Cours G. (1951)

Key: Y= dry matter percentage; x = mass in air/ (mass in air – mass in water) = specific gravity; n/a = information not provided

1.6.5 Inheritance of dry matter content in cassava

Although little progress in understanding the inheritance of the agronomic traits has been achieved in cassava (Jaramillo et al., 2005; Ceballos et al., 2004), few studies conducted on genetic analyses suggest that inheritance of root dry matter content is controlled by polygenic additive factors (Jaramillo et al., 2005; Perez et al., 2005; Kawano et al., 1987). Sakai (1964) working on the sweet potato crop reported that dry matter content is controlled by additive gene effects and the total storage root yield by dominant gene effects.

In an attempt to generate quantitative data in relation to the inheritance pattern in cassava, Jaramillo et al. (2005), using diallel analysis, observed that the SCA effects were relatively more important for the root yield than GCA effects. In addition, the GCA was reported to be high and important for harvest index, plant architecture and dry matter content. Hence, dry matter content was additively controlled. Perez et al. (2005), on the other hand, recorded contrasting results, that GCA was significant for all traits of agronomic relevance except for fresh root yield and dry matter content. They further commented that fresh root yield was the only trait with significant epistatic effects, which combined with a large dominance variance, suggesting the prevalence of non-additive effects. For harvest index and dry matter content, SCA accounted for about 35% of the F_1s crosses' sum of squares (Perez et al., 2005). However, in studies by Easwari-Amma et al. (1995) in India, it was observed that both additive and non-additive gene effects were important in the control of agronomic traits of relevance. They reported that storage root yield and dry matter content indicated the

predominant role of non-additive gene action in the expression of character. However, further studies are required to understand the gene action controlling dry matter content and starch.

1.6.6   Starch in the storage roots

Starch deposition in the roots of cassava commences soon after the development of secondary xylem tissue some three weeks after planting (Hunt et al., 1977). The majority of the starch grains accumulate within the amyloplasts in parenchyma cells of the thickened roots (Wholey and Booth, 1979). The key step in starch biosynthesis in plants takes place inside the amyloplasts where the enzyme adenosine diphosphate glucose pyrophosphorylase (AGPase) catalyses the synthesis of ADP-glucose from Adenosine TriPhosphate (ATP) and glucose-1-phosphate (Hannah and James, 2008). Researchers have reported maximum starch content obtained at 8 MAP (Sriroth et al., 1998a; Ketiku and Oyenuga, 1972). Cock (1976) indicated that maximum starch content was obtained between 8 and 12 MAP. In contrast, Obigbesan and Agboola (1973) observed peak starch content at 15 MAP. However, starch yield declines after the plant reaches maturity, whereafter, the fibre content increases (Obigbesan and Agboola, 1973). In order to attain the maximum starch yield, the optimum age for harvesting cassava differs according to the variety. The age of the crop at which maximum fresh root yield is attained may not necessarily be the same as that of maximum starch yields (Wholey and Booth, 1979). Cock (1976) commented that variety differences exist not only in the starch content of roots but possibly with the time of maximum starch content.

1.6.7   Starch content, composition and properties

The main constituent of cassava carbohydrate is starch. On a dry weight basis, values of starch ranging from 74 to 85% of the total carbohydrate content have been reported for a number of cassava cultivars, using different analytical techniques (Sanchez et al., 2009; Ceballos et al., 2007; Onitilo et al., 2007; FAO, 2005; Rickard et al., 1991; Rickard and Behn, 1987; Wholey and Booth, 1979). Nuwamanya et al. (2010) obtained a much wider range of starch content from 70.4 to 93.8%. Similarly, starch content ranging from 21.2 to 27.8% of the fresh root weight has been reported (Abera and Rakshit, 2003; Tan and Mak,

1995). Other carbohydrate constituents include sugars (sucrose, maltose, glucose and fructose) in limited levels, dextrose and dextrin (Ketiku and Oyenuga, 1972). Among the sugars in cassava carbohydrates, sucrose is prominent, accounting for 70 to 80% of the total sugars (Wholey and Booth, 1979)

Cassava starch granules can be fractionated into two polymers namely amylose and amylopectin (Rickard et al., 1991; Wholey and Booth, 1979). Amylose is a linear polymer consisting of (1-4) linked α-D-glucopyranosyl units, while amylopectin is a highly branched polymer of α-D-glucopyranosyl units, primarily linked by (1-4) bonds, with branches resulting from (1-6) linkages (Rickard et al., 1991) (Table 1.3). The amylose content of cassava starch, evaluated using a variety of methods has been reported to range from 14 to 24% (Freitas et al., 2004; Rickard et al., 1991; Kawabata et al., 1984; Wholey and Booth, 1979; Ketiku and Oyenuga, 1972). Wheatley et al. (1992) studying CIAT germplasm reported a range between 15 and 28% amylose in the roots of cassava plants. In order to understand the variability in the amylose content of Tanzanian germplasm, there is a need to determine amylose content in cassava.

Starch quality is influenced by the amylose content, and for good cooking varieties is 21%, for industrial varieties (more waxy types) 15% and for multipurpose varieties around 17% (IITA, 1977). A range between 15 and 28% amylose has been reported from CIAT germplasm (Wheatley et al., 1992). Zero amylopectin (non waxy) mutants have been detected. However, variations in the ratio of amylose to amylopectin could open new markets for cassava starch (Jennings and Iglesias, 2002). Amylose content determines the stickiness of cooked staple such as rice (*Oryza sativa*). The waxy endosperm of rice consisting of up to 2% amylose, shows low water absorption and expansion on cooking and the grain become sticky (glutinous). Non waxy (non-glutinous) rice may have low (20%), intermediate (21-25%) and high (25%) amylose contents (Singh, 2003). According to Singh (2003) amylose content is governed by a single gene, but is affected by environmental factors.

1.6.8   Granular characteristics of cassava starch

Starch structure properties differ according to the botanical source and stage of development of the plant (Sriroth et al., 1999). The functional properties of the starch are affected by both genetic and environmental conditions (Asaoka et al., 1992). The starch granules of cassava are compound granules and are reported to vary in shape and size (Table 1.2) (Rickard et al., 1991). The granules are found to increase in size only over the first 5-6 months of growth and then remain nearly uniform throughout the 18 month period (Moorthy and Ramanujan, 1986).

Table 1.2 Properties of the amylose and amylopectin components of starch

Property	Amylose	Amylopectin
General structure	Essentially linear	Branched
Colour with iodine	Dark blue	Purple/red
Max. of iodine complex	~ 650nm	~ 540nm
Iodine affinity	19 - 20%	< 1%
Average chain length (glucose residues)	100-10 000	20-30
Degree of polymerization (glucose residues)	100-10 000	10 000-100 000
Solubility in water	Variable	Soluble
Stability In aqueous solution	Retrogrades	Stable
Conversion to maltose by crystalline β-amylase	~ 70%	~ 55%

Source: Shannon and Garwood, 1984

1.6.9   Starch yield

Starch yield in cassava is a product of fresh storage root yield and starch content. Starch yield ranging from 3.6 to 9.0 and from 3.18 to 8.74 t ha^{-1} from improved promising clones have been reported in Indonesia (Shohilin, 2009) and Malaysia (Tan, 2000). The trait is influenced by genetic and environmental factors, including plant maturity (Shohilin, 2009). Few articles regarding the performance and inheritance of starch yield have been published,

yet it is an important economic trait. To address the knowledge gap, there is a need to determine starch yield in Tanzanian cassava germplam.

1.6.10 Genetic modification of cassava for high starch content

Genetic transformation of cassava with enhanced agronomic traits has been reported (Siritunga and Sayre, 2003; Munyikwa et al., 1997). Transgenic cassava plants with enhanced starch content and short crop production cycle have also been reported (Ihemere et al., 2006). They generated transgenic plants with enhanced tuberous root ADP-glucose phosphorylase (AGPase) activity. The AGPase plays a role in the regulation of starch synthesis in plants, and catalyses the rate limiting step in starch biosynthesis and therefore the expression of more active bacterial form of the enzyme expected to lead increased starch production. The modified *Escherichia coli* (glgC) gene has been used to facilitate the maximal AGPase activity. Plants having the highest AGPase activity were observed to have increased total tuberous root biomass and above ground biomass when grown in glasshouse (Ihemere et al., 2006).

1.6.11 Factors affecting starch

Starch functionality shows unpredictable variations, depending on the environmental conditions at the time of harvest, and the age of the crop (Asaoka et al., 1992). Delay in the harvesting of cassava roots until 14-16 months result in increased fiber content, which affects the increased starch and decreased water content attained after 12 months (Chatakanonta et al., 2003). With increased fiber content starch extraction is more difficult. The starch granules from older cassava roots are also characterised by decreased amylose content and an altered granule size distribution, changing gradually from a normal to bimodal distribution with increased harvest time. The environmental conditions also alter the response to the granules uptake to water (swelling power) and subsequent thermal gelatinisation (Chatakanonda et al., 2003).

Santisopasri et al. (1998) studying cassava varieties in Thailand, observed a high content of starch between 26-28% in released varieties; Rayong 90 and Kasetsart 50. Furthermore, they revealed that the roots had the highest accumulation of starch at 8 MAP. They also observed that roots with a high amount of biochemicals like lipid, protein, cyanide, phenolic

compounds and fibre had a resulting lowering of starch quality. The accompanied lipids and phenolic compounds will cause rancidity and darkening of the cassava flour. Moreover, the toxic cyanide and dense fiber will cause difficulties in the industrial starch production process. Therefore, there is a need to consider the age of the crop when harvesting for starch purposes.

Amylose content determines the functional properties of starch such as gelatinisation and pasting. Researchers in Thailand obtained an amylose content of 20% in the roots at 10 months after planting (Santisopasri et al., 1998). However, rainfall one month prior to harvest, affected the content and size of amylose. And rainfall during the harvesting time could influence starch granular properties, possibly reflecting recovery of the plant from the dry period as new foliage develops. During this period starch material is hydrolysed as a source of energy for the growing leaves with preferential hydrolysis of the granules amorphous region (Sriroth et al., 1998b). Roots harvested in the high rainfall period are reported not suitable for starch extraction due to low peak viscosity. In addition, with prolonged harvesting, the amount of amylose decreases with the increasing size (DPn) and chain length of amylopectin. Sriroth et al. (1998c) obtained maximum amylose content at 10 months.

Potassium (K) fertiliser has been reported to increase root yield and starch content (Howeler, 2002; Obigbesan and Agboola, 1973). A similar result of an increase in starch content with increasing application of K have been reported at CIAT as well as in Southern Vietnam (Nguyen et al., 1998; CIAT, 1982). Large doses of nitrogen and magnesium fertilisers are negatively associated with starch content (Tan and Mak, 1995). Therefore care should be taken when choosing a type of fertiliser for use in cassava crop for starch extraction. Cassava diseases such as cassava brown streak have a direct effect on root quality, because they affect the starch tissue in cassava roots (Hillocks et al., 2001).

1.6.12 Genetic and phenotypic correlations

Genetic correlations are of interest to determine the degree of association between traits and how they can enhance selection (Falconer, 1989; Hallauer and Miranda 1988). Genetic correlations are useful for indirect selection; however, they depend on estimates of heritability for each trait and the genetic correlation between them. Kawano et al. (1998) indicated that indirect selection for cassava yield through biomass was not effective;

however, the regression of fresh root yield on harvest index was significant. Kawano (1998) concluded that, direct selection for yield itself in single row trials (SRT) was less effective than indirect selection for yield through harvest index, because of the significant differences between the yield performances of the same genotype in SRT and in replicated trial. A reason for this is border effects caused by inter-genotypic competition (Kawano, 2003). In a single row trial or single-plant planting, those genotypes with a high biomass tend to dominate others with less biomass in competition for light (Kawano and Thung, 1982). Additionally, genotypes with high harvest index are usually weak competitors while those with a large biomass are strong competitors. In plot trials where inter-genotypic competition is absent, weak competitors with a high harvest index tend to perform better than strong competitors with a low harvest index (Kawano, 1990; Kawano and Jennings, 1983). Therefore, there is a need to determine the harvest index at SRT.

The association between two characters that we observe and measure is the phenotypic correlation (Falconer, 1989). Phenotypic correlation is estimated from the phenotypic values observed on a number of individuals for a pair of characters. Phenotypic value is determined by genotypic values and environmental deviations (Dabholkar, 1992). Phenotypic correlation between biomass and fresh root yield in cassava has been reported to be very high (0.97) at the early evaluation stages, and lower (0.54) at the advanced stage of evaluation (Kawano et al., 1998; Cock, 1984; Kawano and Thung 1982; Cock et al., 1979). In contrast, the correlation between harvest index and fresh root yield has been found to be very low (-0.19) at the early stages but very high (0.93) at the later evaluation stage. Furthermore, RDMC and starch have been reported to have a high and significant correlation (r = 0.81; IITA, 1974; CIAT, 1975) hence there is a possibility of employing indirect selection to improve starch content. Starch content can be estimated from root dry matter percentage (Bainbridge et al., 1996).

1.7   Summary of the review

Presently, the main feature of the breeding methodology in cassava involve inter-cultivar recombination of phenotypically selected parents through controlled or open pollination and the selection of superior genotypes followed by clonal perpetuation of the selected ones. Selection in cassava at the early stages include seedling and clonal (single row) stages which are based on high heritability estimates. Parameters such as the harvest index are important in selection for yield at the early stages. At the PYT, AYT and RT stages, the

emphasis of selection shift from high heritability traits of low heritability such as yield. Trials are normally conducted in several locations to determine the stability across locations.

Major diseases of economic importance include cassava bacterial blight (CBB; caused by *X. manihotis*) which is the most important non-virus disease, cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) both caused by *Bemisia spp*. These diseases are the biggest threats to productivity and the health of the crop. The consequences of cassava virus infections are not only a reduction in crop yield but also the undermining of ongoing efforts in genetic improvement for yield, and of quality aspects such as starch and dry matter contents.

Crossing in cassava is relatively easy, but flowering and its control is one of the most important challenges of cassava breeding. Knowledge about flowering capacity is important in order to select a group of materials with synchronised flowering. Since the parent clones are highly heterozygous, selection of suitable parents for hybridization is one of the most important steps in a hybridization programme. Parents have been generally selected on the basis of their *per se* performance both as varieties and as parents in hybridisation programmes which is not a sound procedure. The use of combining ability is important for genetic improvement. Although clonal and recurrent selection have been used extensively in cassava breeding, the development of inbred clones specifically designed for their utilisation as parents in breeding nurseries offers interesting advantages such as the possibility of a gradual and consistent assembly of favourable gene combinations, which in the current system occur just by chance.

The literature indicates that dry matter content and starch are highly correlated; therefore, there is a possibility of employing indirect selection to improve starch content. The concentration of dry matter in cassava roots can vary from 15 to 45% depending on the genotype and environmental conditions thus providing the potential for selection. About 90% of the dry matter is carbohydrate; hence this makes dry matter an important trait for cassava breeders as the crop is grown largely for its carbohydrate content. High dry matter content is important for food, feed and industrial raw material.

According to the literature, selection for dry matter content should be done after 120 DAP, because that's when the accumulation in the storage roots has reached above 50%. However, the maximum rates for dry matter accumulation depend on the genotype and

growing conditions. The maximum rates of dry matter accumulation between 3-7 months have been indicated. Reports also indicated that maximum starch content has been attained between 8-12 months, but there are varietal differences that exist not only in starch content but possibly in time of maximum starch accumulation. Starch functionality is affected by the amylose/amylopectin ratio. The variation in this ratio could open new markets for cassava. Environmental factors immediately prior to harvesting of roots do affect starch quantity and quality. Other factors that affect starch quantity include the age of the crop and the type of fertilisers used.

Polycross design has been extensively used in cassava breeding. However, polycross design does not generate sufficient statistics to estimate all the parameters. North Carolina II and diallel designs provide the same type of information and similar tests of hypothesis. In this research, diallel design has been implemented based on the amount of information which the design supplies, the characteristic of the crop and the traits under evaluation. The general combining ability and specific combining ability were determined. This information has been lacking for Tanzanian germplasm.

Few articles have been published regarding the inheritance of quantitative traits in cassava. There is little information on the relative importance of additive and non-additive genetic effects in cassava. However, some studies have indicated the presence of important non-additive gene action for root yield, dry matter content, and the related starch content. Therefore, improvement through phenotypic selection which exploits additive variation is not adequate. The heritability of dry matter content ranging from intermediate to high with narrow sense heritability ranging from 51 to 67%, and the broad sense heritability of 87% obtained for the clonal mean have been reported. Similarly, High heritability estimates for root dry matter content (95%), harvest index (93%) and fresh foliage (84%) across several locations have been reported at CIAT. The high heritability estimates indicates that the cassava genotypes could be improved through selection which exploits the additive variation. Regression of parent-offspring is most reliable as an estimate of heritability therefore it will be employed in this research.

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Appendices
Appendix 1 Evaluation scheme at IITA, CIAT, SARRNET and National Root and Tuber Crops Research Programme in Tanzania

Year	IITA (Hahn et al, 1979)	CIAT-Colombia (Kawano, 2003)	CIAT- Asia (Kawano, 2003)	CIAT and IITA Jennings and Iglesias (2003)	Tanzania R/T programme/SARRNET (Mahungu and Kanju, 1997)
1	Acqiure or improve the source population by making crosses (20000 – 100000 seedlings produced)	Selection of germplasm and crossing to get F1 seeds	Crossing elite clones as parents	Crosses among elite clones. Up to 100 000 seeds produced	Crosses among elite clones
2	Selected seedlings are cloned (500 – 3000 clones) in a preliminary yield trial (PYT)	Seedling trial. Seeds sown in pots	Seedling trial: F1 seeds sown in plastic bags of 5cm diameter and 8cm depth. Planted in the field at 1 x 1.5m apart	F1: Evaluation of seedlings from botanical seeds. Strong selection for ACMV in Africa. IITA-100 000; CIAT (Col) – 50 000; 17 500 (Asia) seedlings evaluated	F1: seedlings trial, 5000-50 000
3	Advanced yield trial (AYT) (50 -100 clones) selected from PYT	Single row trial (SRT) evaluated in 3 sites	Single row trial (SRT). Single row with 10 cuttings planted at 1 x 1m spacing.	Clonal evaluated trial (CET): 2000-3000 seedlings (IITA, CIAT - Col) and 1800 CIAT - Asia	Clonal evaluation trial (CET), 500-5000 clones evaluated
4	Uniform yield trial (UYT), the most promising 20 clones from AYT evaluated	Replicated yield trial (RT) conducted in 3 locations. 30 cuttings per plot.	Preliminary Yield Trial (PYT). 50 cuttings in a plot of 5 x 10m planted at 1 x 1m spacing.	Preliminary yield trial (PYT): 100 (IITA), 300 (CIAT-Col), 130 (CIAT-Asia) seedlings evaluated	Preliminary yield trial (PYT), 50-500 clones evaluated
5	Elite 5 clones from UYT evaluated for yield and consumer acceptance and adaptation		Advanced Yield Trial (AYT). Superior clones from PYT planted in 4 replications. Planted in 3 sites.	Advanced yield trial (AYT)	Advanced yield trial (AYT), 10-15 clones evaluated. Multilocational trials conducted and first year on-farm
6	Most popular clones multiplied and distributed		Regional Yield Trial (RT). 6 representative clones planted in 4 replications and replicated in 6 sites.	Regional trial (RT) 5- 30 clones	Uniform Yield Trial (UYT). 5-8 breeding lines plus 2 standard checks. Multi-location trials repeated. Confirm with farmer about their selection in on-farm trials.
7.					Selected clones multiplied and distributed.

Chapter 2

Breeding cassava for high dry matter content and starch: understanding farmers preferences and selection criteria for research intervention through participatory rural appraisal in Tanzania

Abstract

Cassava is an important staple in humid and sub-humid lowlands of the eastern agro-ecological zone of Tanzania. Many farmers practise selection, yet the process has rarely been documented. Their involvement in selection and evaluation of cassava germplasm is therefore not new. The objective of this study was to improve researchers' understanding of the farmers' cassava cultivar preferences and selection criteria so as to contribute more effectively to the improvement of the crop. A participatory rural appraisal study was conducted in Bagamoyo and Rufiji districts in Coast region, and Mkinga district Tanga region. The majority of farmers grew cassava in mixed culture, except in Rufiji district where the majority grew cassava as a monoculture, due to socio-economic influences. Major constraints to cassava production and productivity included vermin, pests and diseases. However, drought and lack of market were mentioned as additional important constraints in Mkinga and Rufiji districts respectively. About 32 cultivars were recorded in the surveyed areas, with more that 70% identified as sweet, indicating the relatively high prevalence of sweet type in the coastal belt. The majority of farmers in Bagamoyo and Rufiji cultivated at most three cultivars, while in Mkinga more than 65% farmers grew four to six cultivars per household. The average cassava production recorded was 4 t ha^{-1}, which was very low compared to the district data and previous reports. Preferred traits frequently cited by farmers were categorized into agronomic, culinary, and others. High yield and pests and disease tolerance featured high in the agronomic category. Sweetness, high dry matter content and cultivars that cook well were the attributes frequently mentioned in the culinary category. Marketable roots and root that keep long in ground without rotting were the preferred attributes in the other category. Root dry matter content for the most preferred cultivars was high (above 35%), and found to be important in both sweet and bitter cultivars. These attributes mentioned by farmers do not occur in isolation but are interrelated. Because farmers are selecting cultivars based on multiple criteria, participatory plant breeding at the early stages of evaluation and selection is essential for a successful cassava breeding programme.

2.1　Introduction

As a staple food crop and raw material for many industrial uses, the hardy root crop cassava has an important role in many parts of Tanzania, particularly in the coastal lowland, Lake Victoria and southern agro-ecological zones. Its tolerance to drought and poor soils (El Sharkawy and Cock, 1987) adds to its value in farming communities.

Many farmers practise selection, yet the process has rarely been documented (Soleri et al., 1999). Farmer involvement in selection and evaluation of cassava is not new (Nweke et al., 1998), and they have been carefully selecting their landraces over decades (Fukuda and Saad, 2001). The COSCA study (Collaborative Study of Cassava in Africa) (Nweke et al., 1998) indicated that farmers in rural areas of Tanzania have been practising selection of cassava cultivars by introducing new genotypes and dropping undesired ones. Reasons given for abandoning some of the cassava cultivars were: poor in-ground storability, low root yield, disease and pest susceptibility, late bulking, high level of cyanogens, poor processing qualities, difficulty in harvesting due to root shape and arrangements and low leaf yield (Nweke et al., 1998). Similar results have been reported in Ghana (Manu-Aduening et al., 2005) where farmers introduced new cultivars and abandoned landraces with undesirable root characteristics. Farmers choose between varieties or within populations of a crop species. Within a population, farmers typically practise mass selection or selection of individual plants (Soleri et al., 1999), composing the next generation by bulking the seed of those selections. In addition, their crop populations are subject to ongoing natural selection for fitness during each growing season (Simmonds, 1979). In plant breeding, selection is the discrimination (Soleri et al., 1999) between individuals or populations, that determines which will contribute to the next generation. Through selection, plant breeders try to create a final population that shows most desirable performance for specific selection criteria. This artificial selection in combination with natural selection defines the genetic structure of the crop population (Simmonds, 1979)

The SARRNET (Southern Africa Root Crops Research Network) and the NARS (National Agricultural Research Systems) in Southern Africa proposed (Mahungu, 2002) to involve farmers in the selection of genotypes from segregating F_1 populations. They commented that, while researchers are focusing on recording quantitative data, most farmers' assessments are based on visual observations. In Bukoba region in Tanzania, for example, farmers' participation in the selection of cassava varieties in on-farm trials resulted in the selection of varieties for

specific interests, such as high root yield, suitability for intercropping, leaves for vegetable or high dry matter for processing (Kapinga et al., 1997). Despite this, cassava landraces had remained predominant in Tanzania (Nweke et al., 1998). Reports (Banziger and De Meyer, 2002; Sieglinde, 2002) indicated that farmers participated in the evaluation and selection of cultivars in CIMMYT's (International Maize and Wheat Improvement Center) mother-baby trials in Malawi, Zimbabwe, and elsewhere. Similarly, in Peru, farmers evaluated genotypes at harvest, focusing on yield and tuber characteristics of potato (tuber shape, coluor, and proportion of different sizes), and culinary qualities (Ortiz, 2002). Choice of local varieties based on root formation, colour of the skin and flesh, ease of peeling, cooking time, aroma and taste differed widely from place to place making wide acceptance of improved varieties a difficult task (Ortiz, 2002).

In developing new genotypes and disseminating them to farmers, classical plant breeding faces two major obstacles. First, undesirable traits go undetected during the breeding process consequently new varieties can be disappointing to farmers. Secondly, breeders discard many crosses and varieties during the selection process, because of the traits considered undesirable; however, these traits may actually be of interest to farmers (De Groote et al., 2002; Haugerud and Collison, 1990). On the Kenyan coast, for example, a technician brought home a discarded cassava variety and this variety was rapidly adopted by farmers (De Groote et al., 2000). A survey of cassava in Mukono, Soroti and Apac districts of central, north eastern and north western Uganda respectively revealed that farmers often returned to growing local germplasm that are low yielding and susceptible to virus even when improved clones were available (Fregene et al., 2003). Researchers (Witcombe et al., 2003; Paris and Atlin, 2002; Fukuda and Saad, 2001; Thiele et al., 1997; Joshi and Witcombe, 1996; Sthapit et al., 1996) argued that farmers were involved in final selection and verification of clones/cultivars, consequently, low adoption rate of improved varieties. Therefore, participatory approaches need to be decentralized and implemented even at early stages of selection (Manu-Aduening et al., 2006; Witcombe et al., 2003; Sperling et al., 1993) involving farmers actively in selection from the segregating material to generate improved cultivars that are preferred.

The major socio-economic factor affecting the production and productivity of cassava has been the low adoption rates of improved germplasm in Tanzania and elsewhere. DeVries and Toeniessen (2001) estimated that 80% of the East Africa's cassava harvest comes from late-bulking, unimproved genotypes, while 40% of production in West Africa is from local varieties.

The 60% production from improved varieties in West Africa has made a country like Nigeria to reach 14 t ha^{-1} in terms of productivity. Socio-economic contribution of high yielding cassava varieties in increasing farmers' income has been substantial in Asia (Puspitorini et al., 1998). According to Kawano (2003), new cultivars planted on one million hectares in Asia increased the economic benefits resulting from the increased productivity. The target population of small scale farmers in the poorer rural areas of the tropics captured a large proportion of these economic benefits.

Several hypotheses regarding the adoption of improved varieties have been put forward (Paris and Atlin, 2002; Almekinders and Elings, 2001; Ceccareli et al., 2001). One of the main reasons for this low rate of adoption seemed to be the fact that all the research work has been carried out by breeders at the experimental station, whereby the evaluation agenda and criteria are defined by the researcher. Thus the "promising" varieties brought to the growers/farmers reflected the breeder's opinion (FAO, 2009). Secondly, varieties selected on research station may not outperform traditional varieties under farmer management (Manu-Aduening et al., 2006; Ceccarelli et al., 2003; Paris and Atlin, 2002). Traits such as high yielding and tolerance to pests and diseases may not be enough to ensure adoption of improved cassava varieties (Manu-Aduening et al., 2006). Such a situation suggests that the improved varieties are not adequately satisfying farmers' needs and preferences (Witcombe et al., 2003; Ceccarelli et al., 2001). Therefore, a participatory rural appraisal (PRA) (Chambers, 1994) was introduced with the aim of narrowing the communication gap between scientists and farmers, which is reported elsewhere (Witcombe et al., 1996; Kamara et al., 1996). However, efforts are being made to reduce this gap, in particular by participatory plant breeding (Sperling et al., 2001). Manu-Aduening et al. (2006) implemented a successful participatory plant breeding in the developing superior cassava cultivars in Ghana involving farmers as early as the seedling trial. Schofield et al. (2009) involved farmers in participatory variety selection (PVS) of cassava varieties in the Great Lakes area. Furthermore, Kamau and Migwa (2009) also have implemented participatory plant breeding in Kenya and selected 23 promising cassava lines which are early maturing, high yielding with average dry matter content (30%). These approaches facilitate close interaction among farmers, researchers, and other key stakeholders in the genetic improvement of the crop.

Participatory rural appraisal is a participatory methodology (Chambers, 1989) for interacting with rural and urban people, understanding them and learning from them. It enables rural and urban

people to share, enhance and analyse their knowledge of life and conditions to plan and act (IDS, 1996; Chambers, 1994). The PRA approaches which evolved from rapid rural appraisal (RRA) in the early 1990s (Chambers, 1993) is considered important in assisting researchers to acknowledge the needs of the communities that they work with. The participatory approach is one of the ways that: respondents' feelings and perceptions can be captured and accounted for as hard data; the people's resourcefulness and creativity can be challenged and captured; breeders may demonstrate respect for the insight and knowledge of the farmers (Adebo, 2000; Chambers, 1994). Whilst the statistical analysis of information gathered by participatory means is difficult, it is considered a more accurate picture of the real situation (IDS, 1996). A rapid change in the cultivar composition with an emphasis on higher productivity and value addition is required for cassava to contribute more to food security and to the market economy. The overall objective of this study was to improve researchers' understanding of the cultivars preferences and selection criteria so as to contribute most effectively to improvement of the crop. In addition, it also aimed at understanding farmers cultivars that are high in dry matter content and starch for future improvement for the processing industry.

2.2   Materials and methods

2.2.1   Study area

The PRA study was conducted in the Bagamoyo, and Rufiji districts in Coast and Mkinga district in Tanga regions in the eastern agro-ecological zone during 2007/08. The two regions are located in the eastern agro-ecological zone (MALD, 1994) in the coastal belt of the Indian Ocean. The rainfall pattern received is bimodal, whereby two distinct rainy seasons are experienced in a year. The short rains occur from October to December and the main rains from early March to May-June. The area is characterized as humid and sub-humid lowlands and has a cassava-cashew-coconut farming system. The elevation from sea level, the global positioning system (GPS) coordinates, and the annual rainfall are summarized in Table 2.1. The study area experiences high temperatures and humidity except for the month of June.

Table 2.1 Physical data of the surveyed area

Region	District	Village	Elevation (m)	Coordinates	Annual Rainfall (mm)
Coast	Bagamoyo	Yombo	43	S 06º34.977′ E038^{0}51.105	750-900
	Rufiji	Bungu	157	S 07º38.09′ E 039º 03.69′	700-1000
		J/Mpakani	173	S 07º 32.76′ E 039º 07.67′	700-1000
Tanga	Mkinga	Mtimbwani	37	S 04º57.50′ E 039º 05.37′	800-1000
		B/Mwarongo	81	S 04º 54.18′ E 039º 03.41′	800-1200

Source: District agricultural offices (2007)

2.2.2 Sampling procedure

A purposive sampling procedure was employed to identify district, villages, and farmers included in the study. Two regions, Coast and Tanga were selected for this study, due to their potential for cassava production. The target group for this study involved cassava farmers and processors. Farmers involved in the formal and informal interviews were randomly selected from the village register by the village and hamlet leaders with the help of the agricultural extension officer. In Mtimbwani and Bungu villages cassava processing groups were purposely selected for the study.

2.2.3 Data collection

A number of participatory methods were used in data collection. Both informal and semi-formal methods were implemented to obtain information. For primary data collection, semi-structured questionnaires, focus group discussions, seasonal analysis, and ranking techniques were implemented (Witcombe et al., 2003; Joshi and Witcombe, 1996; Chambers, 1994). Secondary data were obtained from previous reports. In each village, focus group discussions were conducted with groups of between 10 to 30 representative farmers. Focus groups were used to collect general information through discussion. In these groups information on food and cash crops grown, cassava cultivation, production constraints, cultivars grown and their characteristics, seasonal analysis and activity calendar, and cassava processing methods were

discussed. Listing and ranking of crops grown, cassava cultivars, constraints to production and selection criteria were done by local people. A checklist was prepared to guide the discussion. A total of 117 farmers attended focus group discussion in three districts (Table 2.2). The main idea of informal interviews in participatory research was to open up a conversation in a way that allowed the interviewed person to express knowledge and views in their own words and according to their own values, concepts and ways of thinking.

Semi-structured interviewing was the core of the PRA. About 67 interviewees in three districts were allowed to express their opinions through discussions. In semi-structured interviews, questions and topics were pre-determined, whilst the majority of questions were formulated during the interview. The interviews involved: 1) individual farmers or households; and 2) key informants. Randomly selected individuals such as teachers, development staff, village leaders, retired officers and agricultural extension workers were selected as key informants. Ranking technique was employed to complement semi-structured interviews. Different aspects, for example, types of crops, constraints, and opportunities were compared to investigate farmers' preferences and relative importance. A group of comparable variables was chosen, for example cassava varieties. Criteria for assessing the variables were identified through discussion and listing. The local people were asked which items were most preferred or of greatest importance. The resulting information was drawn on a flip chart. The purpose of ranking was to learn about local people's choices and priorities and the complexities of decision-making; to reveal differences in priorities of different social groups.

Table 2.2 Household data for sampled districts in 2007/2008

District	Village	Number of households	Number of people	Group discussion	People interviewed
Rufiji	Bungu	860	4998	15	10
	J/Mpakani	1504	7770	11	8
Bagamoyo	Yombo	489	1693	33	29
Mkinga	Mtimbwani	380	1781	30	10
	Mwarongo	243	887	31	10

Source: District agricultural office, 2007

2.2.4 Root dry matter content

During the survey, cassava roots of the readily available cultivars were collected and put in a cool box with ice to facilitate preservation and transport. Dry matter content of the roots was determined according to Dixon and Nukenine (2000). Cassava roots were washed and cut into thin slices. Duplicate samples of 200 g each were taken and dried in a forced draught oven at 70°C for 72 h. The dried samples were re-weighed to obtain the dry mass, and the dry matter content as percentage were obtained as a proportion of the fresh mass.

2.3 Data analysis

Statistical analysis of both quantitative and qualitative data was performed in SPSS (Release 15) computer package (SPSS Inc., 2006). Descriptive statistics, analysis of variance and mean comparisons were computed for data collected in each village and district. Mean comparisons between districts were performed.

2.4 Results

2.4.1 Household and farm characteristics

Major food crops grown by farmers in Bagamoyo, Mkinga and Rufiji districts are presented in Table 2.3. Cassava, maize (*Zea mays*), cowpea (*Vigna unguiculata*), pigeon pea (*Cajanus cajan*) and banana (*Musa spp.*) were important in all three districts. Sweet potato (*Ipomea batatas*) was important in Bagamoyo district and rice (*Oryza sativa*) was cultivated in Bagamoyo and Rufiji. Major cash crops included coconut (*Cocos nucifera*), cashew (*Anacardium occidentale*) and pineapple (*Ananas comosus*) (Table 2.4). Cashew was one of the most important cash crops reported in all three districts.

The mean land area allocated to different crops per household is presented in Appendix 1. Crop land area planted with cassava, maize, cowpea, and pigeon pea differed significantly. The mean land area in hectares allocated to cassava was relatively higher than other food crops grown in the study area. On average farmers allocated 0.7 ha for cassava, 0.4 ha for maize, 0.2 ha for cowpea, 0.2 ha for sorghum, 0.2 for sweet potato and 0.1 ha for pigeon pea. Most of these crops were grown in mixed culture.

Household resource base refers to household labour, farmland and other economic activities of the household. The survey revealed that the average number of people in the household was 6.8 with the minimum of 1 and maximum of 19 people. However, those who were active in farming activities were 2.9 persons per household (Appendix 2). The average total land area in the three districts was 3.1 ha which ranged between 0.4 and 8.0 ha per household. The common livestock found in the study area were goats and chickens. No goats were recorded from representative farmers in Rufiji and no cattle were observed from representative farmers in Rufiji and Bagamoyo district (Appendix 2). However, the average number of chicken and goats per household was 17.9 and 6.4 respectively. Cattle were observed in Mkinga district with the average of 2.6 cattle per household. Tree crops of importance were coconut, cashew, mangos and citrus; these were good sources of income. The highest number of coconut (169.5) and cashew (172.8) trees per household was recorded in Mkinga and Rufiji districts respectively (Appendix 2). Mango trees were more abundant in Bagamoyo than the other two districts. Each household had at least one radio indicating that they could receive news transmitted everyday from different sources and one bicycle for transport. Each household could at least access one telephone for communication. Television sets were not common.

Table 2.3 Food crops grown by farmers (%) in Bagamoyo, Mkinga and Rufiji districts, 2007/08

Crop	Bagamoyo (N=29)	Mkinga (N=20)	Rufiji (N=18)	Overall mean
Cassava	72.4	100.0	100.0	90.8
Maize	72.4	95.0	77.8	81.7
Cowpea	72.4	30.0	16.7	39.7
Pigeon pea	72.4	15.0	11.1	32.8
Banana	34.5	50.0	27.8	37.4
Rice	48.3	-	33.3	40.8
Sorghum	10.3	-	22.2	16.3
Sweet potato	37.9	5.0	-	21.5
Groundnut	3.4	-	-	3.4

Table 2.4 Cash crops grown by farmers (%) in Bagamoyo, Mkinga and Rufiji districts, 2007/08

Crop	Bagamoyo (N=29)	Mkinga (N=20)	Rufiji (N=18)	Overall mean
Coconut	58.6	70.0	n/a	64.3
Cashew	82.8	80.0	88.9	83.9
Pineapple	27.6	45.0	38.9	37.2

2.4.2 Cassava production

Average area under cassava cultivation and production per household differed significantly between districts (Table 2.5). In general the cassava area ranged from 0.1 to 4.0 ha with the overall mean of 0.7 ha per household. The overall mean of cassava root production in fresh mass basis was 3.8 tonnes per household (equivalent to 4 metric tonnes ha$^-$1), which ranged from 0.6 to 12.8 tons in Bagamoyo, 1.0 to 21.0 tons in Mkinga and 0.8 to 8.5 tons per household in Rufiji districts. However, district data indicated that the average yield in the three districts ranged between 3.0 and 12.0 t ha^{-1} (Table 2.6). The production of cassava roots per household reported was that which could be remembered by farmers during interviews and not what was recorded before.

Results from the survey indicated that the majority of farmers planted cassava on flat seedbeds and very few planted on ridges (Appendix 3). More than 50% farmers planted cassava in rows using a spacing which was wider than the recommended spacing of 1m x 1 m from row to row and plant to plant. Intercropping of cassava with other crops was common and reported by 66.1% farmers, most of them from Bagamoyo and Mkinga district (Appendix 3; Figure 2.2). However, in Rufiji district about 83.3% of farmers practiced monoculture in cassava cultivation.

Table 2.5 Cassava production and mean area under cultivation per household

	Bagamoyo	Mkinga	Rufiji	Overall mean	F probability
Cassava area (ha)					
Mean	0.68	0.50	1.11	0.74	0.001
Min	0.31	0.10	0.41		
Max	1.42	1.21	4.01		
Cassava production (kg household^{-1})					
Mean	3013.8	7170.0	2633.3	3802.5	0.003
Min	640.0	1050.0	750.0		
Max	12800.0	21000.0	8500.0		

Table 2.6 Cassava production data and district population, 2007/08

District	Season	Cassava area (ha)	Cassava production (t)	Yield t ha^{-1}
Rufiji	2004/05	14 616	164,626	11.3
	2005/06	12 856	154,265	12.0
	2006/07	20 241	141,687	7.0
Bagamoyo	2004/05	7 286	21,888	3.0
	2005/06	2 735	22,419	8.2
	2006/07	2 792	22,421	8.0
Mkinga	2005/06	13 053	111,967	8.6
	2006/07	9 101	91,010	10.0
	2007/08	15 444	154,440	10.0
	2008/09	8 653	51,918	6.0

Source: District agricultural offices (2007)

Although a few farmers (22.2%) in the surveyed area weeded four times per season, three weedings per season was common to the majority of farmers. Cassava is propagated vegetatively and the use of planting material derived from the previous crop was a common practice. From the survey, it was established that the farmers' sources of planting material were mainly from their own production fields (60.8%) and neighbours production fields (21.1%) and sometimes from nearby villages (9.7%). A few farmers (8.3%) especially in Mkinga district received improved planting materials from research institutions (Figure 2.3; Appendix 3).

Figure 2.2 Intercropping of cassava with (A) Maize; (B) sugarcane, coconut, cashew
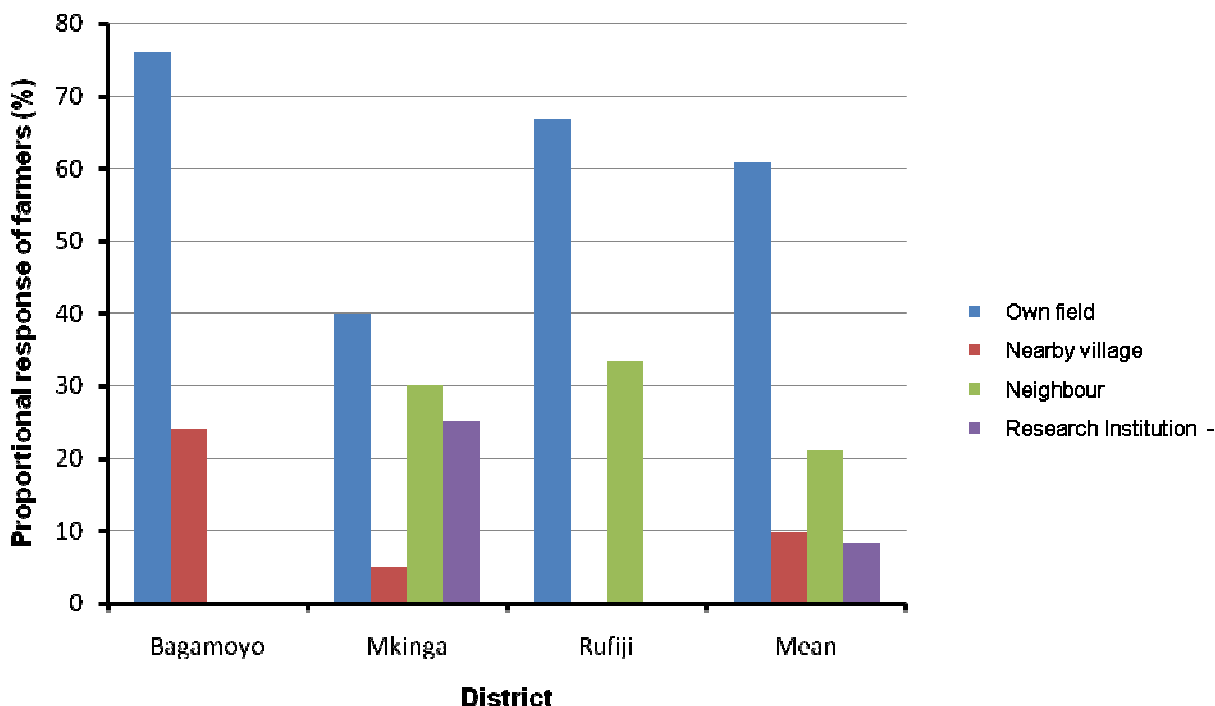
Figure 2.3 Source of cassava planting material as indicated by farmers

2.4.3 Constraints to cassava production and processing

Generally the most important constraints affecting cassava production as identified by farmers were vermin (small mammals), insect pests and diseases (Table 2.7). On average 89.1% of representative farmers said vermin mostly affected the cassava production. Small mammals include wild pigs (*Sus spp*), monkeys (*Catrol spp*), baboons (*Chacma baboon*) and rodents (*Acomys spp*). However, in Bagamoyo district pests especially spiraling whitefly and in Rufiji lack of market was mentioned as the second most important factor limiting cassava production. In Mkinga district, farmers identified bad weather or drought as third most important factor affecting cassava production. In Bagamoyo and Mkinga soil degradation was identified as a constraint to cassava production, while in Rufiji district the low producer price also featured high for 22.2% farmers. Other constraints to production included weeds, lack of reliable market, poor in-ground storability, inadequate extension service, poor transportation of products from farms to cities, lack of manpower as related to farm tools used, and lack of credit to support input purchase.

The post harvest constraints frequently mentioned by farmers included inefficient drying technology (62.7%), root rot caused by CBSD (28.6%), lack of improved processing equipment (14.3%), water shortage (18.2%), storage pests especially large grain borer (10.8%) and difficulty in peeling roots (7.8%) (Figure 2.4; Appendix 4). Shortages of water and storage pests were the second most important constraint in Mkinga and Rufiji districts respectively. Cassava root rot caused by CBSD was the second most important problem in Bagamoyo district (Figure 2.5). Other important constraints were poor working tools in peeling roots which was reported to be very labour intensive, inadequate storage facilities to stock large quantities of dried cassava, transport costs from farm to towns or cities, small margin accrued after selling processed products, and rapid deterioration of fresh cassava roots (Appendix 4).

Table 2.7 Cassava production constraints as identified by farmers in Bagamoyo, Mkinga and Rufiji

Constraint	Bagamoyo	Mkinga	Rufiji	Overall mean
Disease	44.8	40.0	11.1	31.9
Vermin	89.6	100.0	77.8	89.1
Weeds	6.9	10.0	22.2	13.3
Pests	79.3	5.0	22.2	35.5
Lack of manpower	3.4	10.0	16.6	10.0
Lack of reliable market	-	5.0	33.3	12.8
Low price	-	-	22.2	7.4
Lack of credit	3.4	10.0	-	4.5
Poor ground storability	-	-	5.6	1.9
Inadequate ext. service	-	-	5.6	1.9
Poor transportation	-	10.0	5.6	5.2
Poor farm equipment	6.9	10.0	-	5.6
Soil degradation	3.4	5.0	-	2.8
Bad weather	10.3	30.0	5.6	15.3
Poor farming technique	3.4	-	-	1.1
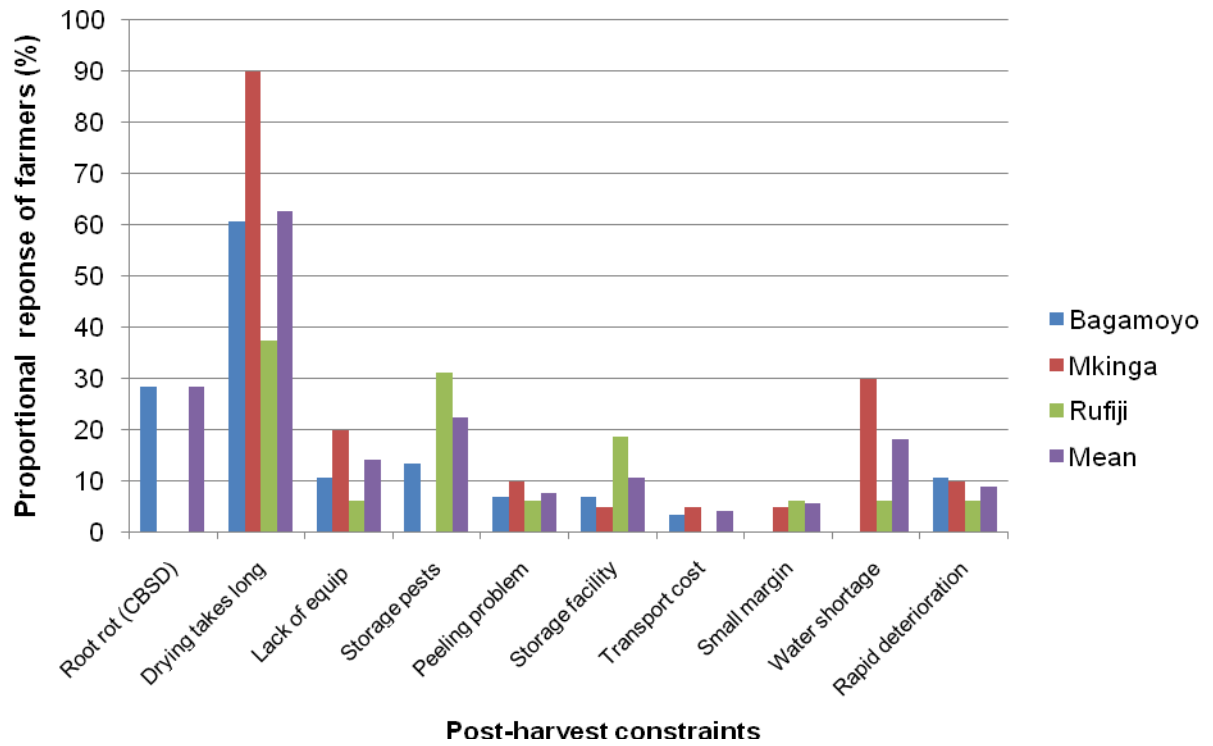
Figure 2.4 Post-harvest constraints in the study area

Figure 2.5 Root rot caused by cassava brown streak disease as reported by farmers

2.4.4 Cassava cultivars grown

The number of cassava cultivars grown per household differed significantly between districts. The mean number of cultivars per household in Mkinga district was 4.9, which was higher than Bagamoyo (2.2) and Rufiji (1.6) (Table 2.8). A minimum of two and maximum of 10 cultivars per household were recorded in Mkinga district, while other districts had at most three cultivars per household. A total of 32 cultivars of cassava were found in the study area, out of which 22 were reported from Mkinga district, 7 from Bagamoyo and 6 from Rufiji districts (Appendix 5). An improved variety Kiroba was reported to be grown across the surveyed districts. Cultivars Kigoma and Kitumbua were common in Mkinga and Rufiji districts. In general, more than 70% farmers in the three districts cultivated at most three cultivars of cassava. However, the majority of cultivars reported by farmers were specific to each agro-ecology (in response to use and preferences).

Farmers indicated that sweet cultivars were relatively more available than bitter types. Of the 32 cultivars identified in the surveyed area, 25.8% were bitter and 74.2% sweet, signifying a higher relative proportion of sweet types than bitter ones in the coastal area. Previous studies have shown similar results (Nweke et al., 1998). Sweet cultivars are used for boiling, roasting, stews or eaten raw, while bitter cultivars are traditionally processed into intermediate products such as chips known as 'makopa' and flour.

Farmers in Mkinga district reported that among many, cultivars Udugu, Gago, Kiroba and Haraka were dominant (Appendix 5). According to Fukuda and Saad (2001) farmers generally maintain broad genetic diversity of cassava varieties on their farms; however only a few occupy a bigger market share. In Bagamoyo district, cultivar Mfaransa was cultivated by all representative farmers in the district, while cultivars Kalolo and Kiroba were grown by 56% and 50% farmers, respectively. Minor cultivars in Bagamoyo district included Mtanga, Mzungu, Kitunguu and Kambinjenga. Almost all farmers in Rufiji district grew cultivar Kiroba which is very marketable. However, some minor cultivars such as Cosmas, Krismas, Usimpejuma, Kichooko and Dihanga were also reported in Rufiji district. These minor cultivars were maintained in small proportions. Cultivars were categorized as early and late bulking types. For example cultivars

Kiroba, Udugu and Haraka from were early bulking and matured within 8-12 months, while Guzo, Agrikacha, and Mwakinyavu were late bulking types and matured within 18-24 months.

Table 2.8 Average number of cassava cultivars grown by farmers in Bagamoyo, Mkinga and Rufiji districts

	Bagamoyo	Mkinga	Rufiji	Overall	F prob
Number of cultivars					
Mean	2.2	4.9	1.6	2.8	0.000
Min	1.0	2.0	1.0	1.0	
Max	6.0	10.0	3.0	10.0	
Std dev.	1.20	1.84	0.62	1.89	

Table 2.9 Number of cassava cultivars grown by farmers (%) in the past five years in Bagamoyo, Mkinga and Rufiji districts

Number of cultivars	Bagamoyo (N=29)	Mkinga (N=20)	Rufiji (N=18)	Overall mean
1	37.9	-	55.6	31.2
2	20.7	5.0	38.9	21.5
3	34.5	15.0	5.6	18.4
4	3.4	20.0	-	7.8
5	-	20.0	-	6.7
6	3.4	25.0	-	9.5
7	-	10.0	-	3.3
8-10	-	5.0	-	1.7

2.4.5 Preferred traits in cassava

The cultivars Mfaransa, Kalolo and Kiroba were the mostly preferred in Bagamoyo district. In Mkinga and Rufiji districts, cultivars Gago, Udugu and Kiroba were mostly preferred (Appendix 5). When asked why those cultivars were mostly preferred the farmers mentioned several attributes that were desired. The attributes are categorized into agronomic, culinary, and others. The most frequently cited attributes considered in selecting cassava varieties were high yield (69.1%) and disease tolerance (48.1%) (Table 2.10). However, early maturity and/or early bulking types were preferred by 46.7% farmers. Cultivars that are sweet were cited by 52.2% farmers as important culinary characteristics. High dry matter content or mealiness was mentioned by 43.5% farmers and roots that cook well by 34.8% farmers as second and third

most important attributes under culinary characteristics. Ease of marketing was the most cited attribute under other characteristics, followed by the size of the root as the second most preferred attribute in this category. For example, consumers preferred medium sized cassava roots. Cultivars Mfaransa from Bagamoyo and Kiroba from Rufiji districts were easily marketed for fresh market. Furthermore, farmers said they would prefer cultivars that have good in-ground storability and that are late bulking as a security for the family. These cultivars should not be susceptible to root necrosis. Cultivars Agrikacha, Gago and Dihanga were mentioned as late bulking and could stay in the ground for up to 36 months. It was apparent that farmers select cultivars based on diverse criteria. For example, farmers commented that they liked cultivars Gago and Macho because they are drought tolerant.

2.4.6 Quality of preferred cultivars

Attributes such as high yield, high dry matter content, early maturity, and disease tolerance are important whether a cultivar is sweet or bitter (Table 2.11). Good cookability, marketability, and sweetness are pertinent to sweet cultivars. Good flour quality is specific to bitter cassava. Despite having preferred attributes, these cultivars also exhibit undesirable attributes such as fibrousness in roots, late bulking, short in-ground storability, and root rot due to CBSD.

Table 2.10 Attributes preferred by farmers (%) in the study area

Characteristic	Bagamoyo (N=29)	Mkinga (N=20)	Rufiji (N=18)	Mean
Agronomic				
Disease tolerance	31.0	80.0	33.3	48.1
Early bulking/maturity	24.1	55.0	61.1	46.7
High yielding	51.7	100.0	55.6	69.1
Resistant to pests	-	5.0	11.1	5.4
Less branching	-	-	5.6	1.9
Drought tolerance	-	30.0	-	10.0
Culinary				
Cook well	62.1	20.0	22.2	34.8
High dry matter/mealy	48.3	60.0	22.2	43.5
Sweet	51.7	55.0	50.0	52.2
Low CNP	-	5.0	-	1.7
Easy peeling	-	5.0	-	1.7
Good flour quality	10.3	10.0	-	6.8
Non fibrous	-	5.0	5.0	3.3
Other				
Good in ground storage	3.4	5.0	-	2.8
Late bulking	-	5.0	-	1.7
Size of the root	24.1	5.0	5.6	11.6
Marketable root	34.5	5.0	11.1	16.9
Shape of the root	-	-	5.6	1.9

2.4.7 Dry matter content of cassava cultivars

Results indicated that root dry matter content (RDMC) of the cultivars collected from farmers ranged between 32.5 and 46.3% from cultivar Mjawa and Kibandameno respectively with the mean RDMC of 38.3%. Majority of the cultivars had RDMC above 36% at the time of collection (season). Most of the cultivars presented were harvested after 12 months. Results also showed that the most preferred cultivars such as Mfaransa in Bagamoyo, Kiroba in Rufiji, and Gago and Udugu in Mkinga had RDMC of 37% and above.

Table 2.11 Strengths and weaknesses of preferred cultivars as presented by key informants

Cultivar	District	Strengths	Weakness
Mfaransa	Bagamoyo	-High yielding -Good cookability -High dry matter -Palatable -Easily marketed -Good in-ground storability -Sweet -Big roots -Disease tolerant -No root rotting	-fibrous if not mature -susceptible to pests -late maturing/bulking
Kiroba	Rufiji Mkinga Bgamoyo	-High yielding -Early bulking -Early maturing -Sweet - Easily marketed -Good cookability -Disease tolerant -Soft leaves for vegetable -Less branching -Palatable -High dry matter content -Easy peeling	-not stable in taste -short in-ground storability
Gago	Mkinga	-Good in-ground storability -High yielding -Bitter taste -High starch content -Drought tolerant -Good flour quality -Tolerant to disease	-fibrous if not mature
Udugu	Mkinga	-Early bulking -Early maturing -Good flour quality -High dry matter content -High yielding -Moderate resistance to diseases -Bitter	-root rotting
Kalolo	Bagamoyo	-Moderate to high yielding -Good flour quality -Bitter -Mealiness -Soft leaves for vegetable -Medium maturity -High dry matter content	-root rotting

2.4.8 Cassava processing

When farmers were asked which cultivars they preferred most for processing, they mentioned cultivars Mfaransa and Kiroba (sweet), and Kalolo, Gago, Udugu, Kichooko and Dihanga (bitter) (Table 2.13). Both sweet and bitter cultivars were processed into intermediate products such as dry chips and flour. The common cassava processing methods used by farmers is presented in Figure 2.6. Other traditional methods are presented in Appendix 7. Processing involves peeling the fresh cassava roots, slicing to reduce size, drying, cleaning or scraping to remove any exogenous material or mould growth, and then milling to get flour. The whole process takes 7-12 days depending on weather conditions. During the rainy season it takes 12 days to produce flour using traditional methods. The long processing time involved in traditional processing resulted in the release of toxic cyanogenic compounds.

Table 2.12 Cultivars mostly preferred for processing by farmers (%) in Bagamoyo, Mkinga and Rufiji districts

Cultivar	Bagamoyo	Mkinga	Rufiji
Mfaransa	62.5	-	-
Kalolo	37.5	-	-
Gago	-	40.0	-
Kiroba	-	15.0	88.9
Udugu	-	45.0	-
Kichooko	-	-	5.6
Dihanga	-	-	5.6

However, due to poor quality of the final product (fungal growth, presence of sand and inadequate drying technologies), improved processing technologies were introduced by the National Root and Tuber Crops Programme in collaboration with the International Institute of Tropical Agriculture (IITA) (Figure 2.7). Essentially roots are harvested, peeled, chipped or grated, pressed (for grating) to reduce water content, then dried over a raised platform to avoid contamination by sand and/or trash. The improved processing technologies have advantages over traditional processing such as fast drying because of the reduced particle size (within one day), white flour, no sand in flour, no fermentation odour, and cyanogenic potentials are reduced to safe levels. The high quality cassava flour can be used to make different novel products (biscuits, buns, bread etc).

Two farmers groups; Sululu in Rufiji and Kiwaumu in Mkinga districts were visited in the study area, where improved cassava processing technologies are implemented. Sululu group are processing cassava roots into high quality cassava flour (HQCF) and had the capacity of producing 4 t of flour per month. The flour produced was sold to a biscuit factory in Dar-es-Salaam. Kiwaumu group was running a small scale starch extraction plant, and had the capacity of producing about 1 t of fine native starch per month, which was sold to two companies in Dar-es-Salaam as well. Data on starch importation was also collected during the PRA study, and indicated that between 1999 and 2005, approximately 2700 -8000 t of starch was imported annually (Appendix 6) into the country. Increased cassava starch production in the country would save foreign exchange money used for importation.

Cassava root peeled

Roots are heaped for 3-4 days
then sun dried for 6-10

Drying

Roots are scraped of mould and
foreign particles before milling

Milling to flour
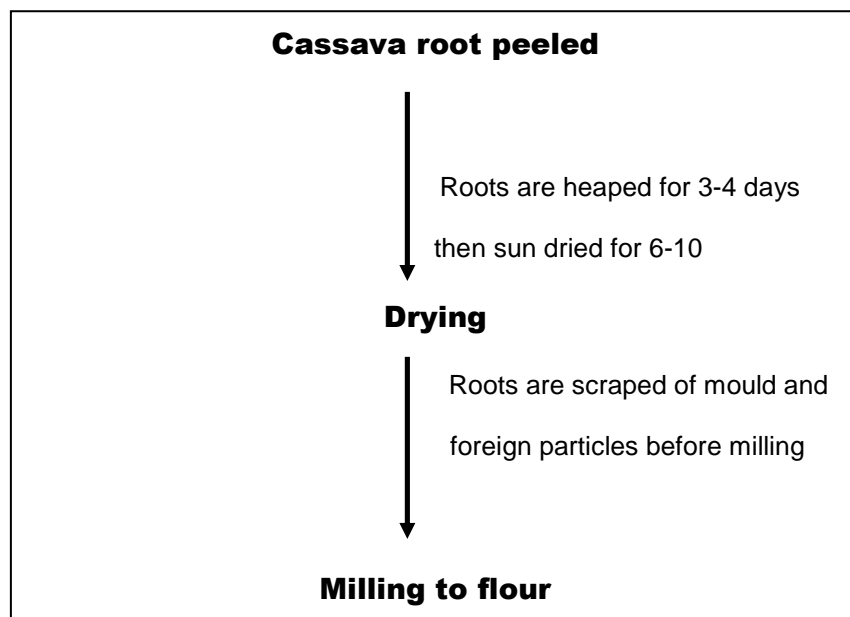
Figure 2.6 Common cassava processing method in the study area

Chipping fresh sweet cassava

Drying cassava chips on raised platform

Figure 2.7. Small scale rural processing of cassava

2.5   Discussion and conclusion

The PRA study was conducted to understand farmer's preferences and priorities in their cultivar selection. The study has clearly established that cassava is an important staple food in Bagamoyo, Mkinga and Rufiji districts. It was established that farmers had good knowledge of cassava cultivars. The crop is used as food in fresh and processed forms. It is also a source of income when traded to towns and cities. Other food crops of importance were maize and rice. Cowpea and pigeonpea were important legumes in the study area. Coconut, cashew, and pineapple were the major cash crops in the study area. The study identified that the crops were sometimes grown as sole crop and/or as intercrops in a mixed culture. However, farmers would decide which one is the major and which one is the minor crop in the mixture. Most of the farm activities such as land preparation, planting and weeding used family labour. The mean total cropped land area per household was generally small.

Generally the cassava root production per household recorded in Bagamoyo, Mkinga and Rufiji districts was very low. The actual yield or productivity was not well captured because of the piecemeal harvesting fashion whereby record keeping is poor. Normally, harvesting would be done according to the objectives. For home consumption, piecemeal harvesting or a few plants would be uprooted according to the family needs. For market purposes, the whole field or plot would be uprooted at once with prior arrangement with a trader and the labour involved will be tagged to the trader. Yield estimates that range from 1.5 to 35.0 t ha^{-1} in farmers' field in Tanzania have been reported (Temu et al., 2003). In this study planting material of improved varieties was inadequately available to few farmers. Investment in planting material of improved varieties and hired labour could improve cassava production and productivity.

Survey results showed that sources of introduced planting materials were limited to own fields, neighbours and nearby villages. Less than 10% farmers received cuttings of improved varieties from the research institutions. Cassava is propagated vegetatively using cuttings; utilization of planting material derived from pest infested or pathogen infected plants is a common way of spreading pests/pathogens of the crop. However, farmers seldom selected for "clean" planting

materials. Selection and use of planting material derived from healthy plants could reduce incidence and severity of important diseases.

Major production constraints included vermin, pests and diseases. Among the vermin, wild pigs, rodents, and monkeys were seriously affecting cassava production. Cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) are a threat to plant health and cassava productivity in the study area. Previous studies established that yield loss of up to 64% occurred due to CBSD in Muheza district (Muhanna and Mtunda, 2002). Thresh and Otim-Nape (1994) indicated that yield loss by CMD ranged between 20% and 90% depending on the variety. Among the pests occurring in the country, spiralling whitefly was frequently mentioned as an important pest threatening crop productivity in Bagamoyo district. Farmers mentioned that weeds were a constraint in cassava production. Studies on weed management have indicated that if weeding is not done within the first two months, there is a 70% reduction in yield. On the other hand, one hand weeding only at one month after planting gave 31% of the expected yield (TARO, 1983).

Inadequate drying techniques were frequently cited as a major post-harvest constraint in the study area. Efficient drying depends on the size of the slice, method of drying and environmental factors such as sunny or rainy days if sun drying is employed. Roots with irregular shapes and small sized roots are difficult to peel by hand, and require more labour. Fresh cassava roots are highly perishable, therefore processing is important to increase shelf life, add value and render products stable.

Farmers distinguished cassava cultivars by local names which were often descriptive of the physical characteristics of a plant. The majority of farmers in Bagamoyo and Rufiji districts grew at most three cultivars, indicating loss of diversity with the exception of Mkinga district where a reasonable number of farmers grew four to six cultivars, and a few farmers grew seven to 10 cultivars per household. Environmental conditions (land, moisture conditions, etc) as well as usefulness of the cultivar to meet specific needs were the major factors determining farmers' choices. Different cultivars fulfil different livelihood functions, and farmers respond to the multiplicity of needs by growing a range of cultivars. However, in areas with easy access to

markets and good roads such as Rufiji district, very few cultivars were recorded, indicating a trend of cultivating few marketable cultivars.

Both sweet and bitter cultivars were processed into intermediate products such as flour and chips. Usually, sweet cultivars were meant for fresh use and the fresh market; however, since they are available throughout the year they are also processed into flour. Secondly, small roots remaining after selling medium and big roots would also be processed into flour. Bitter cultivars are preferred for processing. Several reasons were given as to why bitter cassava is preferred. Reasons mentioned included; bitter cassava makes good flour, has high dry matter content, makes good stiff porridge 'ugali', and has high starch content. Bitter cassava cannot easily be attacked by vermin because of the bitterness and most of them are late bulking, hence keep long in the soil. Therefore they prefer those for processing.

Results also indicated that farmers in Bagamoyo, Rufiji and Mkinga desired high yielding cultivars as the most frequently cited attribute, but they also wanted other related attributes that could strongly affect positively or negatively the adoption of any improved high yielding variety. Sweetness of the root, high dry matter and high starch, roots that cook well, and flour that make good stiff porridge 'ugali' were among the attributes mentioned in this study that could influence the culinary characteristics and farmers felt that they were important. High yield is linked with pests and disease tolerance. Likewise, farmers desired early maturing cultivars to provide the family not only with food but also with cash. Early maturity here refers to 8-10 months after planting (MAP) and cultivars such as Kiroba, Udugu, Haraka and Kitumbua were early bulking types. However, other farmers wanted late bulking type as the family would be assured of food security.

Marketable roots was frequently cited as most important criteria under other characteristics. Farmers select specific cassava cultivars to meet their market needs, which are measured in terms of ease of marketing. This study revealed a well established trade of fresh cassava roots between Rufiji and Bagamoyo districts and Dar-es-salaam city, whereby cultivars Kiroba and Mfaransa respectively were highly marketed. However, the characteristics of marketable roots are root size and shape and colour of the skin, which determine the demand and price for the

different cassava cultivars in the market (Ntumngia, 2008). Cassava cultivars that are selected for the market, should therefore meet most of these qualities if farmers have to stay competitive in the market and increase income from cassava. The combination of desired traits that meet their culinary, agronomic and other needs are based on local knowledge which is translated into their everyday cultivar selection strategies and practices.

Dry matter content of cultivars most preferred by farmers such as Mfaransa, Kiroba, Udugu and Gago was high (≥35%). Studies by Asaoka et al. (1992) indicated considerable variation in glassiness and hardness of texture of cooked roots between varieties. Hardness of texture in cooked roots is a reflection of RDMC and starch contents. Safo-Kantanka and Owusu-Nipah (1992) studying cooking qualities of cassava reported that mealier varieties had higher contents of dry matter and starch. Similarly, Kawano et al. (1987) also indicated that RDMC was positively correlated with the eating quality especially when roots are consumed after boiling. Graham et al. (1999) and Byrne (1984) commented that high RDMC in cassava roots is important to ensure high recovery of dried roots and for the vast majority of uses, cultivars of high dry matter content are preferred.

To bridge the gap between breeders and farmers and to ensure that new varieties satisfy farmers' preferences and suit their socio-economic situations, it is important to develop and adapt participatory methods for identifying farmers' variety preferences from early stages of breeding in Tanzania. Both participatory variety selection and participatory plant breeding should be used to promote collaborations between farmers and breeders for improved adoption. Improved varieties bred specifically for the new markets, for example high dry matter content varieties for the flour and starch markets and simple processing technology, such as grating, chipping and drying machines, can assist the economic growth of cassava farmers in Tanzania.

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Appendix 1 Crop land area in hectare per household in Bagamoyo, Mkinga and Rufiji districts

Crop	Bagamoyo	Mkinga	Rufiji	Mean	F prob
Cassava	0.67	0.50	1.11	0.74	0.001
Maize	0.22	0.32	0.77	0.40	0.000
Cowpea	0.17	0.17	0.71	0.21	0.001
Pigeon pea	0.16	0.19	-	0.12	0.000
Rice	0.36	-	0.28	0.34	0.482
Sorghum	0.11	-	0.30	0.22	0.064
Groundnut	0.08	-	0.10	0.06	0.667
Sweet potato	0.23	0.20	-	0.23	0.837
Banana	0.13	0.14	0.30	0.15	0.008

Appendix 2 Household data, resources and assets per household in Bagamoyo, Mkinga and Rufiji districts.

	Bagamoyo	Mkinga	Rufiji	Mean	F prob
Number of people in hh	6.41	7.84	6.50	6.84	0.337
People involved in farming	3.27	2.89	2.27	2.89	0.056
Land resources (ha)					
Total farmed land	2.38	2.43	2.67	2.49	
Total land area	2.78	3.00	3.67	3.09	0.309
Livestock resources (number)					
Cattle	-	2.6	-	0.86	-
Goat	6.5	12.6	-	6.4	0.461
Chicken	18.7	15.4	19.9	17.9	0.744
Tree crops resources (number)					
Coconut	28.6	169.5	16.5	80.6	0.041
Cashew	28.2	39.9	172.8	58.1	0.000
Citrus	12.3	73.7	24.5	31.25	0.061
Mango	50.0	20.6	-	16.75	0.271
Household assets					
Bicycle	1.12	1.12	1.4	1.2	0.236
Hand hoes	4.0	4.1	4.0	4.04	0.994
Machete	1.7	2.1	2.0	1.9	0.430
Radio	1.3	1.33	1.29	1.30	0.985
Telephone	1.2	1.0	-	1.1	0.407

Key: hh=household

Appendix 3 Crop management practiced by farmers (%) in Bagamoyo, Mkinga and Rufiji districts

Practice	Bagamoyo	Mkinga	Rufiji	Mean
Seed bed type				
Flat land	100.0	95.0	100.0	98.3
Ridges	-	5.0	-	1.7
Planting arrangement				
In rows	24.13	60.0	10.3	50.3
At random	75.86	40.0	33.3	49.7
Number of weeding				
Two times	10.3	5.0	5.6	6.9
Three times	72.4	95.0	72.2	79.9
Four times	11.0	10.8	-	22.2
Cropping pattern				
Intercrop	96.6	85.0	16.7	66.1
Monocrop	3.4	15.0	83.3	33.9
Spacing				
1 m apart	6.9	50.0	38.9	31.9
> 1 m apart	93.1	35.0	61.1	63.1
< 1 m apart	-	15.0	15.0	5.0
Source of planting material				
Own field	75.9	40.0	66.7	60.8
Nearby village	24.1	5.0	-	9.7
Neighbour	-	30.0	33.3	21.1
Research institution	-	25.0	-	8.3

Appendix 4 Percent farmers who indicated post harvest constraints in Bagamoyo, Mkinga and Rufiji

Constraint	Bagamoyo	Mkinga	Rufiji	Mean
% farmers indicated the processing constraint				
Root rot (CBSD)	28.6	-	-	28.6
Drying takes too long	60.7	90.0	37.5	62.7
Lack of proc eqpt	10.7	20.0	6.3	14.3
Storage pests	13.6	-	31.3	22.5
Peeling problem	7.1	10.0	6.3	7.8
Storage facility	7.1	5.0	18.8	10.8
Transport cost	3.6	5.0	-	4.3
Small margin	-	5.0	6.3	5.7
Water shortage	-	30.0	6.3	18.2
Rapid deterioration	10.7	10.0	6.3	9.0

Appendix 5 List of cassava cultivars grown by farmers in Bagamoyo, Mkinga and Rufiji districts

Varieties	Bagamoyo (N=29)	Mkinga (N=20)	Rufiji (N=18)
Mfaransa	100.0	-	-
Kiroba	42.3	55.0	100.0
Kalolo	55.2	-	-
Mtanga	3.4	-	-
Mzungu	3.4	-	-
Kambinjenga	3.4	-	-
Kitunguu	3.4	-	-
Haraka	-	40.0	-
Mjawa	-	5.0	-
Mpemba	-	30.0	-
Agrikacha	-	10.0	-
Gago	-	65.0	-
Kibandameno	-	35.0	5.6
Macho	-	15.0	-
Udugu	-	70.0	-
Kitumbua	-	15.0	5.6
Mahiza	-	5.0	-
Muarusha	-	20.0	-
Kigoma	-	5.0	5.6
Dide	-	5.0	-
Kibangiri	-	5.0	-
Kitingisha	-	35.0	-
Kiberiti	-	5.0	-
Msusa wa nungu	-	10.0	-
Mwakinyavu	-	15.0	-
Karatasi	-	5.0	-
Marasta	-	5.0	-
Guzo	-	5.0	-
Krismas	-	-	22.2
Usimpejuma	-	-	5.6
Cosmas	-	-	5.6

Appendix 6 Aggregate starch imports and values for Tanzania

YEAR	QUANTITIES	TZS VALUE
1999	4,202,960	1,586,981,407
2000	5,182,093	1,657,058,366
2001	3,755,813	1,330,199,894
2002	5,435,263	1,975,344,180
2003	8,025,824	1,933,936,897
2004	7,896,975	3,178,255,998
May 2005	2,771,211	1,201,844,474

Source: Tanzania Revenue Authority, August 2005; TZS (Tanzania shillings)

Appendix 7 Flow chart of traditional processing technologies

A. BADA (Traditional dry fermented product**)**

Harvest

↓

Peel

↓

Heap [3 – 4 days]

↓

Slice

↓

Dry [one day]

↓

Milling

↓

Flour (Bada)
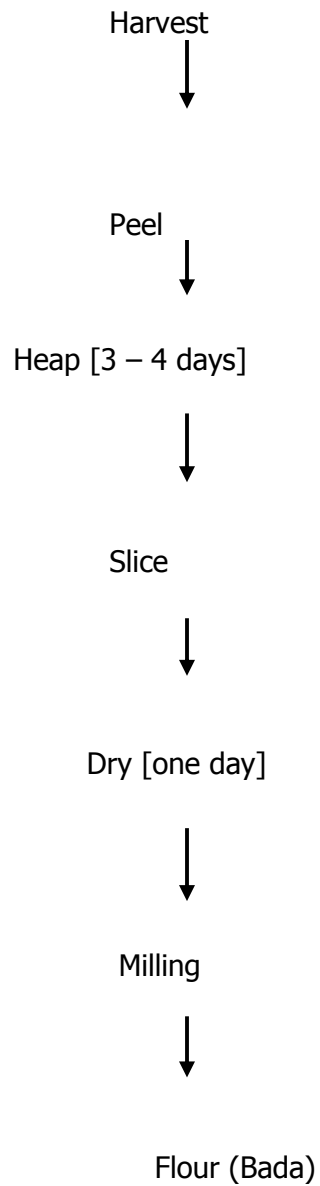
B. KIVUNDE (Traditional wet fermented product)

Harvest

↓

Peel

↓

Soak (3 –4 days) and dewatering

↓

Breaking to small particles

↓

Dry (depend on sun but normally 2-3 days)

↓

Milling

↓

Flour

Chapter 3

Variability in root dry matter content, starch content and yield in cassava cultivars in Tanzania

Abstract

High starch content is an important component of root quality for almost all uses of cassava. The study was conducted to evaluate the variability in root dry matter content, starch quantity and yield of 10 cassava cultivars in Tanzanian environments. The effect of cultivars and harvesting dates were investigated for one season at four locations; SRI-Kibaha, ARI-Chambezi, ARI-Kizimbani and ARI-Hombolo. Harvesting was done at 7, 11, and 14 months after planting (MAP). The root dry matter content (RDMC) ranged between 29 and 40% with the overall mean of 34.3%. Cultivar Namikonga (40%) and Kalolo (29%) had the highest and lowest RDMC respectively. The RDMC at 7 MAP was higher in RDMC than at 11 and 14 MAP. The starch content (StC) ranged between 20.3% (Vumbi) and 24.9% (Namikonga). The StC increased up to 7 MAP, while a decline was observed between 7 and 11 MAP. However, this decline may have commenced during the dry season and continued up to the start of the new season. Starch yield (StY) ranged between 0.54 and 4.09 t ha^{-1}. Cultivar Kiroba had the highest StY. Cassava brown streak disease root necrosis (CBSRN) contributed to poor performance of cultivar Vumbi. From this study it was learned that harvesting could be done at 7-8 MAP for Kibaha and Kizimbani, while at Chambezi and Hombolo, harvesting at 14 MAP could be more profitable. Both StC and fresh storage root yield (FSRY) are important traits when selecting for a commercial cultivar for starch production. Further studies are required to evaluate the effect of CBSRN on starch content and yield, and to determine the accurate trend of starch accumulation considering closer harvest intervals.

3.1   Introduction

Cassava is grown primarily for its enlarged roots, which contain large carbohydrate reserves, mainly starch (Westby, 2002). A typical range of composition in a cassava root includes: water (60-65%); carbohydrate (30-35%); fibre (0.8-1.3%); ash (0.3-1.3%), crude

protein (0.03-0.60%) and ether extracts (0.2-0.6%) (FAO, 2005; Rickard and Behn, 1987). Of its carbohydrate, 64-75% is starch (FAO, 2005). Therefore high starch content is an important component of root quality for almost all uses of cassava (Jennings and Hershey, 1985). Moreover, cassava roots are valued for their starchy properties (Ceballos et al., 2004). Cassava starch has a wide range of applications in both food-related and non-food related industries (Sudarmonowati et al., 2008; Rickard et al., 1991). In food industry starch derivatives have been used as additive compound (candies, bread, canned food, frozen food). In non-food industry they are used in the manufacture of adhesives, paper sizing and textiles (Rickard et al., 1991) and more recently in the production of ethanol and biodegradable polymers (Sudarmonowati et al., 2008). Cassava starch as a raw material in the food industry is bland in taste and has a low tendency to retrograde (Asaoka et al., 1992). Its unique thickening properties, high purity, low cost and its ability to form clear viscous paste gives cassava starch a competitive advantage (Chatakanonda et al., 2003). Starch and starch derivatives, such as dextrins, glucose, and high fructose syrup are the main products of the cassava starch agro-industry.

Variation in RDMC has been reported (Kawano et al., 1987). Studies have shown RDMC ranging between 15-45%, depending on the genotype and environmental conditions (Graham et al., 1999). For the vast majority of uses, cultivars with high dry matter content are preferred (Graham et al., 1999), because increased dry matter content has a positive effect on the extraction efficiency in cassava processing (flour or starch) (Kawano et al., 1987). Variation in starch quantity with values ranging between 13.6 and 35.8% has been reported (Rickard et al., 1991; Rickard and Behn, 1987; Moorthy and Ramanujam, 1986). However, starch content as low as 1.2-3.5% at 6 months after planting (MAP) under stressed conditions and 20.4-25.9% without initial water stress conditions have also been reported (Santisopasri et al., 2001). Both starch quantity and quality are sensitive to the conditions at and immediately after planting. Dry conditions during the early establishment period results in roots with low dry weight and starch content (Sriroth et al., 2001). Starch quantity at harvest is affected by environmental factors such as rainfall and age of the crop prior to harvesting (Sriroth et al., 2001).

Several fibrous roots (3-14) that develop from adventitious roots become storage roots between 60 and 90 days after planting (DAP) (Alves, 2002). At initiation of storage root thickening, the cambium differentiates, the secondary xylem is formed and starch grains are deposited in storage cells, within the amyloplasts (IITA, 2005; Tester et al., 2004) However, storage root initiation is a critical physiological event for the development of root yield. The number of roots initiated, and root enlargement rate (or bulking rate) depend on genotype and environmental factors (IITA, 2005). Rapid root bulking is characterized by a mass of starch-rich parenchymatous tissues (Wholey and Cock, 1974). There is not enough information available regarding the optimum time of harvesting of cassava storage roots for commercially viable starch industry. This study was therefore conducted to evaluate the variability of storage root yield, dry matter content and starch content and yield over time of different cassava cultivars in four cassava growing areas in Tanzania.

3.2   Materials and methods

3.2.1   Germplasm source

Ten cassava cultivars were evaluated in this trial (Table 3.1). Four cultivars were introductions from the Centro Internacional de Agricultura Tropical (CIAT) (AR 42-3, AR 40-6, AR 37-80, CR 25-4) and one from the International Institute of Tropical Agriculture (IITA) (TMS 30001). The other five cultivars (Kalolo, Vumbi, Namikonga, Nanchinyaya and Kiroba) were from local germplasm which included an improved variety (Kiroba) which was released in 2004. The progenitors for the CIAT material include TME 3 (CMD2 gene donor parent), CW66 (green mite resistance), MTAI from Thailand, TMS 30555 from IITA and CM7951-5 from Columbia. The CMD2 gene is believed to enhance resistance against cassava mosaic disease (CMD) (Fregene et al., 2006). Genotypes were considered a fixed effect because they were not randomly sampled to represent an identifiable population of germplasm. The genotypes were evaluated in one season across four locations in Tanzania.

3.2.2 Experimental design

The experiment was laid out in a split plot design, with cultivars the main plots and harvesting dates the sub-plots. The genotypes were evaluated at four sites; SRI-Kibaha (E 038˚58´; S 06˚46´), ARI-Chambezi (E 038˚54´; S 06˚3 4´), ARI-Hombolo (E 03˚55´; S 05˚45´) on the Tanzania mainland and ARI-Kizimbani (E 039˚26´; S 06˚08´) on Zanzibar Island in the 2007/08 season (Table 3.2). At each location the trial was planted in three replications. The genotypes were grown under rain-fed conditions. Planting was done at the beginning of the rainy season, between December and January except for Zanzibar where planting was done in April.

Table 3.1 Description of the ten cultivars used in the study

Cultivar	Description
1. AR 42-3	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
2. AR 40-6	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
3. AR 37-80	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
4. CR 25-4	Clone from CIAT, resistant to CMD, CBB and sweet
5. TMS 30001	Clone from IITA, resistant to CMD, tolerant to CBSD, sweet (Hahn et al., 1980)
6. Kalolo	Local cultivar, bitter taste, high dry matter, good flour quality
7. Namikonga	Local improved cultivar from Amani research centre (EAAFRO), sweet, high dry matter, tolerant to CBSD,
8. Nanchinyaya	Local cultivar, sweet, high dry matter, tolerant to CBSD
9. Vumbi	Local improved cultivar from Amani (EAAFRO) research centre, sweet, early bulking type, good cooking qualities
10. Kiroba	Local improved cultivar, early maturing, tolerant to CBSD, good cooking qualities, sweet, moderate tolerance to CMD

EAAFRO=East African Agricultural and Forestry Research Organization; IITA=International Institute of Tropical Agriculture; CIAT=Centro Internacional de Agricultura Tropical CMD=Cassava mosaic disease; CBSD=Cassava brown streak disease; CGM=Cassava green mite; CBB=Cassava bacterial blight.

Table 3.2 Agro-ecological characteristics of the locations where evaluation was performed, 2007/ 2008

Location	Agro-ecological zones	Soil type	Altitude (m)	Rain (mm)	Wet season	Temp. range (C°)
Kibaha	Sub-humid lowland	Deep clay-sand	158	1028	Oct-Dec Mar-Jun	18-32
Chambezi	Humid lowland	Deep sand Well drained	39	839	Oct-Dec Mar-Jun	22-32
Kizimbani	Humid lowland	Sand loam	72	1730	Sept-Nov March-May	21-32
Hombolo	Semi-arid, mid-altitude	Sand clay	1050	589	Nov-March	11-34

Plants were spaced at 1 m x 1 m giving a population of 10 000 plants ha^{-1}. The plot size was 35 m^2, having seven rows of five plants for each row. No fertilizer or herbicide was applied during the course of the experiment. Hand weeding was done whenever necessary. Harvesting was done at 7, 11 and 14 MAP and data were collected from the middle rows leaving border rows in between plots and border plants at each end of the row to take care of the interference between plots (Kempton, 1997). The harvesting time represents 1) a period at the middle of normal harvesting dates (7 MAP); 2) just before normal harvesting time (11 MAP); and few months after normal harvesting time (14 MAP). The normal harvesting time for breeding trials is 12 MAP.

3.2.3 Data collection

Field data were collected from a net plot of three plants (3 m^2). Samples for RDMC and starch quantity determination were taken. Data on yield and its components were collected at each harvest as follows:

a. Fresh storage root yield (FSRY) included all roots in a plant;
b. Shoot yield (SY) included stems, leaves, and stump;

c. Fresh biomass yield (FBY) included shoot and roots;

d. Dry storage root yield (DSRY) was obtained by multiplying root dry matter content and fresh storage root yield; and

e. Harvest index (HI) was determined by taking a ratio between storage root yield: total biomass

f. Cassava mosaic disease (CMD) severity was subjectively scored at 6 MAP on a scale of 1-5 according to Mahungu and Kanju (1997) as follows:

    1= No symptoms observed;

    2= Mild chlorotic pattern on entire leaflets or mild distortion at base of

    leaflets, the rest of leaflets appearing green and healthy;

    3= Strong mosaic pattern on entire leaf, and narrowing and distortion of

    lower one-third of leaflets;

    4= Severe mosaic with distortion of two-thirds of leaflets and general

    reduction of leaf size;

    5= Severe mosaic, distortion of four-fifths or more of leaflets, twisted and

    misshapen leaves.

g. Cassava brown streak disease (CBSD) severity was assessed subjectively at 6 MAP on above ground parts, on a scale of 1-5 (Mahungu and Kanju, 1997), where;

    1= No visible symptoms;

    2= Slight foliar chlorosis between leaf vein, no stem lesions;

    3= Foliar chlorosis between leaf veins, with mild stem lesions, no die-back

    4= Foliar chlorosis between leaf veins, and pronounced stem lesions with

    beginning of die-back;

    5=Defoliation with pronounced die-back and stem lesions

h. Cassava brown streak disease was assessed subjectively on root necrosis (below ground) as indicated in Figure 3.1 below.
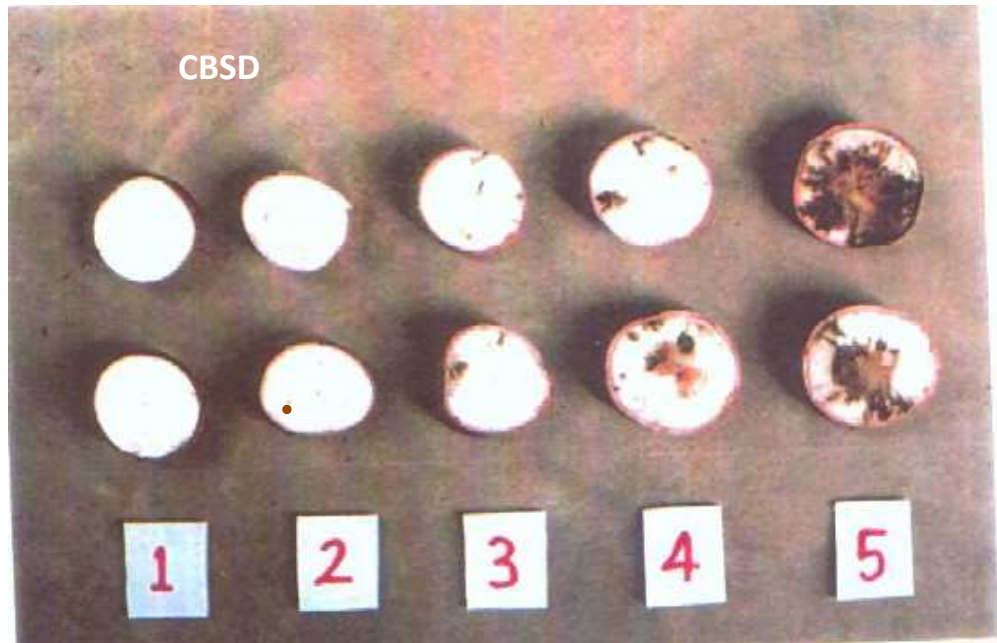
Figure 3.1 Cassava brown streak scoring for severity (class 1-5)

i. Dry mass composition was determined according to Dixon and Nukenine (2000).

- Sampling for root dry matter (RDMC) and starch was done by selecting three representative roots from a bulk of roots harvested from three plants. Cassava roots were washed and cut into thin slices. Duplicate samples of 100 g each were taken and dried in a forced draught oven at 70°C for 72 h. Th e dried samples were weighed to obtain the dry mass, and the dry matter content calculated as percentage of fresh storage root mass were obtained as a proportion of the fresh mass as follows:

$$\text{Dry matter content (\%)} = \left\{ \frac{DM}{FM} \times 100 \right\};$$

Where; FM= Fresh mass and DM= Dry mass

j. Starch content (StC) expressed as percentage of fresh storage root yield was obtained by a modified method of Asaoka et al. (1992).

- The starch granules were isolated by disintegrating 500 g of wet roots using a laboratory Waring blender with excess water. The slurry was double filtered through a sieve mesh and muslin cloth. The residue was rinsed twice with 500 ml of water each time to remove remnants of starch. The filtrate was allowed to settle for 2 h before decanting the liqour. The starch was suspended three times in 3 L water and non-starch materials removed by decanting the supernatant. The starch was then dried in a ventilated oven at 30-33ºC for 72 h, sieved with 200 μm mesh sieve, then placed in polythene bag and stored until required. When a large number of samples were collected and time did not allow prompt analyses, representative samples of roots were put in polythene bags and stored in a deep freezer at -20ºC within 6 h. The dried starch was calculated as a percentage of fresh root weight and dry weight basis as follows.

$$\text{Dry starch (\%)} = \text{DSW} \left\{ \frac{\text{X } 100}{\text{FM}} \right\}$$

Where; FM= Fresh root mass; DSM= Dry starch mass

k. Starch yield in t ha^{-1} was calculated as a product of fresh storage root yield multiplied with the percentage starch of the root.

3.2.4 Statistical analyses

General analyses of variance were performed for all cultivars for yield and other agronomic traits, which included fresh biomass yield, storage root number, fresh storage root yield, dry matter content and starch content using GENSTAT release 11 (Payne et al., 2008) computer package. The F-test and significances of various main effects and interactions were determined using appropriate error term and degree of freedom (McIntosh, 1983).

Mean separation was done by Fisher's protected least significance difference (LSD). Standard analysis of a split plot design was performed according to Cochran and Cox (1992) using the following linear model:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \tau_k + (\alpha\tau)_{ik} + \varepsilon_{ijk}$$

Where:

Y_{ijk} = the response to the ith level factor A and the jth level of factor B in the kth block (replication);

μ = the overall population mean;

α_i = the effect of the ith level of factor A (cultivar);

β_j = the effect of jth level of factor B (harvesting time);

$(\alpha\beta)_{ij}$ = the interaction effect of the ith level of factor A and the jth level of factor

      B;

τ_k = the effect of the kth block (replication)

$(\alpha\tau)_{ik}$ = the interaction effect of the ith level of factor A and the kth block

      (replication)

ε_{ijk} = the random errors (associated with the sub-plots) which are assumed to be independent and normally distributed with mean 0 and variance σ^2;

i   =1, 2,…., a; j=1, 2, …., b; k=1, 2,….., r

Combined analyses of variances (ANOVA) were carried out for fresh storage root yield, root number, dry matter yield, root dry mass expressed as a percentage of root fresh mass (%), starch content (%) and starch yield using Genstat software release 12 (2009). Partitioning of environment was done as location and genotype x location. The following mixed model, with genotype as fixed effect and environment as random was assumed (Bernado, 2002) as follows:

$$P_{ijk} = \mu + g_i + l_j + (gl)_{ij} + e_{ijk}$$

P_{ijk} = phenotypic value of genotype *I* tested in replicate k in environment j

μ = population mean

g_i = genotype effect

l_j = environment/location effect

$(gl)_{ij}$ = genotype x environment interaction effect

e_{ijk} = within environment error term associated with genotype *i*, and

       environment *j* and replicate *k*

Cultivar superiority index for starch content across four environments was determined by calculating the superiority index (Lin and Binns, 1988) using the model: $Pi = \Sigma(X_{ij} - M_j)^2/(2n)$ where Pi = superiority index of ith cultivar in the jth environment (i = 1, 2, 3,…,10; j^{th} = 1, 2, 3,….., 4); Xij= starch content for i^{th} cultivar in j^{th} environment; Mj= maximum starch content for all cultivars in the jth environment; n = number of environments (n = 1, 2, 3, 4). Cultivars with the lowest Pi value were regarded as the most superior and stable across test environments.

The degree of association between FSRY, RDMC and starch content were measured as correlation coefficient (r) as follows (Mead et al., 1993):

r =   <u>Cov(x,y)</u>

       $(S_x S_y)$

Where:

    x = independent variable

    y = dependent variable

    S = sample standard deviation

Variance components for genotype by environment interaction (Bernado, 2002)

$$\sigma^2_p = \sigma^2_G + \sigma^2_E + \sigma^2_{GE} + \sigma^2_e$$

$\sigma^2_G =$ Variance due to phenotype

$\sigma^2_{E\ =}$ Variance due to genotype

$\sigma^2_{GE\ =}$ Variance due to genotype by environment interaction

$\sigma^2_{e\ =}$ Error term

3.3 Results

3.3.1 Agronomic characteristics

Agronomic characteristics considered include storage root number (SRN), SY and FSRY in t ha^{-1}. Other characteristics included are disease mean scores for CMD and CBSD. Results indicated that cultivars and harvesting dates differed significantly ($p \leq 0.001$) in SY across sites with the exception of Hombolo (Table 3.3). Combined means across locations showed that SY ranged from 8.7 to 30.1 t ha^{-1} for cultivar TMS 30001 and AR 37-80 respectively. However, at Hombolo cultivar Namikonga had the highest SY of 20.6 t ha^{-1}, while in other locations cultivar AR 37-80 had the highest SY; Kibaha (12.6 t ha^{-1}), Chambezi (64.7 t ha^{-1}) and Kizimbani (21.0 t ha^{-1}). When the four locations were compared, cultivars at Chambezi site had a higher mean SY of 41.9 t ha^{-1} and the lowest mean SY was recorded at Kizimbani (6.9 t ha^{-1}) (Table 3.3). However, the differences in average SY varied significantly ($p \leq 0.05$) between cultivars within individual harvesting dates, the third harvest (14 MAP) showed significantly higher SY of 24.3 t ha^{-1} (Appendix 1).

Table 3.3 Shoot yield in t ha^{-1} of ten cultivars evaluated at four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7MAP	11MAP	14MAP	Mean†	7MAP	11MAP	14MAP	Mean†
Kalolo	5.78	5.22	6.89	**5.96**	37.81	49.12	31.70	**39.5**
Vumbi	7.39	3.94	6.89	**6.24**	23.90	46.11	40.62	**36.9**
TMS 30001	3.56	5.39	4.28	**4.41**	14.62	29.00	11.13	**18.2**
Namikonga	9.78	8.00	18.90	**12.13**	33.33	51.31	54.41	**46.4**
AR 42-3	6.11	4.39	9.06	**6.52**	22.44	34.45	5.00	**20.6**
AR 40-6	5.22	5.11	17.89	**9.41**	30.12	56.74	91.10	**59.3**
Kiroba	6.78	4.83	9.22	**6.94**	34.25	53.61	57.21	**48.3**
AR 37-80	11.06	7.06	19.67	**12.59**	46.34	86.11	61.73	**64.7**
Nanchinyaya	6.67	7.33	12.33	**8.78**	15.00	44.43	69.41	**43.0**
CR 25-4	2.67	2.89	5.89	**3.81**	15.00	30.41	40.00	**28.5**
Mean	**6.67**	**5.49**	**11.26**	7.81	**29.00**	**49.64**	**47.22**	41.9
LSD (0.05)	4.32	-	8.33	**4.06**	15.90	30.43	35.21	**16.0**
CV (%)	17.9	29.6	36.92	**30.64**	6.70	14.00	7.23	**22.4**
F probability	0.023*	0.107ns	0.006**	**0.003****	0.002**	0.037*	0.002**	**0.001*****

Cultivar	Kizimbani				Hombolo			Overall	
	7MAP	11MAP	14MAP	Mean†	7MAP	11MAP	14MAP	Mean†	Mean‡
Kalolo	3.56	4.67	1.56	**3.26**	4.89	4.30	14.11	**7.76**	**14.23**
Vumbi	4.67	4.22	3.89	**4.26**	12.22	6.91	29.47	**16.20**	**15.75**
TMS 30001	3.11	4.22	1.33	**2.89**	6.33	6.47	15.78	**9.53**	**8.67**
Namikonga	6.89	10.27	11.44	**9.67**	13.56	5.80	42.33	**20.56**	**24.11**
AR 42-3	2.56	5.44	2.67	**3.56**	6.22	5.56	11.20	**7.33**	**9.57**
AR 40-6	4.00	7.78	10.67	**7.48**	16.11	11.33	32.61	**20.02**	**25.09**
Kiroba	6.67	4.44	3.11	**4.74**	14.00	7.63	26.22	**15.95**	**19.45**
AR 37-80	8.44	23.56	31.11	**21.04**	12.56	8.19	29.33	**16.69**	**30.07**
Nanchinyaya	4.22	11.67	4.11	**6.67**	7.56	7.78	11.67	**9.00**	**17.50**
CR 25-4	4.00	6.89	7.56	**6.15**	5.67	3.06	33.50	**14.07**	**13.54**
Mean	**5.08**	**8.30**	**7.16**	6.85	**10.62**	**8.22**	**23.71**	14.16	18.35
LSD (0.05)	-	9.79	-	**10.09**	6.23	5.74	-	-	-
CV (%)	14.00	24.3	38.20	**22.7**	20.51	11.81	12.01	**43.2**	**36.00**
F probability	0.174ns	0.02*	0.104ns	**0.04***	0.003**	0.001***	0.293ns	**0.133**	**0.352**

Significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001   †= cultivar mean over three harvest dates; MAP=months after planting

Results also showed that both cultivars (p≤0.01) and harvesting dates (p≤0.001) differed significantly in SRN plant^{-1} (Table 3.4). The mean SRN across locations ranged between 2.1 (Vumbi) and 5.2 (AR 40-6) roots plant^{-1} (Table 3.4). Cultivar AR 40-6 showed higher SRN at three locations as observed at Hombolo (6.6 roots), Chambezi (7.7 roots), and Kizimbani (2.2 roots plant^{-1}). However, at Kibaha site the highest number of SRN was observed from cultivar Nanchinyaya (4.1 roots ha^{-1}). Among the three harvesting dates, the second harvest (11 MAP) had significantly (p≤0.001) higher SRN of 6.4 roots plant^{-1} than the other two harvests (Appendix 1). Plants at Chambezi site had relatively higher mean SRN (5.1 root plant^{-1}) than the other sites (Table 3.4).

Significant differences were observed between cultivars (p≤0.05) and harvesting dates (p≤0.001) for FSRY (Table 3.5) across locations. The mean FSRY ranged between 4.0 and 17.5 t ha^{-1} from cultivar Vumbi and AR 40-6, respectively. For individual harvesting dates, the mean FSRY of 17.7 t ha^{-1} at 14 MAP was significantly higher than the mean FSRY at 7 and 11 MAP (6.0 and 10.9 t ha^{-1}, respectively) (Appendix 1). Plants at Chambezi site recorded relatively higher mean FSRY of 21.4 t ha^{-1} (Table 3.5).

Cultivars differed significantly (p≤0.05) in mean dry storage root yield (DSRY) across locations. The mean DSRY ranged between 1.4 and 6.6 t ha^{-1} for cultivar Vumbi and Kiroba respectively (Table 3.6). Mean DSRY in t ha^{-1} were significantly higher (p≤0.001) at 14 MAP (5.8 t ha^{-1}) than the other two harvesting dates (Appendix 2). When sites were compared, plants at Chambezi site had relatively higher DSRY of 6.7 t ha^{-1} than other sites (Table 3.6).

Mean harvest index (HI) differed significantly between cultivars (p≤0.001). The differences in HI between harvesting dates were not significant. The HI ranged between 0.23 and 0.50 from cultivars Vumbi and Kiroba respectively (Table 3.7). For individual locations, cultivars at Kizimbani site had relatively higher mean HI (0.47) than the other three sites. When individual cultivars were considered for the same trait, cultivar AR 42-3 had generally higher HI of 0.72 (14 MAP) while cultivar Namikonga recorded the lowest of 0.01 (7 MAP) both at Hombolo site (Table 3.7).

Table 3.4 Storage root number plant^{-1} of 10 cultivars evaluated at four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	2.4	3.0	2.4	**2.6**	6.3	6.4	5.1	**6.0**
Vumbi	2.1	1.8	1.3	**1.7**	4.1	2.6	2.6	**3.1**
TMS 30001	1.9	2.9	2.9	**2.6**	2.1	3.2	1.8	**2.4**
Namikonga	3.4	2.8	3.4	**3.2**	5.1	3.2	7.1	**5.2**
AR 42-3	2.9	2.6	2.6	**2.7**	4.0	4.0	1.1	**3.0**
AR 40-6	3.0	3.1	4.0	**3.4**	6.4	7.7	9.0	**7.7**
Kiroba	3.1	2.8	2.8	**2.9**	6.9	7.8	8.0	**7.5**
AR 37-80	3.8	3.1	1.9	**2.9**	4.1	4.7	4.6	**4.4**
Nanchinyaya	4.3	4.8	3.2	**4.1**	4.1	6.7	6.6	**5.8**
CR 25-4	2.3	1.9	2.1	**2.1**	3.7	5.0	6.4	**5.0**
Mean	**2.9**	**2.8**	**2.7**	**2.8**	**4.7**	**5.2**	**5.3**	**5.1**
LSD (0.05)	15.6	16.6	13.8	**14.8**	25.5	-	34.5	**23.3**
CV (%)	5.8	14.6	11.4	**16.9**	31.7	12.7	12.0	**26.8**
F probability	0.092ns	0.073ns	0.036*	**0.001*****	0.029*	0.136ns	0.001ns	**0.001ns**

Cultivar	Kizimbani				Hombolo				Overall
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	Mean‡
Kalolo	0.7	1.3	0.6	**0.9**	2.2	2.7	4.8	**3.2**	3.2
Vumbi	0.3	0.8	1.3	**0.8**	2.2	1.1	6.2	**3.2**	2.1
TMS 30001	2.6	2.1	1.4	**2.0**	2.2	4.2	4.8	**3.7**	2.9
Namikonga	1.9	1.7	2.4	**2.0**	0.1	0.2	3.8	**1.3**	3.0
AR 42-3	0.3	2.7	0.3	**1.1**	1.9	4.1	5.3	**3.8**	2.8
AR 40-6	1.9	2.3	2.3	**2.2**	4.2	7.2	8.3	**6.7**	5.1
Kiroba	2.1	2.3	1.6	**2.0**	3.1	4.7	7.3	**5.0**	4.4
AR 37-80	1.6	1.9	2.6	**2.0**	3.4	4.0	6.3	**4.6**	3.6
Nanchinyaya	1.9	2.3	1.4	**1.9**	3.4	3.8	6.9	**4.7**	4.1
CR 25-4	1.3	1.8	2.7	**1.9**	1.6	1.7	4.4	**2.6**	3.0
Mean	**1.8**	**2.1**	**1.6**	**1.9**	**2.9**	**4.2**	**5.7**	**4.3**	**3.6**
LSD (0.05)	11.9	17.6	21.1	**10.9**	20.8	27.3	34.0	**26.7**	17.5
CV (%)	19.0	48.4	76.7	**34.1**	29.0	37.9	35.1	**23.6**	50.6
F probability	0.001***	0.057ns	0.325ns	**0.002****	0.001***	0.001***	0.048*	**0.002****	**0.001*****

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001 †= cultivar mean over three harvest dates; ‡=Mean across locations

Table 3.5 Fresh storage root yield (t ha^{-1}) of 10 cultivars evaluated in four locations and three intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	Mean†
Kalolo	4.00	4.92	6.11	**5.02**	18.61	36.72	32.62	**29.29**
Vumbi	2.82	2.06	2.53	**2.47**	4.42	4.71	8.91	**6.00**
TMS 30001	2.36	7.00	7.44	**5.60**	5.91	18.39	13.29	**12.60**
Namikonga	5.50	5.39	11.61	**7.50**	6.74	8.93	40.00	**18.53**
AR 42-3	4.37	4.56	9.19	**6.04**	10.33	23.91	5.63	**13.31**
AR 40-6	3.79	4.89	10.62	**6.43**	14.21	32.39	60.00	**35.53**
Kiroba	6.64	5.83	10.44	**7.64**	27.22	42.64	58.33	**42.69**
AR 37-80	5.46	4.50	3.33	**4.43**	11.91	20.00	12.81	**14.94**
Nanchinyaya	5.08	5.94	6.23	**5.75**	4.74	24.44	34.42	**21.22**
CR 25-4	3.09	3.17	5.44	**3.90**	6.23	18.41	38.33	**21.01**
Mean	**4.30 (2.27)**	**4.69 (2.35)**	**7.38 (2.79)**	**5.45 (2.41)**	**10.81(3.27)**	**23.33 (4.65)**	**29.91 (5.10)**	**21.43 (4.34)**
LSD (0.05)	3.16 (0.67)	4.20 (0.83)	4.78 (0.90)	**2.62 (0.51)**	12.11 (1.41)	26.42 (2.37)	26.44 (2.65)	**13.34 (1.54)**
CV (%)	13.5 (17.1)	29.7 (20.5)	23.9 (18.8)	**28.2 (22.0)**	14.14 (25.4)	66.51 (29.9)	51.82 (30.5)	**36.71 (37.8)**
F probability	0.227 (0.16)	0.48 (0.42)	0.01 (0.01)	**0.115 (<0.001)**	0.021 (0.008)	0.188 (0.055)	0.002 (0.002)	**0.085**

Cultivar	Kizimbani				Hombolo			Overall	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	Mean†	Mean‡
Kalolo	2.00	6.22	2.00	**3.41**	2.34	2.11	11.11	**5.19**	**10.92**
Vumbi	1.44	1.56	2.78	**1.93**	2.33	1.12	18.13	**7.20**	**3.97**
TMS 30001	3.56	9.56	3.78	**5.63**	2.85	5.93	16.73	**8.50**	**9.10**
Namikonga	2.44	8.89	11.33	**7.56**	0.23	0.47	9.44	**3.38**	**9.14**
AR 42-3	0.67	9.78	0.89	**3.78**	1.85	4.44	24.51	**10.27**	**9.12**
AR 40-6	13.33	9.33	7.33	**10.00**	6.17	12.07	37.52	**18.58**	**17.53**
Kiroba	9.78	13.11	7.78	**10.22**	5.33	4.29	27.33	**12.32**	**17.04**
AR 37-80	4.44	15.56	13.11	**11.04**	5.08	4.54	33.38	**14.33**	**12.35**
Nanchinyaya	4.89	13.78	8.00	**8.89**	3.79	7.00	8.39	**6.39**	**10.71**
CR 25-4	2.89	9.11	16.89	**9.63**	1.57	1.37	27.36	**10.10**	**10.36**
Mean	**5.06 (2.25)**	**10.28 (3.21)**	**7.12 (2.64)**	**7.49 (2.63)**	**3.83 (1.93)**	**5.34 (2.16)**	**20.50 (4.42)**	**9.89**	**11.13 (3.14)**
LSD (0.05)	- -	- (1.50)	- (1.72)	**- (0.97)**	3.69 (0.89)	4.91 (0.94)	- (2.83)	**-**	**3.01(-)**
CV (%)	127.3 (40.8)	56.7 (27.3)	89.3 (37.9)	**58.2 (39.1)**	56.6 (26.9)	54.0 (25.4)	70.6 (37.2)	**52.5**	**96.1(31.6)**
F probability	0.319 (0.113)	0.179 (0.100)	0.111 (0.043)	**0.173 (0.002)**	0.001 (0.048)	0.001 (0.002)	0.222(0.24)	**0.106**	**0.001(0.596)**

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations
Values in brackets are transformed using Genstat release 12; Square root = (x + 1.0)**0.5, x=observed value

Table 3.6 Dry storage root yield (t ha^{-1}) of 10 cultivars evaluated at four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	1.36	1.56	1.56	**1.50**	6.20	10.36	9.30	**8.62**
Vumbi	0.98	0.28	0.58	**0.62**	1.47	0.92	2.40	**1.60**
TMS 30001	0.90	2.71	1.93	**1.85**	1.80	5.01	4.60	**3.81**
Namikonga	2.31	2.08	4.71	**3.04**	2.58	3.17	15.57	**7.11**
AR 42-3	1.72	1.66	2.74	**2.04**	3.60	8.08	0.00	**3.89**
AR 40-6	1.56	1.84	3.29	**2.23**	4.98	10.65	17.46	**11.03**
Kiroba	2.41	2.03	3.51	**2.65**	9.49	14.79	18.57	**14.29**
AR 37-80	2.10	1.39	0.87	**1.45**	3.91	0.00	1.04	**1.65**
Nanchinyaya	2.16	2.32	2.07	**2.18**	1.86	9.24	12.45	**7.85**
CR 25-4	1.22	1.08	1.85	**1.38**	2.24	5.97	11.29	**6.50**
Mean	**1.66 (1.62)**	**1.65 (1.61)**	**2.35 (1.78)**	**1.89 (1.67)**	**3.77 (2.10)**	**7.07 (2.63)**	**9.14 (2.90)**	**6.68 (2.55)**
LSD (0.05)	1.18 (0.36)	1.69 (0.47)	1.57 (0.44)	**0.95 (0.26)**	4.25 (0.81)	7.86 (1.25)	8.57 (1.37)	**4.92 (0.85)**
CV (%)	41.7 (12.9)	60.2 (17.2)	39.2 (14.5)	**53.5 (16.7)**	66.1 (22.6)	65.3 (27.8)	55.0 (27.9)	**78.6 (35.4)**
F probability	0.142 (0.105)	0.265 (0.144)	0.001(0.001)	**0.001 (0.001)**	0.026 (0.014)	0.021 (0.002)	0.001 (0.001)	**0.001 (0.001)**

Cultivar	Kizimbani				Hombolo			Overall	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	0.62	2.08	0.60	**1.10**	1.64	0.44	3.53	**1.63**	**3.20**
Vumbi	0.40	0.51	0.93	**0.61**	0.91	0.14	6.65	**2.51**	**1.37**
TMS 30001	1.13	2.80	0.86	**1.60**	1.05	1.37	6.43	**2.95**	**2.15**
Namikonga	1.11	4.11	4.89	**3.37**	0.00	0.00	3.59	**1.20**	**3.82**
AR 42-3	0.22	2.85	0.28	**1.12**	0.72	1.19	10.42	**4.11**	**2.76**
AR 40-6	4.88	3.40	2.75	**3.67**	2.60	3.17	14.92	**6.89**	**6.30**
Kiroba	3.98	4.52	3.18	**3.89**	2.13	1.01	10.43	**4.52**	**6.55**
AR 37-80	1.73	6.14	4.59	**4.15**	2.01	0.72	12.42	**4.63**	**3.54**
Nanchinyaya	2.10	5.56	3.26	**3.64**	1.63	1.31	3.30	**2.08**	**4.16**
CR 25-4	1.17	3.73	6.79	**3.90**	0.63	0.19	10.01	**3.61**	**4.08**
Mean	**1.95 (1.62)**	**3.82 (2.12)**	**2.86 (1.83)**	**2.83 (1.86)**	**1.59 (1.48)**	**1.35 (1.35)**	**7.63(2.86)**	**3.46(1.90)**	**3.84 (1.99)**
LSD (0.05)	4.13 (-)	3.79 (0.80)	4.07 (0.93)	**2.37 (0.53)**	1.40 (0.42)	1.56 (0.44)	9.24 -	**4.35(-)**	**3.78 (-)**
CV (%)	21.1 (31.8)	58.3 (22.2)	39.2 (29.9)	**89.4 (31.0)**	51.6 (16.3)	68.0 (18.7)	71.1(32.7)	**134.4(49.6)**	**107.2(26.2)**
F probability	0.269 (0.103)	0.105 (0.043)	0.062 (0.021)	**0.005 (0.001)**	0.001(0.011)	0.001 (0.004)	0.117(0.17)	**0.369(0.26)**	**0.001(0.232)**

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations
Values in brackets are transformed using Genstat release 12; Square root = (x + 1.0)**0.5, x=observed value

Table 3.7 Harvest index of 10 cultivars evaluated in four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	0.46	0.44	0.51	**0.47**	0.32	0.39	0.50	**0.40**
Vumbi	0.29	0.36	0.27	**0.31**	0.16	0.09	0.16	**0.14**
TMS 30001	0.39	0.49	0.63	**0.51**	0.26	0.33	0.67	**0.42**
Namikonga	0.36	0.37	0.40	**0.38**	0.17	0.13	0.42	**0.24**
AR 42-3	0.42	0.54	0.54	**0.50**	0.32	0.41	0.53	**0.42**
AR 40-6	0.42	0.51	0.55	**0.44**	0.30	0.35	0.39	**0.35**
Kiroba	0.47	0.56	0.55	**0.52**	0.41	0.44	0.51	**0.45**
AR 37-80	0.34	0.39	0.16	**0.30**	0.21	0.19	0.17	**0.19**
Nanchinyaya	0.44	0.44	0.32	**0.40**	0.25	0.35	0.33	**0.31**
CR 25-4	0.55	0.50	0.47	**0.51**	0.28	0.38	0.48	**0.38**
Mean	**0.41**	**0.45**	**0.42**	0.43	**0.26**	**0.30**	**0.41**	0.32
LSD (0.05)	0.15	0.17	0.16	**0.10**	0.12	0.11	0.08	**0.07**
CV (%)	21.8	21.8	19.0	**14.2**	27.8	21.1	11.6	**18.3**
F probability	0.09ns	0.097ns	0.001***	**0.02****	0.006**	0.001***	0.001***	**0.001****

Cultivar	Kizimbani				Hombolo				Overall
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	0.24	0.59	0.27	**0.37**	0.19	0.32	0.19	**0.23**	**0.39**
Vumbi	0.19	0.21	0.31	**0.24**	0.14	0.14	0.39	**0.23**	**0.22**
TMS 30001	0.55	0.65	0.75	**0.65**	0.26	0.47	0.24	**0.33**	**0.45**
Namikonga	0.26	0.46	0.47	**0.40**	0.01	0.07	0.18	**0.09**	**0.27**
AR 42-3	0.21	0.50	0.16	**0.29**	0.19	0.44	0.72	**0.45**	**0.39**
AR 40-6	0.61	0.55	0.41	**0.52**	0.25	0.53	0.54	**0.44**	**0.44**
Kiroba	0.57	0.75	0.68	**0.67**	0.26	0.35	0.47	**0.36**	**0.50**
AR 37-80	0.33	0.38	0.31	**0.34**	0.31	0.37	0.53	**0.40**	**0.31**
Nanchinyaya	0.52	0.56	0.66	**0.58**	0.33	0.41	0.42	**0.39**	**0.42**
CR 25-4	0.43	0.56	0.69	**0.56**	0.20	0.31	0.51	**0.34**	**0.45**
Mean	**0.41**	**0.54**	**0.46**	0.47	**0.23**	**0.35**	**0.44**	0.33	0.39
LSD (0.05)	0.25	0.25	0.36	-	0.16	0.19	0.24	-	-
CV (%)	36.7	27.9	20.2	**23.0**	38.2	33.6	31.1	**40.3**	**32.3**
F probability	0.007**	0.018*	0.029*	**0.246ns**	0.011*	0.003**	0.008**	**0.098ns**	**0.703ns**

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

3.3.2 Virus diseases

Cultivars differed significantly (p≤0.001) in their reaction to cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) (Table 3.8 and 3.9). The mean score across locations showed that cultivars Namikonga (2.7) and Vumbi (2.4) had higher rates of CMD infection than other cultivars. Cultivars AR 40-6 (1.1), AR 42-3 (1.2), AR 37-80 (1.2) and CR 25-4 (1.2) showed the lowest rates of CMD infection. Plants at Chambezi location recorded the highest rate of CMD infection (2.2). Combined mean score across locations indicated significant differences in the rate of CBSD infection between cultivars. Cultivar CR 25-4 (2.9) and AR 37-80 (2.8) had the highest rate of CBSD infection across locations, while cultivar Namikonga showed the lowest rate of CBSD infection (1.3). Hombolo site had significantly lower rate of CBSD (1.5) and CMD (1.2) infection compared to the other sites.

Significant differences in CBSRN were observed between cultivars (p≤0.001). However, harvesting dates did not significantly influence CBSRN, except for Chambezi site. Cultivar Vumbi recorded an overall mean score of 2.8 across locations and harvesting dates (Table 3.10). For individual locations, cultivar Vumbi scored 3.8 (Kibaha); 3.0 (Chambezi); 2.7 (Kizimbani); and 1.7 (Hombolo). However, cultivar AR 42-3 scored 3.5 and 3.1 at Chambezi and Kizimbani, respectively which was relatively higher than other cultivars. Cultivars Namikonga and Nanchinyaya did not exhibit CBSRN at any of the sites or three harvesting dates and appeared to have tolerance to CBSD.

Table 3.8 Cassava mosaic disease (CMD) severity of 10 cultivars recorded at six months after planting at four locations in Tanzania, 2007/08

	Location				
Cultivar	Kibaha	Chambezi	Kizimbani	Hombolo	**Overall mean**
Kalolo	1.91	3.07	2.13	1.07	**2.05**
Vumbi	2.85	3.27	2.09	1.21	**2.36**
TMS 30001	1.82	2.44	1.82	1.00	**1.77**
Namikonga	2.24	3.57	2.83	2.25	**2.72**
AR 43-2	1.02	1.00	1.96	1.00	**1.25**
AR 40-6	1.00	1.13	1.43	1.00	**1.14**
Kiroba	1.80	2.85	2.36	1.07	**2.02**
AR 37-80	1.00	1.02	1.62	1.13	**1.19**
Nanchinyaya	2.44	2.87	2.13	1.05	**2.12**
CR 25-4	1.00	1.00	1.89	1.00	1.22
Mean	1.84	2.20	2.03	1.17	**1.82**
LSD (5%)	0.35	2.22	0.37	0.33	**0.44**
CV (%)	3.70	7.80	5.20	4.00	**3.70**
F probability	0.001***	0.001***	0.001***	0.001***	**0.001***

Significance levels: * p≤0.05**; p≤0.01; *** p≤0.001

Table 3.9 Cassava brown streak disease (CBSD above ground) severity recorded at six months after planting of 10 cultivars evaluated at four locations in Tanzania, 2007/08

	Location				
Cultivar	Kibaha	Chambezi	Kizimbani	Hombolo	**Overall mean**
Kalolo	2.43	2.12	3.00	1.17	**2.18**
Vumbi	1.47	2.08	2.98	1.36	**1.98**
TMS 30001	2.33	2.62	1.52	1.08	**1.89**
Namikonga	1.09	1.27	1.92	1.05	**1.33**
AR 42-3	3.74	2.93	2.10	1.56	**2.58**
AR 40-6	2.64	2.65	1.72	1.90	**2.23**
Kiroba	2.28	1.82	2.20	1.27	**1.89**
AR 37-80	3.54	2.97	2.72	2.11	**2.83**
Nanchinyaya	2.07	2.16	1.98	1.16	**1.84**
CR 25-4	3.25	2.68	3.29	2.43	**2.91**
Mean	2.38	2.31	2.34	1.46	**2.11**
LSD (5%)	0.35	0.85	0.72	0.39	**0.58**
CV (%)	2.30	7.30	12.4	9.70	**7.20**
F probability	0.001***	0.013**	0.001***	0.001***	**0.001***

Significance levels: * $p \leq 0.05$**; $p \leq 0.01$; *** $p \leq 0.001$

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Table 3.10 Root necrosis scores (for CBSD) of 10 cultivars recorded at each harvest date at four locations in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	1.67	1.67	2.33	**1.89**	1.33	1.00	2.33	**1.56**
Vumbi	3.67	4.00	3.67	**3.78**	3.67	4.00	1.33	**3.00**
TMS 30001	3.00	2.00	3.00	**2.67**	3.33	2.00	2.17	**2.50**
Namikonga	1.00	1.00	1.00	**1.00**	1.00	1.00	1.00	**1.00**
AR 42-3	2.33	2.33	2.67	**2.44**	3.67	2.67	4.17	**3.50**
AR 40-6	1.00	1.00	1.00	**1.00**	1.00	1.33	1.33	**1.22**
Kiroba	1.33	1.00	1.00	**1.11**	1.00	1.00	1.00	**1.00**
AR 37-80	3.00	3.67	3.67	**3.44**	3.00	3.33	3.33	**3.22**
Nanchinyaya	1.00	1.00	1.00	**1.00**	1.67	1.00	1.00	**1.22**
CR 25-4	1.67	1.67	2.00	**1.78**	2.33	2.00	2.33	**2.22**
Mean	**2.03**	**2.00**	**2.18**	**2.07**	**2.15**	**1.94**	**2.03**	**2.04**
LSD (0.05)	0.93	0.68	1.63	**1.12**	1.31	1.06	1.15	**1.15**
CV (%)	26.8	19.8	43.8	**16.1**	35.8	32.1	33.1	21.9
F probability	0.001***	0.001***	0.006**	**0.991ns**	0.001***	0.001***	0.001***	**0.004**

Cultivar	Kizimbani				Hombolo			Overall	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	2.33	2.33	2.83	**2.50**	1.47	2.00	1.13	**1.53**	**1.80**
Vumbi	1.34	3.83	2.83	**2.67**	1.00	2.67	1.33	**1.67**	**2.77**
TMS 30001	2.00	2.67	2.00	**2.22**	2.00	2.33	1.67	**2.00**	**2.38**
Namikonga	1.00	1.00	1.00	**1.00**	1.01	1.00	1.00	**1.02**	**1.00**
AR 42-3	3.53	2.67	3.20	**3.13**	1.92	2.33	1.00	**1.75**	**2.63**
AR 40-6	1.33	1.67	1.33	**1.44**	1.00	1.33	1.00	**1.11**	**1.19**
Kiroba	1.00	1.00	1.00	**1.11**	1.00	1.33	1.00	**1.11**	**1.08**
AR 37-80	2.00	1.67	2.00	**1.89**	1.33	2.33	2.00	**1.89**	**2.61**
Nanchinyaya	1.00	1.00	1.00	**1.00**	1.00	1.33	1.00	**1.11**	**1.08**
CR 25-4	1.33	1.33	1.33	**1.33**	1.00	2.00	1.00	**1.33**	**1.67**
Mean	**1.63**	**1.86**	**1.87**	**1.78**	**1.25**	**1.82**	**1.19**	**1.42**	**1.82**
LSD (0.05)	1.06	1.14	-	-	0.72	-	0.39	-	**0.63**
CV (%)	37.6	36.3	55.3	**43.1**	33.6	35.9	19.9	**37.0**	**37.5**
F probability	0.004**	0.002**	0.272ns	**0.472ns**	0.022*	0.55ns	0.001***	**0.432ns**	**0.001***

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

3.3.3   Root dry matter content

Root dry matter content (RDMC) differed significantly between cultivars (p≤0.05) within individual locations (Table 3.11) and harvesting dates (p≤0.05). However, harvesting dates across locations did not cause significant differences in RDMC (Appendix 2). The RDMC based on cultivar averages over locations and harvesting dates ranged from 29.1% (Kalolo) to 40.3% (Namikonga) with the overall mean of 34.1% (Table 3.11). However, individual cultivar averages for the trait ranged from 10.0% (Kalolo; 14 MAP) to 46.5% (Namikonga; 11 MAP) both at Kizimbani. For individual locations, the lowest RDMC was observed from cultivar AR 37-80 at Chambezi (16.0%; 14 MAP) and Hombolo (13.8%; 11 MAP) and the highest for the same locations was observed from cultivar Nanchinyaya (39.3% and 42.8% respectively). At Kibaha the RDMC ranged from 22.0% (Vumbi; 11 MAP) to 42.2% (Nanchinyaya; 7 MAP) and at Kizimbani RDMC ranged between 10.0% (Kalolo; 14 MAP) and 46.5% (Namikonga; 11 MAP). The RDMC at 7 MAP was significantly higher (37.2%) than other harvesting dates across locations, (Appendix 2).

3.3.4   Starch content

Significant differences (p≤0.01) in starch content (StC) were observed between cultivars within individual harvesting dates (Appendix 2; Table 3.12). The overall mean StC was 22.8%, with the maximum StC of 24.9% (Namikonga) and the minimum content of 20.29% (Vumbi) across locations, cultivars and harvesting dates. However, for individual cultivars the same trait ranged from 2.8% (Hombolo; 11 MAP) to 35.2% (Kizimbani; 14 MAP) both from cultivar TMS 30001 observed at different harvesting dates (Table 3.12). For individual harvesting dates across locations, the mean StC ranged from 20.0% (11 MAP) to 24.8% (14 MAP) (Appendix 2). However, at 7 MAP, cultivar AR 42-3 had StC of 26.9% which was the highest for the harvesting date; the lowest was recorded from cultivar Vumbi (16.1%; 7 MAP), (Appendix 2). However, cultivar Vumbi had the highest StC of 24.0% (11 MAP) and cultivar AR42-3 the lowest (17.0%; 11 MAP) (Appendix 2). At 14 MAP, cultivar TMS 30001 had the highest StC (30.6%) across all locations and cultivars, while the lowest at 14 MAP was observed from cultivar Kalolo (16.3%). Different locations had relatively different StC for the same cultivars. At Kibaha, the highest StC was observed from cultivar AR 37-80 (30.1%;

7 MAP), and the lowest from cultivar Kalolo (14.5%; 14 MAP), (Table 3.12; Figure 3.2). At Chambezi cultivar Namikonga showed the highest StC (28.5%; 14 MAP) while the lowest was from cultivar AR 42-3 (13.0%; 11 MAP) (Figure 3.3). At Kizimbani, cultivar TMS 30001 had the highest (35.2%) while cultivar Kalolo had the lowest (10.5%) StC both at 14 MAP (Figure 3.4). At Hombolo, the StC ranged between 2.8% (Kalolo; 11 MAP) and 31.9% (AR 42-3; 14 MAP) (Figure 3.5). When sites were compared, Kizimbani site had relatively higher mean StC (25.2%) than other sites.

Significant differences between harvesting dates were observed ($p \leq 0.001$) in StC as a proportion of DSRY (dry starch/dry storage root yield) (Table 3.13). Cultivar TMS 30001 showed highest StC of 72% on dry weight basis, while AR 40-6 was the lowest (58%). The StC of 70% at 14 MAP was significantly higher than at 7 and 11 MAP ($p \leq 0.01$) (Table 3.13).

Table 3.11 Root dry matter content (%) of 10 cultivars evaluated in four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	34.17	31.33	25.67	**30.39**	33.17	29.00	28.67	**30.28**
Vumbi	35.33	27.70	22.00	**28.35**	33.17	36.42	32.17	33.92
TMS 30001	36.33	36.83	25.83	**33.00**	33.40	31.65	33.71	**32.92**
Namikonga	42.17	37.50	40.17	**39.94**	38.33	36.83	39.00	**38.06**
AR 42-3	39.33	36.33	29.00	**34.89**	35.33	33.83	30.96	**33.58**
AR 40-6	41.00	36.83	32.67	**36.83**	35.17	32.67	29.67	**32.50**
Kiroba	36.17	34.17	33.67	**34.67**	35.33	34.83	31.50	**33.89**
AR 37-80	38.50	31.50	29.17	**33.06**	33.00	24.79	16.04	**24.61**
Nanchinyaya	42.17	39.17	33.17	**38.17**	39.33	37.67	34.67	**37.22**
CR 25-4	38.83	33.50	33.00	**35.11**	36.00	32.33	29.50	**32.61**
Mean	**38.30**	**34.43**	**30.68**	34.47	**35.40**	**37.22**	**30.75**	33.16
LSD (0.05)	3.91	4.81	7.17	**5.29**	2.61	2.88	6.66	**4.04**
CV (%)	6.00	8.10	13.7	**9.80**	4.3	4.8	12.2	**7.10**
F probability	0.003**	0.004**	0.003**	**0.001***	0.001***	0.001***	0.001***	**0.001***

Cultivar	Kizimbani				Hombolo			Overall	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	28.88	33.50	10.00	**24.13**	40.04	19.33	29.77	**29.78**	**28.12**
Vumbi	29.67	20.45	28.22	**26.11**	38.00	22.05	35.50	**31.84**	**30.95**
TMS 30001	31.67	32.17	33.17	**32.33**	33.87	22.33	40.20	**32.00**	**32.44**
Namikonga	45.00	46.50	42.67	**44.72**	40.19	26.41	38.00	**34.87**	**40.16**
AR 42-3	34.33	30.83	31.46	**32.21**	26.00	27.00	41.00	**31.33**	**33.37**
AR 40-6	38.33	36.33	36.83	**37.33**	41.50	26.00	40.08	**34.74**	**35.63**
Kiroba	39.33	35.50	40.50	**36.97**	40.17	20.67	39.67	**33.50**	**35.13**
AR 37-80	37.33	35.50	40.50	**38.44**	39.33	13.83	34.00	**29.06**	**32.04**
Nanchinyaya	42.67	39.50	41.37	**41.18**	42.83	21.33	38.83	**34.33**	**33.59**
CR 25-4	40.33	40.50	40.17	**40.33**	39.33	35.83	37.33	**37.50**	**35.54**
Mean	**37.08**	**35.84**	**34.55**	35.82	**38.19**	**24.40**	**37.31**	32.86	34.27
LSD (0.05)	5.34	12.66	10.76	**9.91**	-	-	6.16	**10.43**	-
CV (%)	8.4	20.7	17.6	**14.8**	20.00	28.9	9.6	**19.6**	19.7
F probability	0.001***	0.041*	0.001***	**0.034***	0.356ns	0.054ns	0.048*	**0.023***	**0.098**

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

Table 3.12 Mean starch content in percentage (fresh mass basis) of 10 cultivars evaluated in four locations in Tanzania

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	26.87	22.75	14.53	**21.10**	22.00	15.41	16.13	**17.58**
Vumbi	20.87	23.36	17.33	**18.69**	24.29	14.33	22.41	**18.44**
TMS 30001	28.07	15.83	22.84	**21.01**	25.78	16.44	22.41	**22.22**
Namikonga	29.73	22.70	25.13	**24.43**	25.63	22.07	28.47	**25.39**
AR 42-3	27.43	23.33	19.83	**22.33**	25.00	13.00	22.41	**17.56**
AR 40-6	29.73	22.63	18.67	**21.08**	20.80	15.00	19.00	**18.27**
Kiroba	24.97	21.37	23.00	**21.21**	22.60	19.00	21.13	**20.91**
AR 37-80	30.07	25.97	24.80	**25.43**	23.73	16.44	22.41	**20.38**
Nanchinyaya	29.20	28.47	24.50	**26.63**	26.72	19.53	28.40	**24.88**
CR 25-4	27.77	24.92	17.47	**21.52**	25.17	14.13	18.53	**19.28**
Mean	**28.04**	**23.45**	**20.90**	**22.25**	**24.29**	**16.44**	**22.41**	**20.60**
LSD (0.05)	-	-	-	-	-	4.062	6.623	-
CV (%)	18.1	12.5	19.4	**17.5**	10.9	13.7	16.6	**16.3**
F probability	0.361	0.12	0.166	**0.112**	0.153	0.006	0.007	**0.060**

Cultivar	Kizimbani				Hombolo			Overall	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	17.62	20.60	10.48	**15.11**	15.11	2.79	21.70	**13.14**	**20.72**
Vumbi	24.79	22.15	28.30	**28.45**	17.82	5.49	24.24	**15.85**	**20.28**
TMS 30001	22.83	20.86	35.20	**28.11**	17.41	10.25	28.47	**18.66**	**24.19**
Namikonga	29.60	24.60	31.90	**28.27**	18.09	5.76	24.51	**16.12**	**24.91**
AR 42-3	24.79	22.15	28.10	**25.19**	24.77	11.77	31.86	**22.80**	**23.25**
AR 40-6	25.21	24.79	30.40	**26.21**	20.26	7.27	25.47	**17.67**	**20.68**
Kiroba	26.09	15.53	26.10	22.72	20.35	9.76	30.24	**20.11**	**22.67**
AR 37-80	26.58	23.47	32.40	**25.06**	23.51	6.70	27.87	**19.36**	**23.66**
Nanchinyaya	24.59	22.13	28.30	**25.14**	20.92	10.94	29.33	**20.39**	**24.50**
CR 25-4	24.79	22.73	27.10	**24.61**	17.77	5.45	24.19	**15.86**	**23.27**
Mean	**24.79**	**22.15**	**28.10**	**25.20**	**19.71**	**7.95**	**26.49**	**18.01**	**22.81**
LSD (0.05)	2.98	6.61	11.84	**8.81**	-	-	6.74	-	-
CV (%)	5.7	17.0	22.4	**19.7**	12.8	22.2	14.8	**20.0**	**19.8**
F probability	0.003	0.156	0.051	**0.033**	0.564	0.095	0.051	**0.766**	**0.060**
Cultivar									**0.732**
Harvest date									**0.002**

MAP (months after planting); significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations
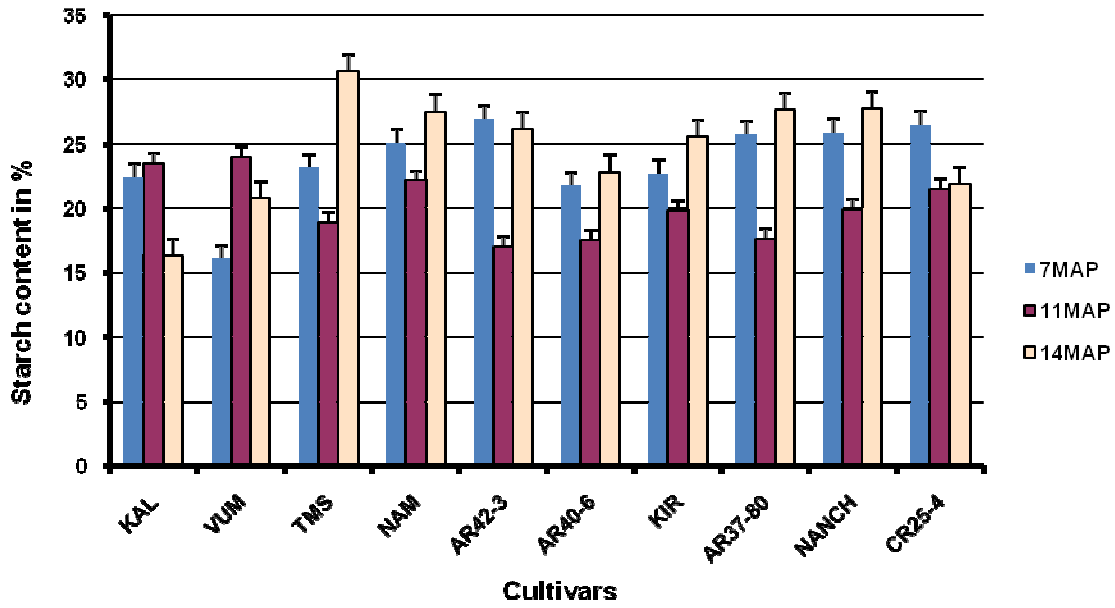
Figure 3.1 Starch content of 10 cultivars across sites
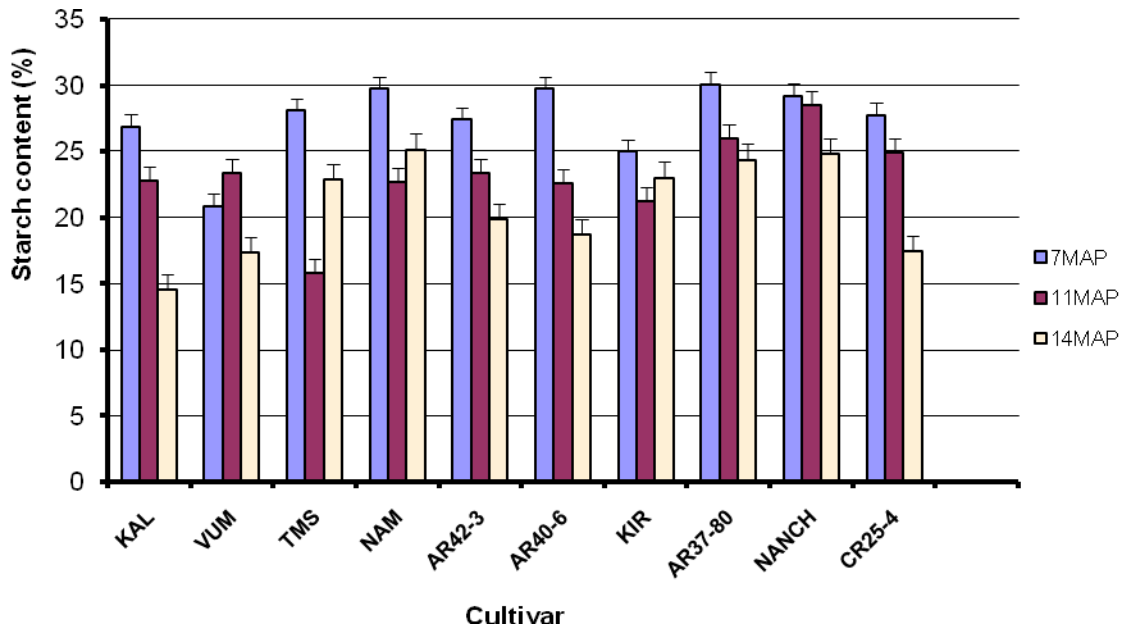
Figure 3.2 Starch content at Kibaha for different cultivars and harvesting dates
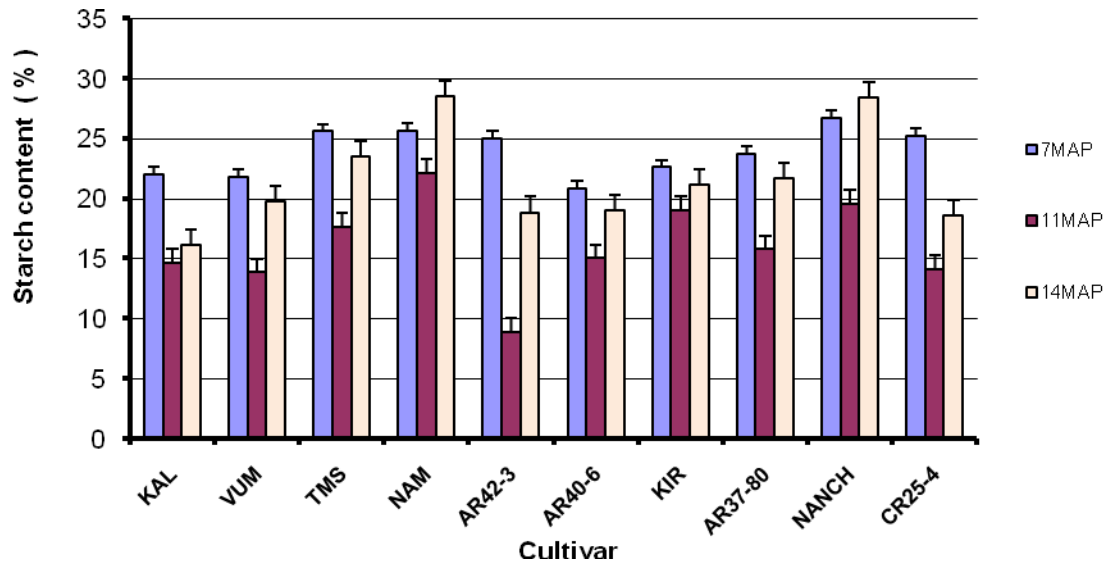
Figure 3.3 Starch content at Chambezi for different cultivars and harvesting dates
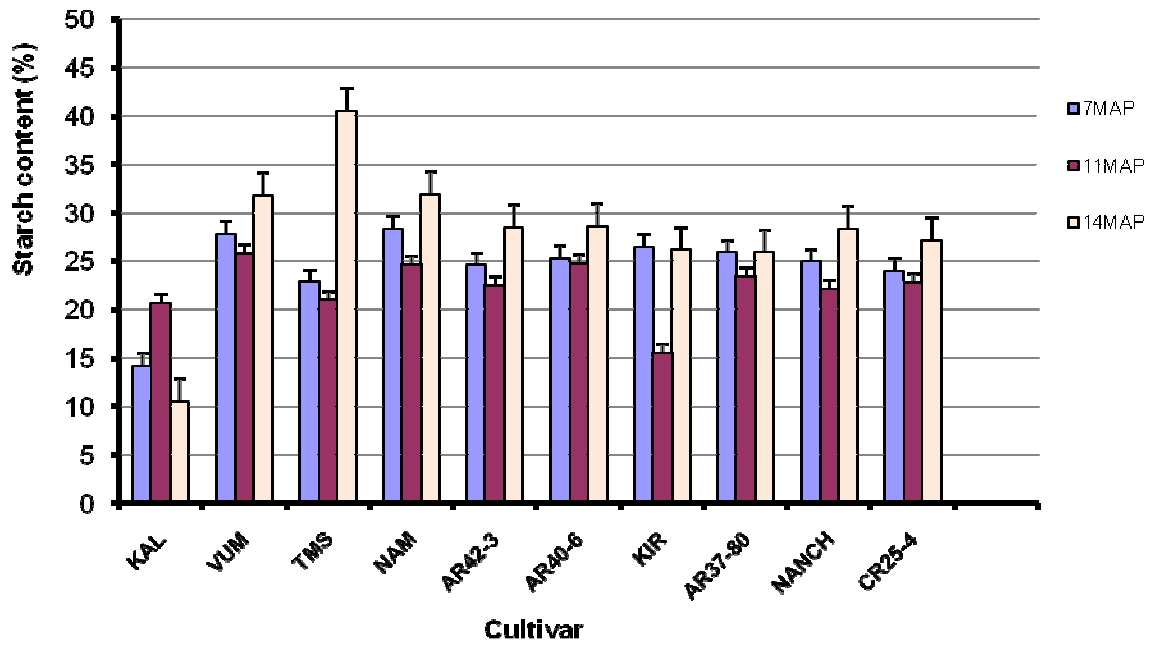
Figure 3.4 Starch content at Kizimbani for different cultivars and harvesting dates

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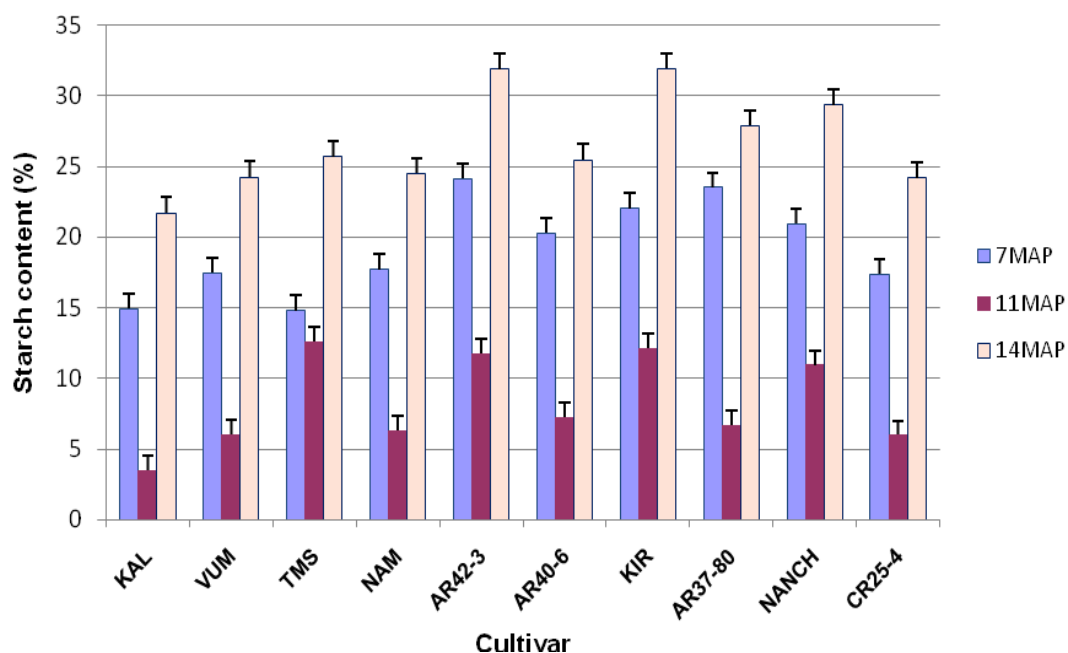
Figure 3.5 Starch content at Hombolo for different cultivars and harvesting dates

Table 3.13 Mean starch content as a proportion of dry root yield of 10 cultivars, 2007/08

Cultivar	7 MAP	11 MAP	14 MAP	**Mean**
Kalolo	0.64	0.66	0.58	**0.64**
Vumbi	0.32	0.42	0.67	**0.60**
TMS 30001	0.67	0.63	0.83	**0.72**
Namikonga	0.63	0.58	0.69	**0.62**
AR 42-3	0.68	0.57	0.69	**0.65**
AR 40-6	0.58	0.53	0.65	**0.58**
Kiroba	0.62	0.54	0.70	**0.62**
AR 37-80	0.69	0.66	0.82	**0.70**
Nanchinyaya	0.63	0.54	0.74	**0.65**
CR 25-4	0.55	0.57	0.62	**0.62**
Mean	**0.60**	**0.57**	**0.70**	0.64
LSD (0.05)	0.12	-	0.134	-
CV (%)	0.26	33.2	14.9	**23.4**
F probability	0.001	0.07	0.023	**0.231**
Cultivar				**0.863**
Harvest date				**0.001**

Figures 3.6 to 3.9 summarize the performance of each cultivar at each site in terms of StC. At Kibaha (Figure 3.6) highest StC was attained at 7 MAP, whereby cultivar Namikonga and Nanchinyaya showed higher StC. However, cultivar TMS 30001 showed a major decline from 7 to 11 MAP, probably due to its reaction to CBSD infection in the roots or it was not stable to the environmental changes from the dry and wet season. At Chambezi (Figure 3.7), almost all cultivars showed a decline in StC between 7 and 11 MAP. At Kizimbani (Figure 3.8) all cultivars had a decline between 7 and 11 MAP with the exception of cultivar Kalolo. However, the decline at Kizimbani site was small compared to cultivars at Chambezi site. Cultivar Kalolo did not recover even at 14 MAP at Kizimbani. The CBSRN was high (2.83≈3) for cultivar Kalolo at 14 MAP such that StC was affected. At Hombolo (Figure 3.9), all cultivars except TMS 30001 had a major decline in StC between 7 and 11 MAP. However, starch accumulation resumed later and an increase was observed at 14 MAP.
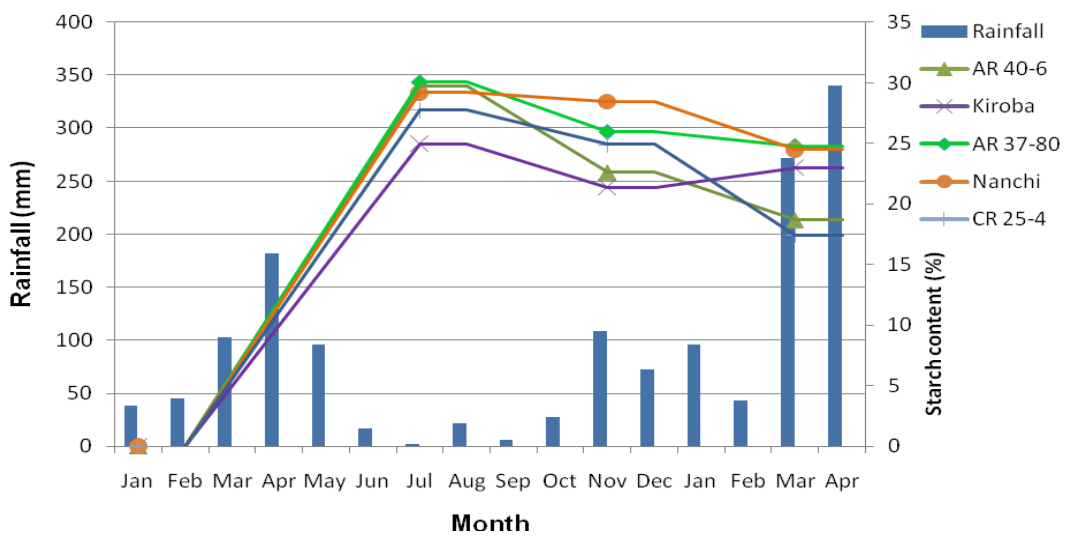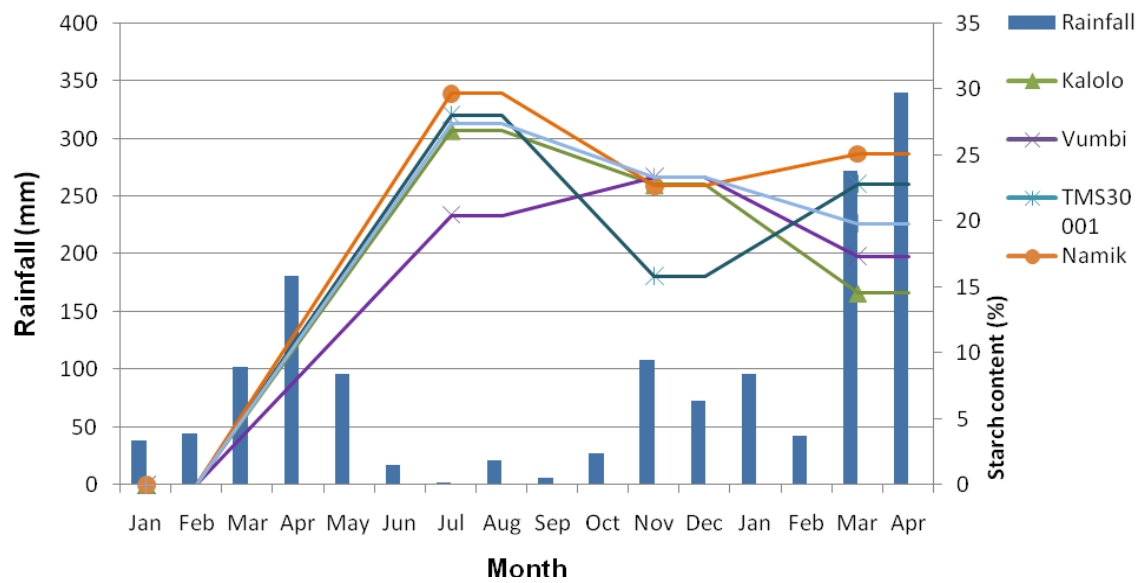
Figure 3.6 Starch content of 10 cultivars at 7, 11, and 14 months after planting, Kibaha, site
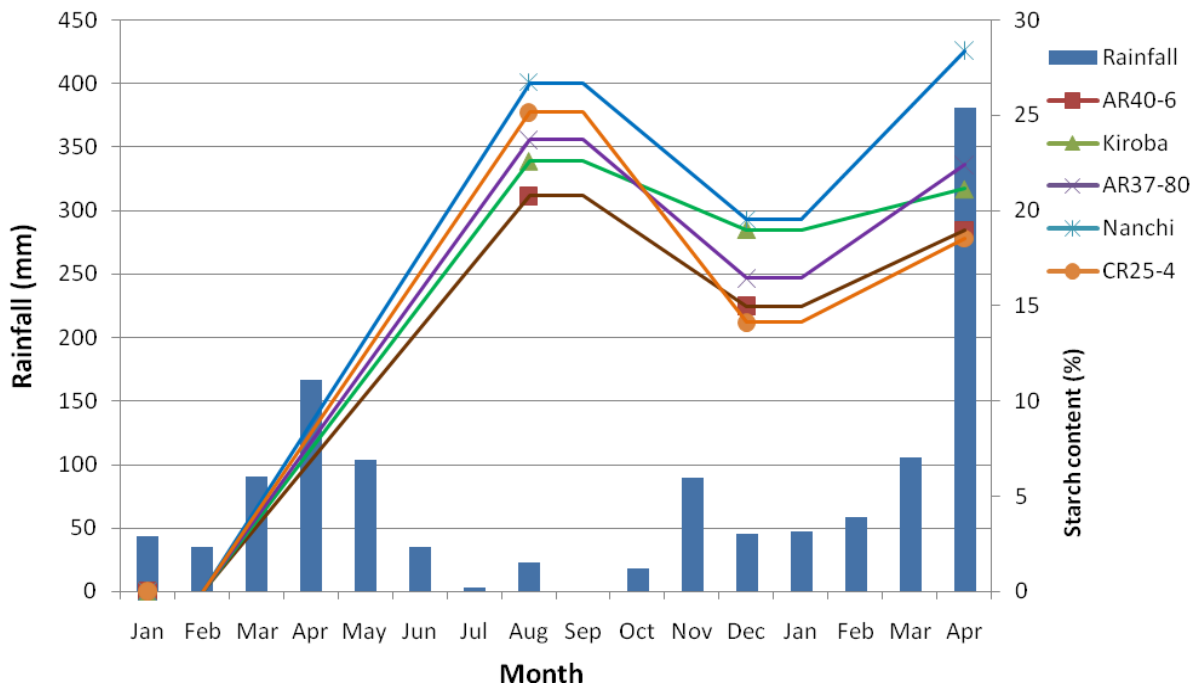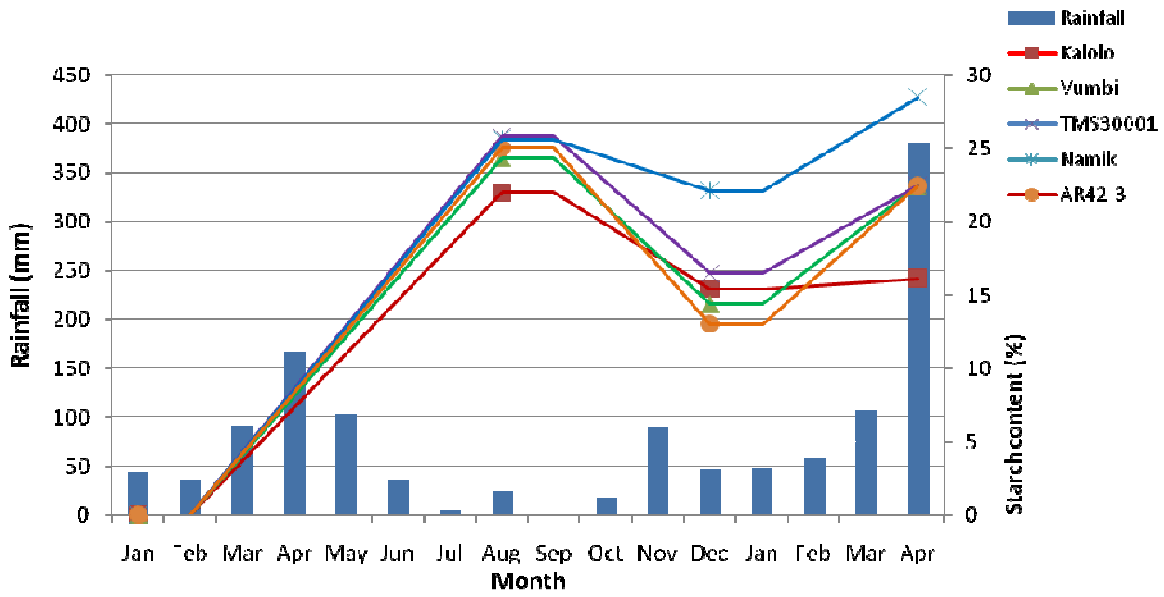
Figure 3.7 Starch contents of 10 cultivars at 7, 11, and 14 months after planting, Chambezi site
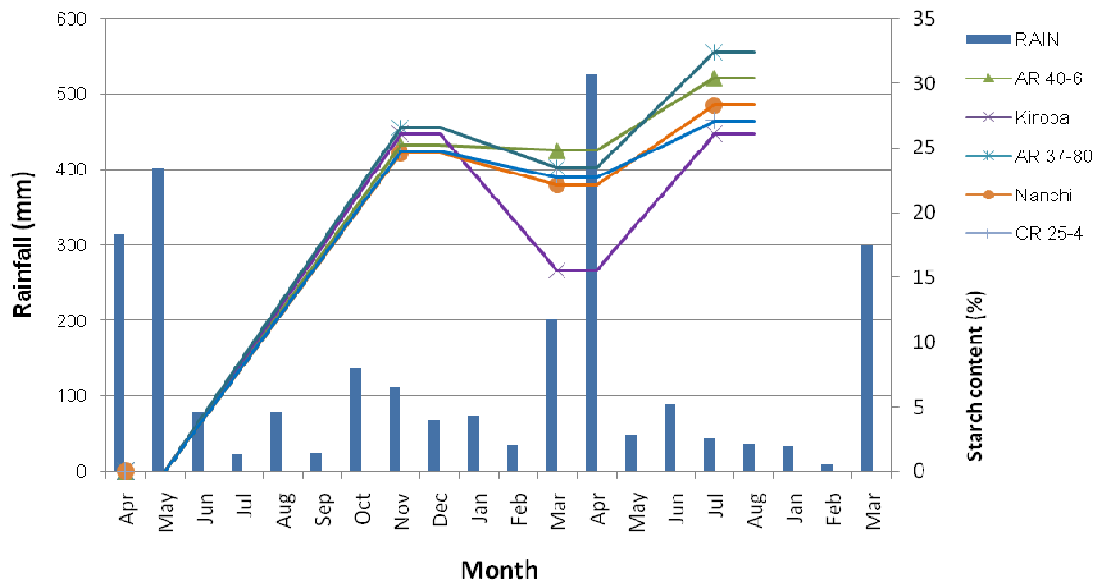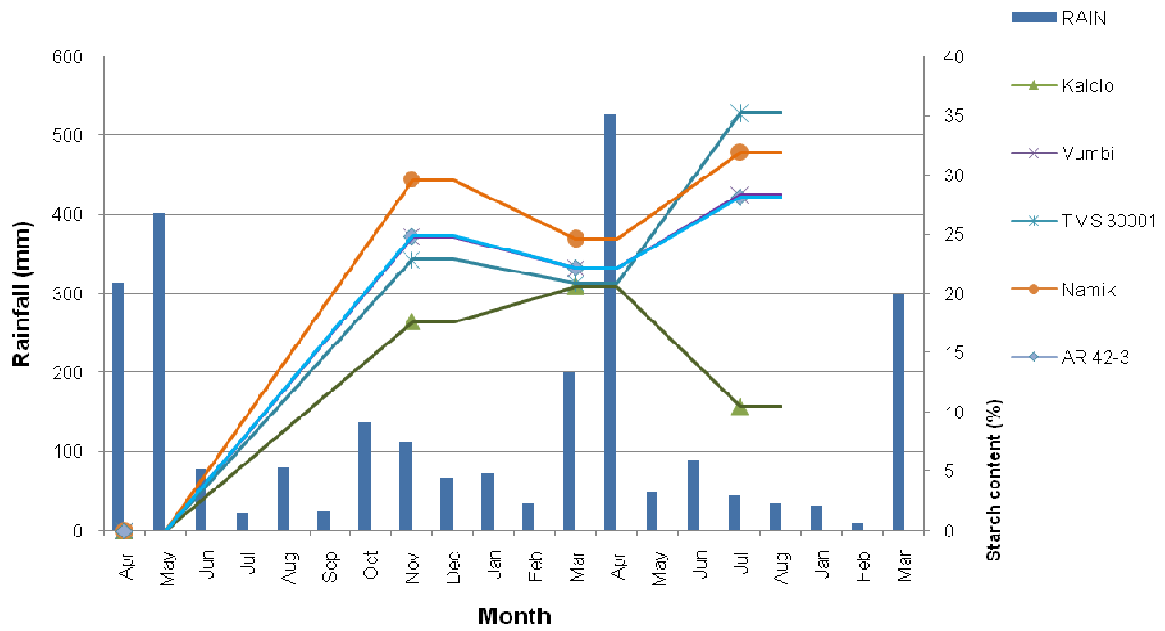
Figure 3.8 Starch content of 10 cultivars at 7, 11, and 14 months after planting, Kizimbani site
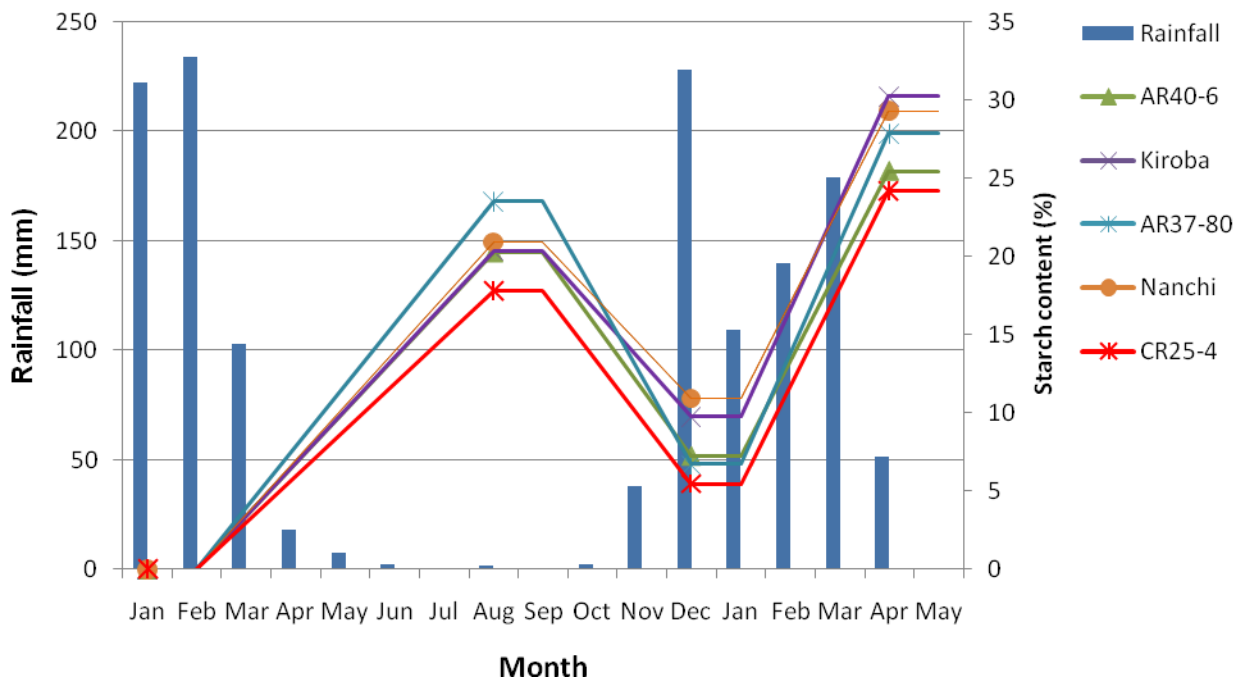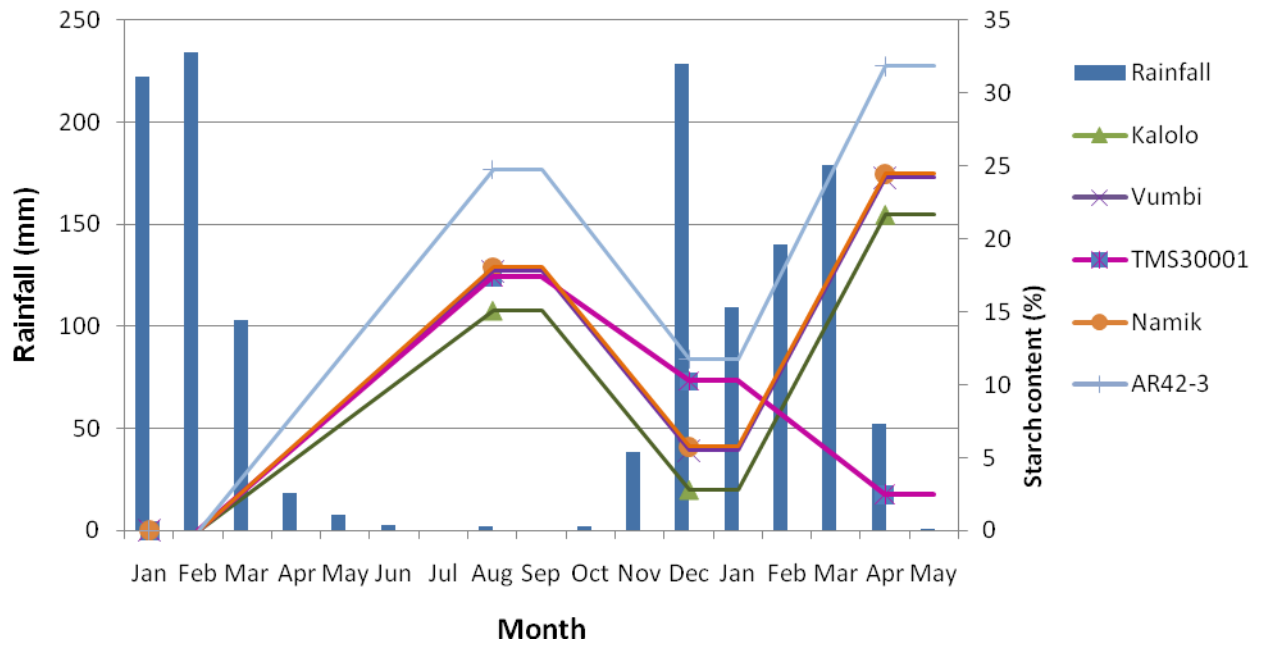
Figure 3.9 Starch content of 10 cultivars at 7, 11, and 14 months after planting, Hombolo site

3.3.5 Starch yield

Significant differences in StY (p≤0.001) were observed between harvesting dates (Appendix 2) as well as between cultivars across locations (Table 3.14). The StY ranged from 0.54 (Vumbi) to 4.09 t ha^{-1} (Kiroba). Cultivar Namikonga which had the highest StC of 24.9%, had a StY of 2.5 t ha^{-1} (Table 3.14). However, the mean StY for different harvesting dates ranged from 0.02 to 6.97 t ha^{-1} from cultivars Vumbi (7 MAP) and Kiroba and AR 40-6 (14 MAP) (Appendix 2). For individual sites, plants at Chambezi site indicated relatively higher mean StY of 4.96 t ha^{-1} than other sites (Figure 3.10; Table 3.14). There were small increase (≈25%) in mean StY between 7 and 11 MAP, but more than 100% increase between 11 and 14 MAP with the exception of cultivars Kalolo and TMS 30001 (Figure 3.11; Appendix 2). However, cultivars at Kibaha and Kizimbani sites had no definitive increase in StY between different harvesting dates, this has been contributed with poor FSRY obtained (Figures 3.11; Table 3.14, Appendix 2)
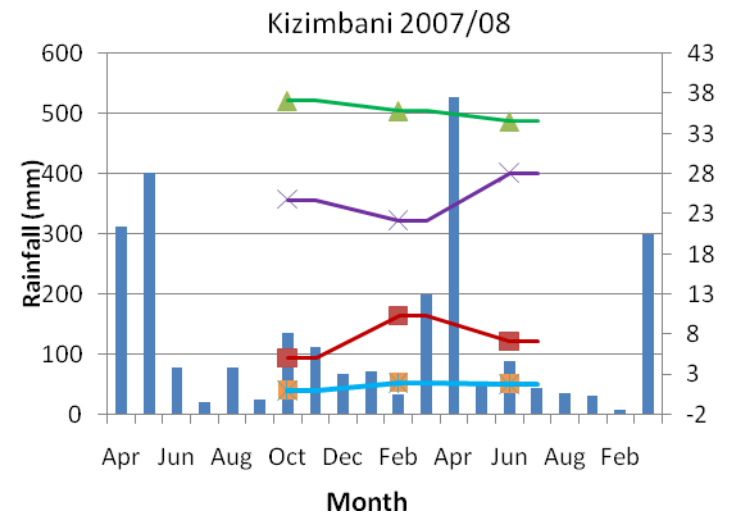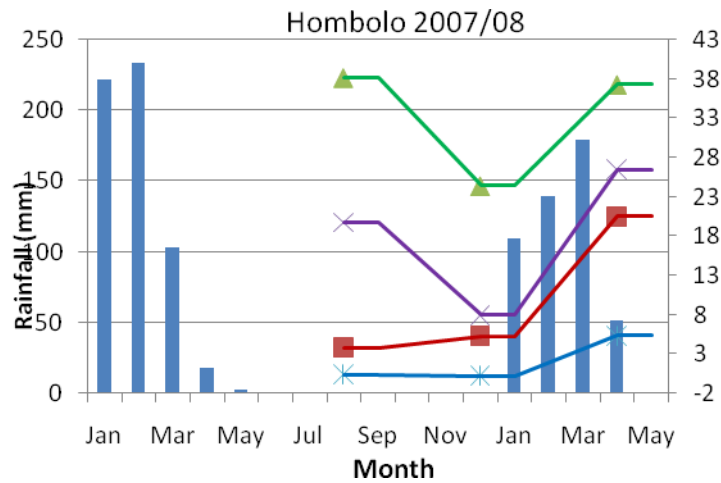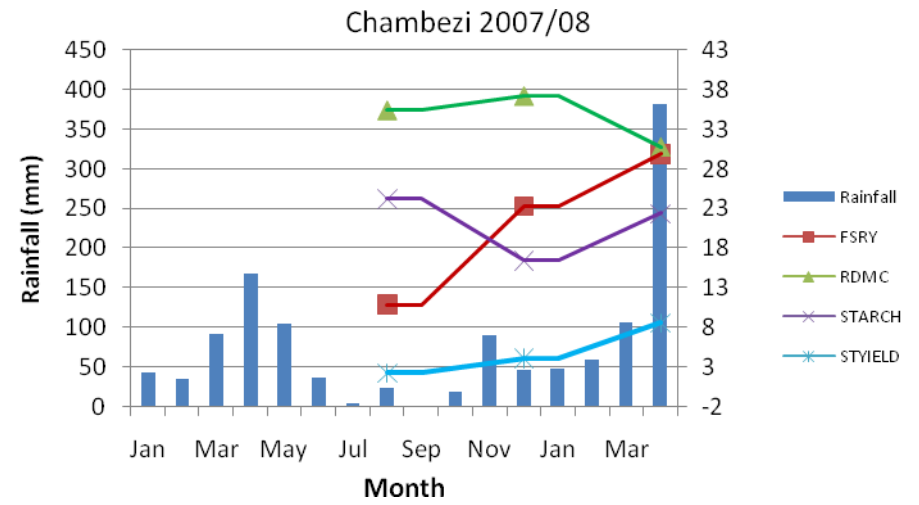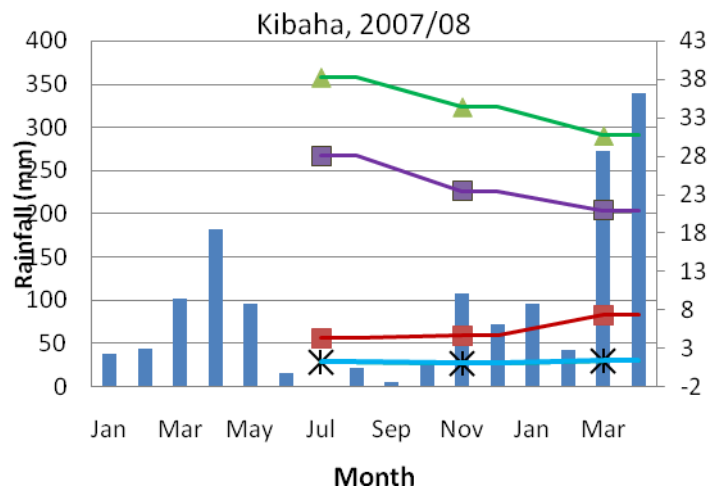
Figure 3.10 Rainfall amount, fresh storage root yield, starch content and starch yield of 10 cultivars over three harvesting times

Table 3.14 Mean starch yield (t ha^{-1}) of 10 cultivars evaluated in four locations and three harvesting intervals in Tanzania, 2007/08

Cultivar	Kibaha				Chambezi			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	1.06	0.95	0.92	**0.97**	3.95	7.60	5.73	**5.76**
Vumbi	-	-	0.11	**0.11**	1.52	0.33	4.81	**1.21**
TMS 30001	0.40	1.78	1.01	**1.06**	1.70	3.55	8.03	**4.43**
Namikonga	1.65	1.46	2.32	**1.81**	1.79	1.95	11.04	**4.92**
AR 42-3	1.19	0.94	1.09	**1.07**	2.57	3.05	8.22	**4.61**
AR 40-6	1.15	1.05	1.30	**1.17**	2.88	5.02	10.85	**6.25**
Kiroba	1.59	1.36	1.99	**1.65**	6.27	8.20	12.44	**8.97**
AR 37-80	1.64	0.62	-	**0.76**	2.87	4.72	9.20	**5.60**
Nanchinyaya	1.49	1.56	1.37	**1.47**	0.34	4.79	10.24	**5.22**
CR 25-4	0.83	0.56	0.53	**0.64**	1.59	1.89	7.07	**3.51**
Mean	**1.07 (1.43)**	**0.99 (1.39)**	**1.06 (1.40)**	**1.10 (1.41)**	**2.23 (1.78)**	**4.08 (1.83)**	**8.56 (2.35)**	**4.96 (1.98)**
LSD (0.05)	0.84 (0.27)	(0.43)	1.09 (0.36)	-	3.19 (0.66)	4.57 (0.95)	7.59 (0.88)	**4.98 (0.64)**
CV (%)	44.9 (11.0)	30.1 (18.3)	45.7 (14.9)	**36.7 (16.1)**	68.0 (21.7)	59.3 (30.6)	62.6 (22.0)	**33.0 (34.5)**
F probability	0.006 (0.002)	0.272 (0.179)	0.007 (0.003)	**0.456 (0.001)**	0.12 (0.008)	0.03 (0.003)	0.011 (0.001)	**0.39 (0.001)**

Cultivar	Kizimbani				Hombolo			Across	
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**	**Mean‡**
Kalolo	0.33	0.88	0.44	**0.55**	0.00	0.00	2.50	**0.83**	**1.76**
Vumbi	-	-	0.88	**0.88**	0.00	0.00	4.37	**1.46**	**0.38**
TMS 30001	0.81	1.75	0.41	**1.03**	0.42	0.31	4.95	**1.89**	**1.10**
Namikonga	0.30	2.24	3.57	**2.04**	0.00	0.00	2.30	**0.77**	**2.36**
AR 42-3	-	-	-	-	0.00	0.10	7.86	**2.65**	**1.47**
AR 40-6	3.16	2.28	1.56	**2.33**	0.10	0.65	9.46	**3.40**	**3.26**
Kiroba	2.12	1.98	1.79	**1.96**	0.40	0.00	7.39	**2.60**	**3.51**
AR 37-80	0.81	3.73	2.74	**2.42**	0.97	0.14	9.40	**3.50**	**2.22**
Nanchinyaya	0.95	3.13	2.15	**2.08**	0.40	0.08	2.56	**1.01**	**2.54**
CR 25-4	0.00	2.13	4.40	**2.18**	0.00	0.00	6.65	**2.22**	**1.94**
Mean	**1.01 (1.33)**	**2.01 (1.67)**	**1.78 (1.56)**	**1.60 (1.48)**	**0.44 (1.09)**	**0.23 (1.06)**	**5.37 (2.47)**	**2.01(1.54)**	**2.09 (1.629)**
LSD (0.05)	-	3.01 (0.62)	-	-	0.92	0.49	-	**4.94 (-)**	**1.96 (-)**
CV (%)	19.9 (0.79)	24.3 (21.7)	37.9 (33.8)	**77.4 (33.0)**	122.0 (17.0)	126.5 (11.5)	74.6 (31.9)	**67.0(19.9)**	**127.2 (26.9)**
F probability	0.349 (0.216)	0.02 (0.006)	0.275 (0.117)	**0.174 (0.004)**	0.001 (0.274)	0.001 (0.218)	0.177 (0.22)	**0.039(0.79)**	**0.001(0.82)**

MAP =months after planting; significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; †= cultivar mean over 3 harvest dates; ‡=Mean across locations; Values in brackets are transformed using Genstat release 12; Square root = (x + 1.0)**0.5, x=observed values
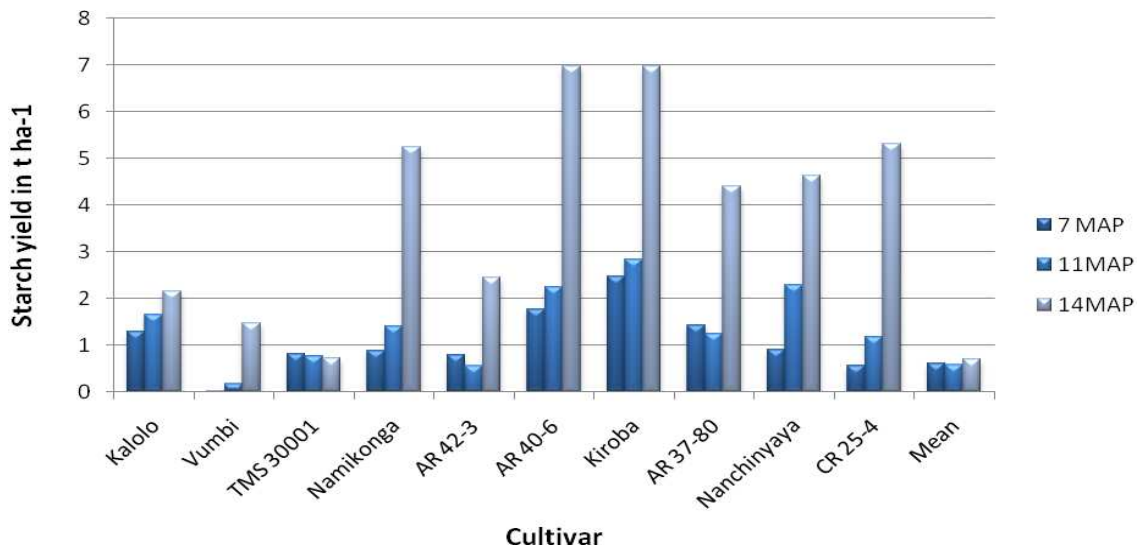
Figure 3.11 Starch yield across sites

3.3.6 Genotype x environment interaction

The combined analyses of variances for the FSRY, SRN, DSRY, RDMC, StC and StY revealed significant variation between cultivars for all the traits and at each harvesting date (Table 3.15). The effect of location was also significant for almost all the traits with the exception of StC at 7 MAP. Genotype x environment effects was highly significant at 14 MAP for FSRY, DSRY and StY ($p \leq 0.001$). The proportion of treatment sum of squares due to the main effects of location ranged between 14.5 to 62.5%, while that due to genotypes ranged from 19.9 to 37.2%, and that due to cultivar x location from 15.5 to 42.8%. Contribution of genotype effects to the treatment sum of squares was more than location effects for RDMC and StC suggesting that genetic control was more important than environment. Location means ranged between 5.48 (Kibaha) and 21.50 (Chambezi) for FSRY in t ha^{-1}, 33.07% (Hombolo) and 35.54% (Kizimbani) for RDMC, 21.23% (Chambezi) and 24.91% (Kizimbani) for StC, and 1.04 (Kibaha) and 3.68 (Chambezi) for StY in t ha^{-1} (Appendix 4). The six yield traits presented in Table 3.16 appear to be influenced partly by the genotype. In comparison with other sources of variation, the genotype component for RDMC and StC were apparently strong at 7 and 14 MAP. However, based on the F test of significance, strong environment effects were detected for all the traits in the combined anova, and were the main source of variation for FSRY, SRN, DSRY and starch yield.

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Table 3.15 Combined analyses of variance for six traits of 10 cultivars evaluated in four locations, 2007/08

Source	df	Mean square					
		SRN	FSRY	DSRY	RDMC	StC	StY
7 MAP							
Cultivar	9	1306.0***	107.9***	15.1***	107.9***	57.8***	8.7***
Location	3	4542.6**	349.9***	35.1***	66.3	48.6	47.9***
Rep/Loc	2	173.5	38.0	5.5	17.3	452.6	2.8
G X E	27	476.8***	39.8	4.9	23.5	15.8	6.2***
Error	78	126.4	25.1	3.3	17.4	10.7	2.3
11 MAP							
Genotype	9	2319.9***	211.6**	30.1***	138.2***	18.7	8.5***
Location	3	6322.4***	2457.8***	230.0***	868.5***	1545.9**	41.3***
Rep/Loc	2	46.8	41.9	2.9	3.4	80.1	4.1
G X E	27	890.9* **	97.0	16.4**	66.1**	25.1**	6.5***
Error	78	260.9	72.1	7.0	29.3	9.5	2.5
14 MAP							
Genotype	9	2256.9(19.9)***	708.3(21.5)***	97.7(24.7)***	204.9(37.2)***	147.2(33.3)***	53.9(23.8)***
Location	3	23606.1(62.5)***	4890.9(44.6)***	483.2(36.6)***	266.6(14.5)*	379.2(25.7)**	260.0(33.5)***
Rep/Loc	2	1188.6(2.1)	71.7(0.44)	6.6(0.34)	12.3(0.5)	436.8(19.7)	6.8 (0.53)
G X E	27	585.2(15.5)*	365.8(33.4)***	50.5(38.3)***	90.8(47.8)***	39.3(21.3)*	32.4 (42.2)***
Error	78	355.5	138.5	17.1	19.9	19.2	10.9

Significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; SRN (storage root number); FSRY (fresh storage root yield in t ha^{-1}); DSRY (dry storage root yield t ha^{-1}); RDMC (root dry matter content in %); StY (Starch yield in t ha^{-1}); StC (starch content in %); Values in brackets are contributions to total variations calculated as percentage of the sum of squares

Table 3.16 Variance components of yield, yield components, starch content and starch yield of 10 cultivars evaluated in four locations in Tanzania, 2007/08

7 MAP Trait	σ^2_g	σ^2_l	σ^2_{gl}	σ^2_e
SRN	30.11	176.93	54.53	131.3
FSRY	6.81	11.70	4.40	24.7
DRY	0.95	1.16	0.43	3.3
RDMC	8.34	1.68	1.70	19.5
StC	12.21	0.86	1.07	21.1
StY	0.29	0.82	0.33	1.6
11 MAP				
SRN	98.69	171.25	58.0	213.9
FSRY	10.33	73.29	7.8	75.5
DRY	1.36	6.49	3.28	7.2
RDMC	8.28	28.85	11.3	30.2
StC	1.89	43.90	1.57	20.9
StY	0.39	1.25	1.33	2.50
14 MAP				
SRN	167.98	662.65	88.0	362.7
FSRY	44.68	148.81	86.3	141.1
DRY	6.38	14.54	12.6	18.0
RDMC	14.53	10.22	19.8	20.6
StC	11.58	9.22	7.47	19.4
StY	3.33	7.72	7.87	11.6

σ^2_g= genotypic variance; σ^2_l = variance due to location/environment; σ^2_{gl} = variance due to interaction (gxl); σ^2_e = error term; SRN (storage root number); FSRY (fresh storage root yield in t ha^{-1}); DSRY (dry storage root yield t ha^{-1}); RDMC (root dry matter content in %); StY (Starch yield in t ha^{-1}); StC (starch content in %).

3.3.7   Cultivar superiority index

Cultivar superiority index (Pi) for StC ranged between 1.34 and 29.55. Cultivar Nanchinyaya showed the lowest superiority index of 1.338, which implicate that the cultivar is superior for starch content compared to the other cultivars (Table 3.17). The second most superior

cultivar was Namikonga (3.84) and the most inferior with the highest Pi value of 29.55 was cultivar Kalolo.

Table 3.17 Superiority index (Pi) for starch content and percent response of 10 cultivars

Cultivar	Mean starch (%)	% response	Pi
Nanchinyaya	24.50	107.36	1.34
Namikonga	24.91	109.16	3.84
AR 37-80	23.66	103.68	4.04
TMS 30001	24.19	106.00	5.47
Kiroba	22.67	99.34	6.88
AR 42-3	23.35	102.32	7.54
AR 40-6	20.68	90.62	9.54
CR 25-4	23.27	101.97	10.29
Vumbi	20.29	88.91	13.04
Kalolo	20.72	90.79	29.55

3.3.8   Correlation between traits in yield and yield components

Correlations between DSRY and SRN (0.75; p≤0.001), FSRY (0.98; p≤0.001), SY (0.77; p≤0.001), StY (0.96; p≤0.001) were highly significant across all locations (Table 3.18). The StC and RDMC correlated highly, positively and significantly at 7 (0.38; p≤0.001), 11 (0.60, p≤0.001) and 14 MAP (0.71; p≤0.001). Starch yield correlated positively and significantly with DSRY (0.96; p≤0.001), SRN (0.70; p≤0.001), FSRY (0.93; p≤0.001), SY (0.72; p≤0.001) and StC (0.24; p≤0.001) across locations. In addition, SY had a significant but negative correlation with HI (-0.36; p≤0.001).

Table 3.18 Phenotypic correlation between traits of 10 cultivars evaluated in four locations in Tanzania, 2007/08

Trait   7MAP

		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY
DSRY	1	-							
HI	2	0.2232	-						
RDMC	3	-0.1513	0.0334	-					
SRN	4	0.5351***	-0.2061	-0.0641	-				
FSRY	5	0.9936***	0.1975	-0.2412*	0.5279***	-			
SY	6	0.4915***	-0.5849***	-0.3272**	0.5664***	0.5243***	-		
StC	7	-0.2374	0.1034	0.3826***	-0.2007	-0.2642*	-0.3036**	-	
StY	8	0.9823***	0.2252*	-0.1912	0.4975***	0.9830***	0.4805***	-0.1164	-
		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY

11 MAP

		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY
DSRY	1	-							
HI	2	-0.0633	-						
RDMC	3	0.0674	0.0169	-					
SRN	4	0.6101***	-0.1718	-0.2163	-				
FSRY	5	0.9782***	-0.0551	-0.0863	0.6374***	-			
SY	6	0.7854***	-0.5580***	-0.0361	0.5786***	0.7816***	-		
StC	7	-0.1244	0.2220*	0.6003***	-0.4785***	-0.2024	-0.2541*	-	
StY	8	0.9601***	0.0215	0.0870	0.4745***	0.9429***	0.6985***	0.0825	-
		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY

Significance levels: * p≤0.05; ** p≤0.01; *** p≤0.001; SRN=storage root number; FSRY=fresh storage root yield in t ha^{-1}; DSRY= dry storage root yield t ha^{-1}; HI= harvest index; SRN=storage root number; RDMC=root dry matter content in %; StY= Starch yield in t ha^{-1}; StC=starch content in %

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Table 3.18 Phenotypic correlation between traits of 10 cultivars at 14 MAP and across four locations in Tanzania, 2007/08

Trait   14 MAP

		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY
DSRY	1	-							
HI	2	0.1343	-						
RDMC	3	0.1888	0.3435***	-					
SRN	4	0.7532***	-0.0661	0.1575	-				
FSRY	5	0.9707***	0.0988	0.0551	0.7470***	-			
SY	6	0.7398***	-0.3004**	-0.0083	0.6459***	0.7913***	-		
StC	7	0.2413*	0.1942	0.7147***	0.2321*	0.1459	0.1340	-	
StY	8	0.9665***	0.1065	0.1836	0.7290***	0.9337***	0.7401***	0.3721***	-
		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY

MEAN ACROSS LOCATIONS

		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY
DSRY	1	-							
HI	2	0.1303	-						
RDMC	3	0.0003	0.0633	-					
SRN	4	0.7494***	-0.1000	-0.0755	-				
FSRY	5	0.9805***	0.1215	-0.1174	0.7558***	-			
SY	6	0.7677***	-0.3622***	-0.1012	0.7055***	0.7877***	-		
StC	7	0.0772	0.1226	0.5059***	0.0024	0.0066	-0.0206	-	
StY	8	0.9578***	0.1316*	0.0005	0.6973***	0.9341***	0.7212***	0.2392***	-
		DSRY	HI	RDMC	SRN	FSRY	SY	StC	StY

Significance levels:* $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$; SRN (storage root number); FSRY (fresh storage root yield in t ha^{-1}); DSRY (dry storage root yield t ha^{-1}); HI (harvest index); SRN (storage root number); RDMC (root dry matter content in %); StY (Starch yield in t ha^{-1}); StC (starch content in %).

3.4   Discussion and conclusion

The study was conducted to establish the variation in FSRY, RDMC, StC and StY of 10 cassava cultivars in four locations in Tanzania. The participatory rural appraisal study (Chapter 2) and other reports (Nweke et al., 1998), have indicated that farmers sell cassava roots from sweet cultivars for cash income while roots from bitter cultivars and small roots from sweet cultivars are processed into more stable products (Westby, 2002). The starch industry is one of the potential markets for cassava roots in Tanzania. In order to maximize their economic returns farmers need high starch varieties. The information on the right time to harvest the tuberous root for optimum starch yield is also important.

Variations in FSRY, RDMC, StC and StY were observed between cultivars. Cultivars also varied in SRN, HI and their reaction to diseases. Cultivars from CIAT exhibited tolerance to CMD but were rather susceptible to CBSD. The RDMC was highest at 7 MAP. Similar findings have been reported elsewhere (Kawano et al., 1987). However, RDMC was strongly influenced by genotype, suggesting that selection pressure could be applied to improve the trait. Variations in StC and StY were observed between cultivars as well as harvesting dates. Cultivars Namikonga and Vumbi gave the highest and lowest StC respectively across locations. The differences in StC might however be due to the genetic composition of the cultivars, cultural practices on the field as well as a combination of environmental factors (Rickard et al., 1991). The StC showed an increasing trend up to 7 MAP followed by a decline in starch content between 7 and 11 MAP. Studies (Setter and Fregene, 2007) have indicated that during water deficit conditions, leaf and stem growth ceases, limiting demands for assimilates. Sources of assimilates to meet respiratory and other tissue maintenance requirements are provided by starch quantities stored in stems and leaf petioles (Setter and Fregene, 2007). This study shows that some starch reserves are drawn from the roots to support plant maintenance during the dry season. The accumulation of starch resumes after the rains return. An increased starch percentage was observed at 14 MAP for Hombolo and Chambezi sites. Similar findings have been reported elsewhere (Sriroth et al., 1999; Asaoka et al., 1992) where the lowest starch content was observed at 10 MAP.

When the rain returns after a dry spell, new leaves develop rapidly and a dramatic gain in root starch content occurs as starch synthesis and accumulation resume. The results have shown that it is best to harvest between 7 and 8 MAP at Kibaha, because after this period a decline in StC was observed; and even at 14 MAP not much improvement in starch content was noted. However, at Chambezi and Hombolo sites, plants could be left in the field for up to 14 MAP, as StC and yield increased rapidly between 11 and 14 MAP. At Kizimbani, cultivars Kalolo and Kiroba did not show much increase in StC at 14 MAP, therefore they could be harvested earlier to enable the land to be used for other crops. Early maturing varieties with high root yield and starch content would be appropriate at Kibaha and Kizimbani sites.

The StY (t ha^{-1}) indicates the potential economic return expected from a cultivar for processing. High StC in a cultivar is important, but it has to be matched with high FSRY in order to maximize StY. For example, cultivar Namikonga which had the highest StC did not have high FSRY, resulting in moderate StY. Instead, cultivar Kiroba, which had moderate StC but a high FSRY gave the highest StY. Breeders need to strike a balance for optimum FSRY and StC to attain maximum economic StY. A high FSRY with low StC would mean increased costs for root crushing, pulp homogenization, water usage, filtration and decantation.

In conclusion, cultivars Kiroba and AR 40-6 performed well in terms of starch yield. However, cultivars such as Namikonga and others with high starch content could be improved by breeding and selection to increase storage root yield for the starch industry. Farmers need to know the cyclic trend in starch content and be informed on when the appropriate time is to harvest at each site. Both StC and FSRY are important traits to maximize StY for economic returns; therefore selection for StY should consider both StC and FSRY. There is a need to develop varieties for specific location as evidenced in this study. Early maturing varieties that have high StC are also required. However, further studies are required to more accurately determine starch accumulation trends in relation to environmental factors. Close intervals between harvesting dates should be considered. Effect of CBSD root necrosis on starch content should be further explored.

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Appendix 1 Yield components of 10 cultivars evaluated at 7, 11, and 14 MAP across four locations in Tanzania, 2007/08

Cultivar	Shoot yield t ha⁻¹				Root number plant⁻¹			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	13.00	15.82	13.87	**14.23**	2.9	3.4	3.0	**3.1**
Vumbi	12.17	15.30	19.78	**15.75**	2.2	1.6	2.8	**2.2**
TMS 30001	6.89	11.27	7.85	**8.67**	2.2	3.1	2.7	**2.7**
Namikonga	15.89	18.95	37.49	**24.11**	2.6	2.0	5.3	**3.3**
AR 42-3	9.33	12.46	6.93	**9.57**	2.3	3.3	2.4	**2.7**
AR 40-6	13.86	20.22	41.19	**25.09**	3.9	5.1	6.7	**5.2**
Kiroba	15.42	17.62	25.32	**19.45**	3.8	4.4	5.4	**4.5**
AR 37-80	19.60	31.23	39.39	**30.07**	3.2	3.4	4.7	**3.8**
Nanchinyaya	8.36	17.81	26.34	**17.50**	3.4	4.4	5.2	**4.3**
CR 25-4	6.83	10.82	22.97	**13.54**	2.2	2.6	4.4	**3.1**
Mean	**12.84**	**17.89**	**24.32**	18.35	**5.6**	**6.4**	**4.8**	3.7
LSD (0.05)	4.35	8.05	11.88	-	9.5	13.1	-	-
CV (%)	41.8	55.4	60.2	**56.1**	37.6	44.7	45.0	**43.1**
F probability	0.001	0.015	0.004	**0.352**	0.001	0.001	0.058	**0.508**

Cultivar	Root yield t ha⁻¹				Harvest index			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	6.74	12.49	13.17	**10.80**	0.33	0.44	0.40	**0.39**
Vumbi	2.75	2.35	8.58	**4.56**	0.20	0.20	0.28	**0.23**
TMS 30001	3.68	10.23	10.32	**8.08**	0.37	0.49	0.51	**0.45**
Namikonga	3.73	5.91	19.21	**9.62**	0.20	0.26	0.36	**0.27**
AR 42-3	4.31	10.67	10.21	**8.40**	0.28	0.47	0.42	**0.39**
AR 40-6	9.36	14.68	32.61	**18.89**	0.39	0.49	0.43	**0.44**
Kiroba	12.24	16.45	27.28	**18.65**	0.43	0.52	0.55	**0.50**
AR 37-80	6.72	11.15	20.33	**12.73**	0.29	0.33	0.29	**0.31**
Nanchinyaya	4.63	12.79	15.95	**11.12**	0.38	0.44	0.44	**0.42**
CR 25-4	3.44	8.02	23.53	**11.66**	0.37	0.44	0.54	**0.45**
Mean	**6.01**	**10.90**	**17.72**	11.54	**0.33**	**0.41**	**0.42**	0.38
LSD (0.05)	3.98	-	9.26	-	0.085	0.088	0.124	-
CV(%)	81.8	78.4	64.4	**75.2**	32.0	26.8	36.8	**24.4**
F probability	0.038	0.158	0.001	**0.693**	0.002	0.046	0.001	**0.701**

MAP (months after planting); significance levels: * p=0.05; ** p=0.01; *** p=0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

Appendix 2 Mean DRY, FSRY, starch content and starch yield in t ha^{-1} of 10 cultivars evaluated in four locations in Tanzania, 2007/08

Cultivar	Dry matter yield t ha^{-1}				RDMC (%)			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	2.42	3.61	3.70	**3.20**	34.02	28.29	24.96	**29.09**
Vumbi	0.94	0.46	2.70	**1.37**	34.04	26.87	30.94	**30.62**
TMS 30001	1.22	2.97	2.27	**2.15**	33.72	30.65	33.27	**32.54**
Namikonga	1.50	2.34	7.61	**3.82**	41.17	39.62	39.96	**40.25**
AR 42-3	1.57	3.44	3.28	**2.76**	33.75	32.00	34.99	**33.58**
AR 40-6	3.50	4.76	10.63	**6.30**	39.00	33.08	33.97	**35.35**
Kiroba	4.50	5.59	9.55	**6.55**	37.75	31.29	36.33	**35.12**
AR 37-80	2.44	2.06	6.13	**3.54**	37.04	25.50	28.70	**30.41**
Nanchinyaya	1.94	4.61	5.94	**4.16**	41.75	34.42	37.01	**37.73**
CR 25-4	1.31	2.74	8.19	**4.08**	38.62	35.33	35.00	**36.32**
Mean	**2.24**	**3.47**	**5.84**	3.84	**37.21**	**32.09**	**33.48**	34.26
LSD (0.05)	-	4.37	6.65	**3.79**	6.92	8.68	7.35	**7.62**
CV (%)	80.5	77.7	70.2	**106.2**	11.4	16.6	13.5	**16.3**
F probability	0.073	0.002	0.001	**0.001**	0.246	0.004	0.001	**0.919**

Cultivar	Starch content (%)				Starch yield t ha^{-1}			
	7 MAP	11 MAP	14 MAP	**Mean†**	7 MAP	11 MAP	14 MAP	**Mean†**
Kalolo	22.42	23.46	16.29	**20.72**	1.29	1.65	2.16	**1.70**
Vumbi	16.13	24.00	20.74	**20.29**	0.02	0.16	1.46	**0.54**
TMS 30001	23.13	18.87	30.58	**24.19**	0.80	0.76	0.71	**0.76**
Namikonga	25.10	22.13	27.49	**24.91**	0.88	1.40	5.25	**2.51**
AR 42-3	26.91	17.02	26.11	**23.35**	0.79	0.55	2.44	**1.26**
AR 40-6	21.76	17.48	22.80	**20.68**	1.76	2.25	6.97	**3.66**
Kiroba	22.72	19.76	25.54	**22.67**	2.46	2.84	6.97	**4.09**
AR 37-80	25.78	17.60	27.60	**23.66**	1.42	1.25	4.40	**2.36**
Nanchinyaya	25.90	19.88	27.72	**24.50**	0.90	2.29	4.62	**2.61**
CR 25-4	26.48	21.51	21.83	**23.27**	0.56	1.17	5.30	**2.34**
Mean	**23.64**	**20.02**	**24.80**	22.82	**1.09**	**1.43**	**4.03**	2.18
LSD (0.05)	3.29	3.46	3.89	-	1.10	1.48	3.27	-
CV(%)	17.7	24.3	19.5	**23.7**	116.7	120.5	101.9	**104.7**
F probability	0.001	0.024	0.001	**0.060**	0.001	0.001	0.001	**0.001** HVD
								0.850 Cult x hvd

MAP (months after planting); significance levels: * p=0.05; ** p=0.01; *** p=0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

Appendix 3 Mean fresh yield, RDMC, starch content and starch yield of 10 cultivars combined across four locations in Tanzania, 2007/08

Cultivar	Fresh root yield t ha^{-1}				Root dry matter content (%)			
	7 MAP	11 MAP	14 MAP	**Mean**	7 MAP	11 MAP	14 MAP	**Mean**
Kalolo	6.74	12.49	13.2	**10.80**	34.15	28.29	25.21	**28.31**
Vumbi	2.75	2.35	8.60	**4.56**	34.04	26.62	30.85	**30.95**
TMS 30001	3.68	10.23	10.30	**8.08**	34.17	30.58	33.31	**32.16**
Namikonga	3.73	5.91	19.2	**9.62**	42.14	37.56	39.96	**40.16**
AR 42-3	4.31	10.67	10.2	**8.40**	33.75	32.00	33.63	**33.35**
AR 40-6	9.36	14.68	32.6	**18.89**	39.00	33.08	33.97	**35.35**
Kiroba	12.24	16.45	27.3	**18.65**	37.75	31.29	36.33	**35.12**
AR 37-80	6.72	11.15	20.3	**12.73**	37.04	28.70	28.95	**32.05**
Nanchinyaya	4.63	12.79	16.0	**11.12**	41.75	34.42	37.01	**37.72**
CR 25-4	3.44	8.02	23.5	**11.66**	38.63	35.46	35.00	**36.52**
Mean	**5.76**	**10.47**	**18.10**	**11.45**	**37.24**	**31.80**	**33.42**	**34.16**
LSD (5%)		14.13	19.31	-	7.186	8.97	7.4	-
F-probability	0.07	0.179	0.001	**0.003**	0.219	0.008	0.001	**0.001**
Cultivar	0.001	0.007	0.001	**0.001**	0.001	0.001	0.001	**0.057**
Site	0.001	0.001	0.001	**0.001**	0.016	0.001	0.001	**0.030**

Cultivar	Starch content (%)				Starch yield t ha^{-1}			
	7 MAP	11 MAP	14 MAP	**Mean**	7 MAP	11 MAP	14 MAP	Mean
Kalolo	18.99	18.29	16.34	**18.69**	1.29	1.65	2.16	**1.70**
Vumbi	13.52	14.04	24.21	**22.25**	0.02	0.16	1.46	**0.54**
TMS 30001	22.92	15.82	28.59	**22.74**	0.80	0.76	0.71	**0.76**
Namikonga	25.84	20.17	27.49	**25.66**	0.88	1.40	5.25	**2.51**
AR 42-3	24.38	17.11	26.54	**24.32**	0.79	0.55	2.44	**1.26**
AR 40-6	22.18	17.26	23.23	**20.93**	1.76	2.25	6.97	**3.66**
Kiroba	23.48	15.65	25.54	**23.52**	2.46	2.84	6.97	**4.09**
AR 37-80	25.78	18.48	27.56	**24.24**	1.42	1.25	4.40	**2.36**
Nanchinyaya	24.94	20.11	27.72	**25.04**	0.90	2.29	4.62	**2.61**
CR 25-4	23.50	17.68	21.83	**22.57**	0.56	1.17	5.30	**2.34**
Mean	**22.55**	**17.46**	**24.91**	**23.00**	**1.09**	**1.43**	**4.03**	**2.18**
LSD (5%)	7.605	7.570	3.595	**5.059**	2.03	2.55	5.55	**2.99**
F probability	0.347	0.294	0.013	**0.001**	0.046	0.001	0.001	**0.002**
Cultivar	0.001	0.049	0.001	**0.001**	0.001	0.001	0.001	**0.001**
Site	0.097	0.001	0.001	**0.001**	0.001	0.001	0.001	**0.001**

MAP (months after planting); significance levels: * p=0.05; ** p=0.01; *** p=0.001; †= cultivar mean over three harvest dates; ‡=Mean across locations

Appendix 4 Location means for yield and yield components, starch and starch yield of ten cultivars, 2007/08

Cultivar	FSRY (t ha^{-1})					RDMC (%)				
	KBH	CHZ	KIZ	HBL	**Mean**	KBH	CHZ	KIZ	HBL	**Mean**
Kalolo	5.02	29.28	3.41	5.48	**10.80**	30.39	30.26	24.17	28.00	**28.21**
Vumbi	2.47	5.98	1.93	7.85	**4.56**	28.53	33.90	26.96	34.41	**30.95**
TMS 30001	5.60	12.57	5.63	7.56	**8.08**	33.72	32.81	32.74	29.35	**32.16**
Namikonga	7.50	18.54	7.56	4.86	**9.62**	39.94	38.06	44.72	37.92	**40.16**
AR 42-3	6.04	13.26	3.78	10.50	**8.40**	34.89	34.58	32.60	31.33	**33.35**
AR 40-6	6.43	35.54	10.00	23.57	**18.89**	36.83	32.50	37.33	34.74	**35.35**
Kiroba	7.64	42.69	10.22	14.06	**18.65**	34.67	33.89	38.44	33.50	**35.17**
AR 37-80	4.43	14.89	11.04	20.58	**12.73**	33.06	29.10	36.97	29.06	**32.05**
Nanchinyaya	5.75	21.21	8.89	8.64	**11.12**	38.17	37.22	41.18	34.33	**37.72**
CR 25-4	3.90	20.99	9.63	12.13	**11.66**	35.11	32.61	40.33	38.03	**36.52**
Mean	**5.48**	**21.50**	**7.21**	**11.62**	**11.45**	**34.54**	**33.49**	**35.54**	**33.07**	**34.16**
LSD (0.05) cult x site					**11.26**					**6.124**
CV (%)					**106.1**					**19.3**
F probability					**0.003**					**0.030**
Cultivar					**0.001**					**0.001**
Site					**0.001**					**0.057**

Cultivar	Starch content (%)					Starch yield (t ha^{-1})				
	KBH	CHZ	KIZ	HBL	**Mean**	KBH	CHZ	KIZ	HBL	Mean
Kalolo	20.46	18.20	15.57	20.54	**18.69**	0.86	4.96	0.55	0.55	**1.70**
Vumbi	20.19	13.72	30.87	24.24	**22.25**	0.07	0.16	0.29	1.65	**0.54**
TMS 30001	22.43	25.46	24.46	18.61	**22.74**	0.83	0.47	1.03	0.69	**0.76**
Namikonga	24.43	25.39	28.30	24.51	**25.66**	1.92	4.92	2.04	1.14	**2.51**
AR 42-3	21.86	21.77	26.23	27.42	**24.32**	1.15	1.21	0.00	2.68	**1.26**
AR 40-6	21.08	18.27	25.85	18.53	**20.93**	1.22	6.25	2.33	4.84	**3.66**
Kiroba	21.21	20.91	22.25	29.71	**23.52**	1.54	8.97	1.96	3.89	**4.09**
AR 37-80	24.94	23.73	25.42	22.88	**24.24**	0.82	0.96	2.42	5.23	**2.36**
Nanchinyaya	25.88	24.80	25.18	24.31	**25.04**	1.32	5.42	2.08	1.61	**2.61**
CR 25-4	21.12	20.01	24.93	24.19	**22.57**	0.71	3.51	2.18	2.98	**2.34**
Mean	**22.36**	**21.23**	**24.91**	**23.49**	**23.00**	**1.04**	**3.68**	**1.49**	**2.52**	**2.18**
LSD (0.05) cult x site					**5.059**					**2.99**
CV (%)					**23.6**					**147.7**
F probability					**0.001**					**0.002**
Cultivar					**0.001**					**0.001**
Site					**0.001**					**0.001**

Significance levels: * p=0.05; ** p=0.01; *** p=0.001; †= cultivar mean over three harvest dates

Chapter 4

Performance of F_1 seedling populations for yield and yield components in cassava

Abstract

Ten parents with desirable characteristics were planted in a crossing block at SRI-Kibaha in January 2007. A 10 x 10 half diallel mating design was used to generate the F_1 population. Collected botanical seeds from 36 families (excluding selfs) were raised on raised seed beds in November 2006 and transplanted to the main field in March 2007. The progeny were evaluated in a 6x6 triple lattice design. Data on yield, yield components and diseases were recorded. Each family comprised 150 genotypes divided equally across the three replications. Plants were harvested 12 months after planting (MAP). Seed set ranged between 14.5 and 71.5% with a mean of 34.9%. Seed germination recorded 1 MAP ranged between 40.0 and 83.4% with the mean of 63.4%. Significant differences in fresh storage root mass (FSRM), total biomass (FBM), storage root number (SRN), harvest index (HI), and root dry matter (RDMC) were observed between families. The mean values for the families for SRN were 4.1, for FSRM was 0.84 kg plant^{-1}, 2.3 kg plant^{-1}for FBM, 0.35 for the HI, and 34.0% for the RDMC. Fresh storage root mass had a negative correlation with RDMC. The high level of variation in the segregating F_1 progeny for almost all the traits provided good potential for genetic gain.

4.1   Introduction

Genetic improvement of crops depends on the extent of genetic variation present in available germplasm (Poehlman and Sleper, 1995). Genetic diversity provides farmers and plant breeders with variability that can be used to develop, through selection and breeding, crops that are resistant to virulent pests and diseases, have high yield potential, and are adapted to adverse environments (Okogbenin et al., 2007).

Clonally propagated crops are generally improved by crossing two or more desirable parental clones (Ceballos et al., 2004; Hahn et al., 1979). Sexual reproduction leading to recombination and segregation should provide new genetic variation in clonal crops (Singh,

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2003; Poehlman, 1987). The seedlings obtained from sexual reproduction would be genotypically different from the asexually derived progeny of either parental clone. Selection and clonal propagation of superior genotypes in the segregating progeny population would then follow (Kawano, 2003; Kawano et al., 1998). Clonal advancement of superior genotypes is relatively easy and quick because all genetic variability is instantly fixed (Simmonds, 1979).

Selection at the early stages of a cassava breeding programme is from seedling and clonal (single row) trials, and is based on high heritability traits such as plant type, branching habits and reaction to certain diseases (Iglesias et al., 1994; Hershey, 1984; Hahn et al., 1980). In addition, the selection is based on single plant performance (Ceballos et al., 2004) within each family at seedling stage. Intermediate to high heritability values for root dry matter composition (RDMC) have been reported (Iglesias and Heshey, 1994), with narrow sense heritability ranging from 51 to 67%, while a broad sense heritability estimate of 87% was obtained for the clonal mean (Kawano et al., 1987; Byrne, 1984). At CIAT, high heritability estimates for RDMC (95%), HI (93%) and fresh foliage composition (84%) across 13 locations have also been reported (Perez et al., 2005). Harvest index is a highly heritable trait in cassava and therefore a better selection criterion than single plant yield in segregating populations (Kawano et al., 1978; CIAT, 1974). Kawano and Thung (1982) and Kawano et al. (1998) reported high correlation and regression coefficients for HI with root yield and demonstrated the effectiveness of using the trait at all stages of selection as an indirect selection for root yield.

Root number, a trait affecting root yield, is known to be determined early in the growth cycle (Hunt et al., 1977; Wholey and Cock, 1974; Magoon, 1970), and can be used as an early selection criteria. However, storage root number can be affected by growing conditions such as fertilizer application (Hunt et al., 1977). Cours (1951) noted that new storage roots could be formed at the onset of a new filling period after a dry season.

Phenotypic correlation between total biomass and fresh root yield in cassava has been observed to be very high (0.97) at the early evaluation stages, and lower (0.54) at an advanced stage of evaluation (Kawano et al., 1998; Cock, 1984; Kawano and Thung, 1982; Cock et al., 1979). Kawano et al. (1998) reported very low correlation (-0.19) between HI

and fresh root yield at the early stages (seedling and clonal), but very high (0.93) at advanced evaluation stages. However, cassava genotypes perform differently in terms of yield, harvest index and biomass at different stages of evaluation and selection (Kawano and Thung, 1982). Those genotypes with higher biomass at seedling or clonal evaluation trial tend to dominate others with less biomass in competition for light. Likewise, genotypes with high harvest index are weak competitors while those with greater biomass are strong competitors. Byrne (1984) observed that there were significant correlations (r=0.48**) in root dry matter content between seedling and single row trials.

The objectives of this study were to evaluate the performance of a diallel derived seedling population for yield characteristics in general, with the specific objective of improving root yield and dry matter content as a step towards starch content improvement. Virus diseases (cassava mosaic disease and cassava brown streak disease) affecting production were taken into consideration.

4.2   Materials and methods

4.2.1   Germplasm source

Parent genotypes for this study comprised five local cultivars, one from IITA and four CIAT (Table 4.1). Both the local germplasm and exotic varieties were selected based on their characteristics of good performance in terms of dry matter, pest and disease resistance and flowering ability.

Table 4.1 Description of parent genotypes used in the diallel mating design

Cultivar	Description
1. AR 42-3	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
2. AR 40-6	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
3. AR 37-80	Clone from CIAT, resistant to CMD, CBB and CGM, sweet
4. CR 25-4	Clone from CIAT, resistant to CMD, CBB and sweet
5. TMS 30001	Clone from IITA, resistant to CMD, tolerant to CBSD, sweet (Hahn et al., 1980)
6. Kalolo	Local cultivar, bitter taste, high dry matter, good flour quality
7. Namikonga	Local improved cultivar from Amani, sweet, high dry matter, tolerant to CBSD,
8. Nanchinyaya	Local cultivar, sweet, high dry matter, tolerant to CBSD
9. Vumbi	Local improved cultivar from Amani research centre, sweet, early bulking type, good cooking qualities
10. Kiroba	Local improved cultivar, early maturing, tolerant to CBSD, good cooking qualities, sweet, moderate tolerance to CMD

CIAT= Centre for Cassava Improvement; IITA= International Institute of Tropical Agriculture
CMD=Cassava mosaic disease; CBSD=Cassava brown streak disease; CBB=Cassava bacterial blight; CGM=Cassava green mite.

4.2.2 Crossing block

Selected parents with desirable characteristics were planted in a crossing block at SRI-Kibaha, in January 2006. The parents were arranged to facilitate a 10x10 half diallel mating design (Stuber, 1980). A spacing of 1.0 m intra-row and 1.5 m inter-row was used to provide enough space for plant growth. Normally flowering is rare during the dry season, therefore plants were irrigated as required to ensure adequate flowering and seed set (Kawano, 1980). Hand weeding was performed as required but no chemical control was exercised over insects or diseases. Controlled hand pollination was done according to the standard procedure described by Kawano (1980).

Plants were observed for signs of flowering each morning. Muslin bags were used to enclose flowers about to open to prevent fertilization by stray pollen upon opening. Pollen from the corresponding male parent in accordance with the diallel mating design was collected in the morning before 10h00 and pollination done later in the day (primarily between 11h00 and 14h00) after flowers had opened by dusting on the stigma of a matching

female. However, as both male and female flowers are large and pollen is sticky, pollination did not need any tool.

One male flower could pollinate up to three female flowers. After pollination the female flowers were covered with the muslin bags for one to two weeks. Each flower branch was marked by a tag indicating cross combination with female parent listed first, date of pollination and pollinator. Developing fruits were covered with netting bags three to four weeks after pollination to catch the dehisced seeds when ripe. Seeds were collected after two months, labeled and stored ready for planting. Percent seed set was determined by dividing pollinated fruits (survived after pollination) with total number of seeds per cross. For pollinated fruits it was assumed that every fruit had three ovules.

Figure 4.1 Pollinated flowers covered with muslin bag

4.2.3 Propagation of the progeny

Seed of the F_1 generation were sown on raised seed beds end of November 2006, at SRI-Kibaha. The number of seeds per cross ranged between 250 and 300 depending on the amount of seeds available. During this time of the year soil temperatures were high (30-35°C) which facilitated fast germination (Jennings and Hershey, 1985). Germinating seeds were hand-watered on a daily basis. Hardening of seedlings was done one week before transplanting to the main field by reduced watering regimes.

Figure 4.2 Seed bed with germinating seedlings at SRI-Kibaha, February 2007.

4.2.4   Seedling field trial

The seedling trial was established at SRI-Kibaha at the end of February 2007. The trial was laid out as 6x6 triple lattice with six plots in each of six blocks per replication. The 36 families were randomly allocated to plots within blocks, and blocks randomly allocated within each replication. The seedlings were planted at 1 x 1 m spacing. Each family comprising 150 progeny was divided equally across the three replications i.e. 50 progeny per plot in each replication. Seedlings were watered at establishment and thereafter whenever necessary. Spreader rows of the cultivar Mreteta which was infected by cassava brown streak (Cassava brown streak virus; *Ipomovirus*; *Potyviridae*) were planted around each replication and between replications to enhance transmission of the disease by white flies (*Bemisia tabaci* Gennadius). No fertilizer was applied.

4.2.5 Data collection

The seedling trial was harvested at the end of March 2008, delayed by three weeks by the onset of the main rains. Plants were harvested on an individual basis. Shoot and roots were weighed to obtain fresh yield. All storage roots in a plant (SRN) were counted. Harvest index (HI) was determined by dividing fresh storage root mass (FSRM) by total biomass (FBM). Percent dry matter (RDMC) was determined using a forced draught oven (Dixon and Nukenine, 2000) as follows: cassava roots were washed and cut into thin slices. Duplicate samples of 100 g each were taken and dried at 70°C for 72 h. The dried samples were weighed to obtain the dry mass, which was expressed as a percentage of the fresh mass. Dry storage root yield (DSRY) was derived as a product of RDMC and FSRY. Disease assessment was done at 3, 6, and 9 MAP. However, data presented are disease scores recorded at 6 MAP. Cassava mosaic and cassava brown streak diseases were rated as follows:

    i.   Cassava mosaic disease (CMD) severity was assessed subjectively at 6 MAP on a scale of 1-5 (Mahungu and Kanju,1997) as follows:

1= No symptoms observed;

2= Mild chlorotic pattern on entire leaflets or mild distortion at base of leaflets, the rest of leaflets appearing green and healthy;

3= Strong mosaic pattern on entire leaf, and narrowing and distortion of lower one-third of leaflets;

4= Severe mosaic with distortion of two-thirds of leaflets and general reduction of leaf size; and

5= Severe mosaic, distortion of four-fifths or more of leaflets, twisted and misshapen leaves.

    ii.   Cassava brown streak disease (CBSD) severity was assessed subjectively at 6 MAP on above ground parts, on a scale of 1-5 (Mahungu and Kanju, 1997), where:

1= No visible symptoms;

2= Slight foliar chlorosis between leaf vein, no stem lesions;

3= Foliar chlorosis between leaf veins, with mild stem lesions, no die-back

4= Foliar chlorosis between leaf veins, and pronounced stem lesions with beginning of die-back; and

5=Defoliation with pronounced die-back and stem lesions

4.2.6 Data analysis

All data were analysed using Genstat Version 12 (Payne et al., 2008). The REML linear mixed model was used to analyse family and progeny data at seedling stage. Families and progeny were declared as fixed effects in the model, while replications, blocks, and plots were declared as random effects. Phenotypic correlation between traits on a family mean basis was performed using the Pearson correlation procedure. Principal component analysis was done to study the relative contribution of various traits in genotype improvement. Principal component analysis involves a mathematical procedure that transforms a number of correlated variables into a smaller number of uncorrelated variables called principal components (PC) (Jollife, 2002). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

4.3 Results

4.3.1 Seed set and germination

A total of 45 crosses were expected from a 10 x 10 half diallel. However, two crosses did not produce seed, and another seven crosses produced less than 150 seeds. The required number of seed was between 250 to 300 seed per family to account for potential germination and transplanting losses. Therefore the nine crosses were left out remaining with 36 families. Seed set per cross ranged from 14.5 to 71.5% with a mean of 34.9% (Table 4.2). The family CR 25-4 x AR 40-6 had relatively more seeds (71.5%) than other families, while the lowest seed set (14.5%) was observed in family Kiroba x AR 37-80. The rate of seed germination determined four weeks after sowing ranged between 40.0 and 83.4% with a mean of 63.4% (Table 4.2). The highest and lowest rates of seed germination were recorded from families Kalolo x Namikonga (83.4%) and Vumbi x AR 40-6 (40.0%) respectively.

Table 4.2 Percent seed set per cross and seed germination of the diallel crosses at SRI-Kibaha, 2006/07

Cross	Seed set		Seed germination	
	%	Rank	%	Rank
1. Kalolo x Vumbi	42.6	8	70.6	8
2. Kalolo x Namikonga	26.9	26	83.4	1
3. Kalolo x AR 40-6	17.5	34	68.0	10
4. Kalolo x TMS 30001	55.9	4	82.2	3
5. Kalolo x AR 42-3	31.8	21	62.6	21
6. Kalolo x AR 37-80	33.3	17	57.4	28
7. Kiroba x Namikonga	19.3	33	67.5	12
8. Kiroba x Vumbi	16.9	35	70.3	9
9. Nanchinyaya x Vumbi	60.5	2	63.6	20
10. Kiroba x AR40-6	22.6	32	64.5	18
11. Kiroba x TMS 30001	26.0	29	61.3	24
12. Kiroba x AR 42-3	22.9	31	64.0	19
13. Kiroba x AR 37-80	14.5	36	67.5	13
14. Nanchinyaya x Namikonga	29.1	23	79.2	4
15. Nanchinyaya x AR 40-6	34.3	16	66.0	16
16. Nanchinyaya x TMS 30001	32.1	20	82.6	2
17. Nanchinyaya x AR 42-3	28.7	24	74.6	5
18. Nanchinyaya x AR 37-80	38.3	12	66.8	14
19. Vumbi x Namikonga	37.0	14	42.7	35
20. Vumbi x AR 40-6	38.1	13	40.0	36
21. Vumbi x TMS 30001	30.5	22	60.7	25
22. Vumbi x AR 42-3	36.6	15	55.3	29
23. Vumbi x AR 37-80	50.4	5	47.0	33
24. TMS 30001 x AR 37-80	42.1	10	65.9	17
25. Namikonga x AR 40-6	27.5	25	54.3	30
26. Namikonga x TMS 30001	24.5	30	71.0	7
27. TMS 30001 x AR 42-3	42.9	7	73.0	6
28. Namikonga x AR 42-3	32.2	19	61.8	23
29. Namikonga x AR 37-80	41.0	11	66.0	15
30. AR 40-6 x TMS 30001	26.6	27	67.7	11
31. AR 40-6 x AR 42-3	33.3	18	52.3	31
32. AR 40-6 x AR 37-80	44.0	6	46.0	34
33. AR 42-3 x AR 37-80	26.4	28	58.3	26
34. CR 25-4 x AR 42-3	42.3	9	58.0	27
35. CR 25-4 x AR 40-6	71.5	1	62.2	22
36. CR 25-4 x AR 37-80	58.7	3	49.1	32
Mean	**34.9**		63.4	
Maximum	71.5		83.4	
Minimum	14.5		40	
Standard error of the mean	2.14		1.78	
Standard deviation	12.8		10.7	
Skewness	0.89		-0.21	

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4.3.2 Yield and yield components of the progeny

The FBM for the 1653 progeny ranged from 0.20 to 21.5 kg plant[-1] with a mean of 2.4 kg plant[-1]. Genotype 131-21 R2 had the highest FBM of 21.5 kg plant[-1]. Storage root number (SRN) ranged from 0.0 to 16 roots plant[-1] with a mean of 4.3 roots plant[-1], and the (HI) from 0.01 to 0.8. The highest SRN of 16 roots plant[-1] was recorded from family Kalolo x TMS 30001 (genotype 213-16 R2). The mean FSRM was 0.9 and ranged between 0.0 and 6.5 kg plant[-1], with genotype 105-02 R1 from the family (Kalolo x AR 42-3) having the highest individual progeny FSRM of 6.5 kg plant[-1]. Family Kalolo x AR 42-3 had FSRM values ranging from 0.0 to 6.5 kg plant[-1], compared with family such as Nanchinyaya x TMS 30001 which had ranged from 0.0 to 2.5 kg plant[-1], indicating genetic variability within families and the potential for selection (Tables 4.3; 4.4). Mean RDMC was 34.3%, and ranged between 6.4 and 60.5%. Genotype 125-8 R2 (Namikonga x AR 40-6) had the highest RDMC value of 60.5%, followed by genotype 121-22 R2 (Vumbi x TMS 30001) with the RDMC value of 53.2%. It is also important to note that some families recorded very low RDMC of 8.8% and 6.4% (Kalolo x AR 42-3 and Kiroba x Namikonga, respectively) (Table 4.5). Plant height (PLht) and first branching height (BRht) ranged from 15 to 285 cm, and 15 to 235 cm, respectively (Table 4.3).

Table 4.3 Minimum, maximum and mean values for yield and yield components of the 1653 genotypes on individual progeny evaluated at the seedling evaluation trial 2007

Variable	Min	Max	Mean	SD	SEM	Skew
FBM	0.20	21.5	2.4	1.5	0.04	3.2
SRN	0.00	16.0	4.3	0.7	0.02	1.9
HI	0.01	0.8	0.4	0.2	0.03	-0.2
FSRM	0.00	6.5	0.9	0.7	0.02	1.9
RDMC	6.40	60.5	34.3	5.5	0.14	-0.7
PLht	15.00	285.0	135.4	36.7	0.51	0.10
BRht	15.00	235.0	115.3	29.1	0.61	0.25

FBM (fresh biomass in kg plant[-1]); SRN (total number of storage roots); HI (harvest index); FSRM (fresh storage root mass in kg plant[-1]); RDMC (root dry matter content in %); PLht (plant height in cm); BRht (branching height in cm); Min (minimum); Max (maximum); SD (standard deviation); SEM (standard error of the mean); skew (skewness)

Table 4.4 Minimum, maximum, mean of fresh root mass (kg plant^{-1}) evaluated at the seedling evaluation trial, SRI-Kibaha, 2007

Cross	Min	Max	Mean	SD	SEM	Rank
1. Kalolo x Vumbi	0.1	5.4	1.5	1.1	0.2	2
2. Kalolo x Namikonga	0.05	2.7	1.0	0.7	0.1	8
3. Kalolo x AR 40-6	0.0	3.8	1.2	0.8	0.1	3
4. Kalolo x TMS 30001	0.0	3.9	1.1	0.8	0.1	5
5. Kalolo x AR 42-3	0.0	6.5	1.7	1.2	0.2	1
6. Kalolo x AR 37-80	0.0	4.0	1.2	0.9	0.1	4
7. Kiroba x Namikonga	0.0	2.3	0.5	0.5	0.1	36
8. Kiroba x Vumbi	0.0	1.8	0.6	0.5	0.1	35
9. Nanchinyaya x Vumbi	0.0	2.2	0.6	0.5	0.1	24
10. Kiroba x AR40-6	0.0	2.5	0.7	0.6	0.1	25
11. Kiroba x TMS 30001	0.0	2.3	0.9	0.5	0.1	11
12. Kiroba x AR 42-3	0.0	2.3	0.9	0.6	0.1	12
13. Kiroba x AR 37-80	0.0	2.6	0.8	0.5	0.1	13
14. Nanchinyaya x Namikonga	0.0	3.2	0.6	0.6	0.1	34
15. Nanchinyaya x AR 40-6	0.0	4.0	0.9	0.7	0.1	14
16. Nanchinyaya x TMS 30001	0.0	1.4	0.7	0.4	0.1	26
17. Nanchinyaya x AR 42-3	0.0	1.6	0.7	0.4	0.1	27
18. Nanchinyaya x AR 37-80	0.0	1.6	0.7	0.4	0.1	28
19. Vumbi x Namikonga	0.0	2.2	0.8	0.7	0.1	18
20. Vumbi x AR 40-6	0.0	2.0	0.8	0.5	0.1	19
21. Vumbi x TMS 30001	0.0	2.5	0.9	0.7	0.1	15
22. Vumbi x AR 42-3	0.0	3.6	0.8	0.7	0.1	20
23. Vumbi x AR 37-80	0.0	3.6	0.9	0.8	0.1	16
24. TMS 30001 x AR 37-80	0.0	1.7	0.6	0.5	0.1	33
25. Namikonga x AR 40-6	0.0	4.5	0.6	0.7	0.1	29
26. Namikonga x TMS 30001	0.0	3.5	0.7	0.7	0.1	30
27. TMS 30001 x AR 42-3	0.0	2.5	0.9	0.6	0.1	9
28. Namikonga x AR 42-3	0.0	2.5	0.7	.06	0.1	31
29. Namikonga x AR 37-80	0.0	2.1	0.7	0.5	0.1	21
30. AR 40-6 x TMS 30001	0.0	2.0	0.8	0.5	0.1	22
31. AR 40-6 x AR 42-3	0.0	2.2	0.8	0.5	0.1	23
32. AR 40-6 x AR 37-80	0.0	2.6	0.7	0.6	0.1	17
33. AR 42-3 x AR 37-80	0.0	6.2	1.0	1.1	0.2	6
34. CR 25-4 x AR 42-3	0.0	3.7	1.1	1.0	0.6	7
35. CR 25-4 x AR 40-6	0.1	4.0	0.9	0.8	0.1	10
36. CR 25-4 x AR 37-80	0.0	4.5	0.5	0.9	0.1	32

Min (minimum); Max (maximum); SD (standard deviation); SEM (standard error of the mean)

Table 4.5 Minimum, maximum, and mean for root dry matter (%) evaluated at the seedling evaluation trial, SRI-Kibaha

Cross	Min	Max	Mean	SD	SEM	Rank
1. Kalolo x Vumbi	17.0	44.0	32.9	0.6	0.8	28
2. Kalolo x Namikonga	14.0	42.0	31.8	6.3	0.9	32
3. Kalolo x AR 40-6	19.0	46.0	34.0	6.8	1.0	17
4. Kalolo x TMS 30001	15.3	42.0	30.2	6.5	1.0	36
5. Kalolo x AR 42-3	8.8	43.0	33.3	5.7	0.8	24
6. Kalolo x AR 37-80	17.7	36.0	31.6	5.3	0.8	33
7. Kiroba x Namikonga	6.4	44.0	30.8	7.5	1.2	34
8. Kiroba x Vumbi	17.5	40.1	32.4	4.2	0.7	29
9. Nanchinyaya x Vumbi	20.0	43.8	35.7	0.8	0.8	8
10. Kiroba x AR40-6	22.8	45.1	35.7	4.9	0.8	9
11. Kiroba x TMS 30001	14.8	40.0	33.0	5.0	0.7	27
12. Kiroba x AR 42-3	27.0	42.0	36.4	3.3	0.5	5
13. Kiroba x AR 37-80	18.2	44.0	33.3	5.8	0.9	22
14. Nanchinyaya x Namikonga	23.0	44.0	35.2	5.0	0.8	13
15. Nanchinyaya x AR 40-6	26.0	43.0	34.6	4.4	0.7	14
16. Nanchinyaya x TMS 0001	25.0	44.0	34.3	4.9	0.7	16
17. Nanchinyaya x AR 42-3	21.0	43.0	35.3	4.5	0.7	11
18. Nanchinyaya x AR 37-80	21.0	43.0	35.4	4.5	0.7	10
19. Vumbi x Namikonga	26.0	43.0	35.7	3.4	0.5	7
20. Vumbi x AR 40-6	23.7	43.0	36.9	4.3	0.7	3
21. Vumbi x TMS 30001	27.0	51.7	35.8	4.7	0.7	6
22. Vumbi x AR 42-3	26.0	43.0	35.2	3.6	0.6	12
23. Vumbi x AR 37-80	22.0	42.0	33.8	5.1	0.8	19
24. TMS 30001 x AR 37-80	18.0	46.7	33.6	5.8	0.9	20
25. Namikonga x AR 40-6	16.0	60.5	36.7	7.2	1.2	4
26. Namikonga x TMS 30001	19.2	42.7	33.6	5.3	0.8	21
27. TMS 30001 x AR 42-3	13.2	42.3	33.3	5.6	0.8	23
28. Namikonga x AR 42-3	22.9	44.0	37.5	4.4	0.7	1
29. Namikonga x AR 37-80	13.0	50.0	33.2	6.6	1.0	25
30. AR 40-6 x TMS 30001	24.2	42.0	34.5	4.5	0.7	15
31. AR 40-6 x AR 42-3	30.1	43.0	37.4	2.9	0.5	2
32. AR 40-6 x AR 37-80	23.2	39.0	33.1	3.9	0.6	26
33. AR 42-3 x AR 37-80	17.5	45.3	32.1	5.2	0.8	30
34. CR 25-4 x AR 42-3	16.1	38.0	32.1	4.5	0.7	31
35. CR 25-4 x AR 40-6	23.0	42.6	33.9	4.2	0.6	18
36. CR 25-4 x AR 37-80	16.2	39.0	30.4	6.5	1.2	35

Min (minimum); Max (maximum); SD (standard deviation); SEM (standard error of the mean)

4.3.3 Family yield and yield components

Large and significant (p≤0.001) differences among families were observed in FBM, RDMC, SRN, FSRM, and HI (Table 4.6). The overall mean SRN for all 36 families was 4.1, and ranged between 2.4 and 5.8 roots plant^{-1} (Tables 4.6; 4.7). The family Kalolo x AR 42-3 had the highest mean SRN of 6.4 roots plant^{-1} (Table 4.7). The FSRM for the 36 families ranged between 0.5 and 1.7 with a mean of 0.8 kg plant^{-1} (Tables 4.6; 4.7). Family Kalolo x AR 42-3 had the highest mean FSRM of 1.7 kg plant^{-1} (Table 4.7). The HI ranged from 0.3 to 0.5 for the 36 families evaluated, with a mean of 0.4 (Tables 4.6; 4.7). Family Kalolo x AR 42-3 recorded the highest mean HI of 0.5 (Table 4.7). Plant height ranged between 104.8 (Nanchinyaya x AR 42-3) and 149.5 cm (Kalolo x TMS 30001), while the first branching height ranged between 93.5 (CR 25-4 x AR 40-6) and 140.2 cm from family (Namikonga x AR 42-3). The top five individual progeny for FSRM were recorded from three different families, namely: Kalolo x AR 42-3 (105-02 R1, 105-14 R2, 105-22 R1), Kalolo x Vumbi (101-18 R1), and AR 42-3 x AR 37-80 (133-04 R1). Families differed significantly from one another (p≤0.001) in RDMC, and the family means ranged from 30.3 (Kalolo x TMS 30001) to 37.5% (Namikonga x AR 42-3) with an overall mean of 34.0% (Table 4.7). Family AR 40-6 x AR 42-3 had the second highest RDMC (37.4%).

Table 4.6 Residual maximum likelihood Wald's F statistic for yield and yield components of 36 families evaluated at
the seedling evaluation trial

Variable	Degrees of freedom Family	F Statistic Family	Min	Max	Mean	SEM	SED
FSRM	35	3.16***	0.53	1.71	0.84	0.15	0.21
FBM	35	2.71***	1.53	3.55	2.31	0.29	0.39
SRN	35	2.17***	2.38	5.81	4.11	0.52	0.68
HI	35	2.80***	0.26	0.45	0.35	0.02	0.04
RDMC	35	4.67***	30.32	37.48	34.02	1.65	1.60
PLht	35	4.74***	104.80	149.50	128.8	6.76	9.83
BRht	35	9.36***	93.50	146.10	118.15	3.87	5.41

FSRM (fresh storage root mass in kg plant^{-1}); HI (harvest index); FBM (fresh biomass in kg plant^{-1}); SRN (total number of storage roots);
RDMC (root dry matter content in %); PLht (plant height); BRht (branching height);Min (minimum); Max (maximum);
SEM (standard error of the mean); Significance levels: * p≤0.05; ** p≤0.01; ***p≤0.001;

Table 4.7 Family means of yield and yield components evaluated at the seedling evaluation trial, SRI-Kibaha, 2007

Cross	FBM	SRN	FSRM	RDMC	HI	PLht	BRht
1. Kalolox Vumbi	3.3	6.2	1.5	32.9	0.44	141.2	127.7
2. Kalolo x Namikonga	2.3	5.0	1.0	31.8	0.40	142.3	132.7
3. Kalolo x AR 40-6	2.7	6.2	1.2	33.9	0.44	127.8	110.0
4. Kalolo x TMS 30001	2.7	6.2	1.1	30.3	0.40	149.5	138.4
5. Kalolo x AR 42-3	3.6	6.4	1.7	33.3	0.45	131.9	119.5
6. Kalolo x AR 37-80	2.9	6.3	1.2	31.6	0.41	133.1	131.5
7. Kiroba x Namikonga	1.8	3.8	0.5	30.9	0.30	148.7	136.7
8. Kiroba x Vumbi	2.1	3.5	0.6	32.4	0.27	128.2	112.4
9. Nanchinyaya x Vumbi	2.4	4.5	0.6	35.7	0.27	139.7	125.8
10. Kiroba x AR40-6	2.1	4.0	0.7	35.7	0.31	121.0	106.1
11. Kiroba x TMS 30001	2.2	4.5	0.9	33.0	0.39	139.9	127.1
12. Kiroba x AR 42-3	2.4	4.0	0.9	36.4	0.35	123.6	121.1
13. Kiroba x AR 37-80	2.3	4.3	0.8	33.3	0.31	124.7	116.9
14. Nanchinyaya x Namikonga	1.8	4.5	0.7	35.2	0.35	117.3	119.1
15. Nanchinyaya x AR 40-6	2.5	5.5	0.9	34.6	0.35	117.3	100.7
16. Nanchinyaya x TMS 30001	1.9	4.3	0.7	34.3	0.36	112.2	108.6
17. Nanchinyaya x AR 42-3	2.5	4.2	0.7	35.3	0.31	104.8	96.4
18. Nanchinyaya x AR 37-80	2.1	5.6	0.7	35.4	0.33	107.7	94.8
19. Vumbi x Namikonga	2.5	3.8	0.8	35.7	0.31	137.4	124.7
20. Vumbi x AR 40-6	2.5	3.5	0.8	36.9	0.29	126.5	107.6
21. Vumbi x TMS 30001	2.3	4.2	0.9	35.8	0.38	126.8	122.2
22. Vumbi x AR 42-3	2.4	3.4	0.8	35.2	0.33	132.2	122.4
23. Vumbi x AR 37-80	2.5	3.5	0.9	33.8	0.31	140.6	126.6
24. TMS 30001 x AR 37-80	1.9	3.5	0.6	33.6	0.30	153.3	134.8
25. Namikonga x AR 40-6	1.9	3.5	0.6	36.7	0.34	120.3	113.2
26. Namikonga x TMS 30001	1.8	3.7	0.7	33.6	0.34	133.7	138.0
27. TMS 30001 x AR 42-3	1.9	5.1	0.9	33.3	0.45	112.8	118.2
28. Namikonga x AR 42-3	1.9	3.4	0.7	37.5	0.31	124.0	140.1
29. Namikonga x AR 37-80	2.1	4.1	0.7	33.2	0.33	135.4	146.1
30. AR 40-6 x TMS 30001	2.0	4.8	0.8	34.5	0.40	129.1	114.9
31. AR 40-6 x AR 42-3	2.7	4.5	0.8	37.4	0.38	128.5	101.9
32. AR 40-6 x AR 37-80	1.7	4.4	0.7	33.1	0.37	129.0	100.5
33. AR 42-3 x AR 37-80	2.7	4.6	1.0	32.2	0.35	131.0	109.7
34. CR 25-4 x AR 42-3	2.7	5.1	1.1	32.1	0.38	129.4	114.1
35. CR 25-4 x AR 40-6	2.2	5.2	0.9	33.9	0.38	117.1	93.5
36. CR 25-4 x AR 37-80	1.5	2.7	0.5	30.4	0.26	120.0	99.2
Mean	**2.3**	**4.1**	**0.84**	**34.0**	**0.35**	**0.78**	**118.2**
SEM	0.29	0.52	0.15	1.65	0.02	0.02	3.87
SED	0.39	0.68	0.21	1.6.0	0.04	0.02	5.41

FBM (fresh biomass plant[-1]); SRN (storage root number); FSRM (fresh storage root mass plant[-1]); RDMC (root dry matter in %); HI (harvest index); PLht (plant height); BRht (branching height); SEM (standard error of the mean); SED (standard error of the difference)

4.3.4 Virus diseases

Significant differences between families (p≤0.001) were observed in the expression of cassava mosaic disease (CMD) and cassava brown streak disease symptoms (CBSD). The CMD severity ranged between 1.4 (Kiroba x TMS 30001, Vumbi x TMS 30001, TMS 30001 x AR 37-80, Namikonga x TMS 30001, AR 40-6 x TMS 30001, and CR 25-4 x AR 37-80) and 2.5 (Kalolo x AR 37-80) with a mean score of 1.7, while for CBSD only a few families (Vumbi x AR 40-6, Namikonga x AR42-3, CR 25-4 x AR 40-6,and CR 25-4 x AR 37-80) expressed the disease with a mean of 1.03 (Table 4.8).

Table 4.8 Family means for yield, yield components and disease scores evaluated at the seedling evaluation trial SRI-Kibaha, 2007

Cross	CMD	CBSD
1. Kalolo x Vumbi	2.3	1.0
2. Kalolo x Namikonga	1.9	1.0
3. Kalolo x AR 40-6	2.0	1.0
4. Kalolo x TMS 30001	1.5	1.0
5. Kalolo x AR 42-3	2.0	1.0
6. Kalolo x AR 37-80	2.5	1.0
7. Kiroba x Namikonga	1.7	1.0
8. Kiroba x Vumbi	2.0	1.0
9. Nanchinyaya x Vumbi	2.2	1.0
10. Kiroba x AR40-6	1.6	1.0
11. Kiroba x TMS 30001	1.4	1.0
12. Kiroba x AR 42-3	1.6	1.0
13. Kiroba x AR 37-80	1.6	1.0
14. Nanchinyaya x Namikonga	1.9	1.0
15. Nanchinyaya x AR 40-6	1.8	1.0
16. Nanchinyaya x TMS 30001	1.6	1.0
17. Nanchinyaya x AR 42-3	2.0	1.0
18. Nanchinyaya x AR 37-80	2.0	1.0
19. Vumbi x Namikonga	1.7	1.0
20. Vumbi x AR 40-6	1.7	1.1
21. Vumbi x TMS 30001	1.4	1.0
22. Vumbi x AR 42-3	1.6	1.0
23. Vumbi x AR 37-80	1.6	1.0
24. TMS 30001 x AR 37-80	1.4	1.0
25. Namikonga x AR 40-6	1.6	1.0
26. Namikonga x TMS 30001	1.4	1.0
27. TMS 30001 x AR 42-3	1.5	1.0
28. Namikonga x AR 42-3	1.6	1.1
29. Namikonga x AR 37-80	1.6	1.0
30. AR 40-6 x TMS 30001	1.4	1.0
31. AR 40-6 x AR 42-3	1.5	1.0
32. AR 40-6 x AR 37-80	1.5	1.0
33. AR 42-3 x AR 37-80	1.6	1.0
34. CR 25-4 x AR 42-3	1.7	1.0
35. CR 25-4 x AR 40-6	1.7	1.2
36. CR 25-4 x AR 37-80	1.4	1.4
Mean	**1.7**	**1.03**
SEM	0.07	0.01
SED	0.16	0.04

CMD (cassava mosaic disease scores); CBSD (cassava brown streak disease scores); SEM (standard error of the mean); SED (standard error of the difference)

4.3.5 Correlation between traits

The trait DSRY was highly, positively and significantly correlated (p≤0.001) with almost all yield traits evaluated as follows: HI (r=0.66; p≤0.001), SRN (r=0.59; p≤0.001), FSRM (r=0.97; p≤0.001) (Table 4.9). The RDMC correlated positively with DRSY (r=0.17; p≤0.001), HI (r=0.08; p≤0.001), and SRN (r=0.07; p≤0.001). Negative and non-significant association was observed between FSRY and RDMC (r=-0.018) indicating that these two traits were independent.

Table 4.9 Correlations between five traits of the families in the seedling evaluation trial

		DSRY	HI	RDMC	SRN	FSRM
DSRY	1					
HI	2	0.6591***				
RDMC	3	0.1669***	0.0822***			
SRN	4	0.5890***	0.5002***	0.0678***		
FSRM	5	0.9709***	0.6532***	-0.018	0.6165***	1.00

DSRY (dry storage root yield); HI (harvest index); RDMC (root dry matter in %); SRN (storage root number); FSRM (fresh storage root M); FSRY (fresh storage root yield); Significance levels: * p≤0.05; ** p≤0.01; ***p≤0.001;

4.3.5 Principal component analysis

Principal component analysis was used to explain the relative contribution of the various traits to the performance of the progeny. The first four PCs accounted for 99.86% of the total variation (Table 4.10). The PC1 accounted for 78% of the total variance. The RDM was the main contributing trait to PC1. The PC2 accounted for 17.51% of the total variance, with SRN, FBM and FSRM contributing most to the variation. The PC3 and PC4 contributed 4.02 and 0.42% of the total variance, with SRN and HI contributing to PC3, and FBM and SRN to PC4.

Table 4.10 Principal component coefficients of five traits evaluated on 36 families at seedling evaluation trial, SRI-Kibaha, 2007

Trait	PC1	PC2	PC3	PC4
HI	-0.002	0.028	0.011	-0.233
RDMC	0.999	0.041	0.002	0.005
SRN	-0.038	0.899	0.428	0.085
FSRM	-0.004	0.207	-0.256	-0.918
FBM	-0.015	0.383	-0.867	0.311
Percent variation	78.03	17.51	4.02	0.42
Cumulative variation	78.03	95.54	99.56	99.98

HI (harvest index); RDMC (root dry matter %); SRN (storage root number); FSRM (fresh storage root mass); FBM (fresh biomass)

Frequency distributions of progeny within the top nine families for RDMC (Figures 4.2) indicate that in general most of the families were negatively skewed, while for FSRM (Figure 4.3) almost all nine families were positively skewed which imply that FSRM can be improved through hybridization with elite parents and selection done in order to make improvement in yield response.
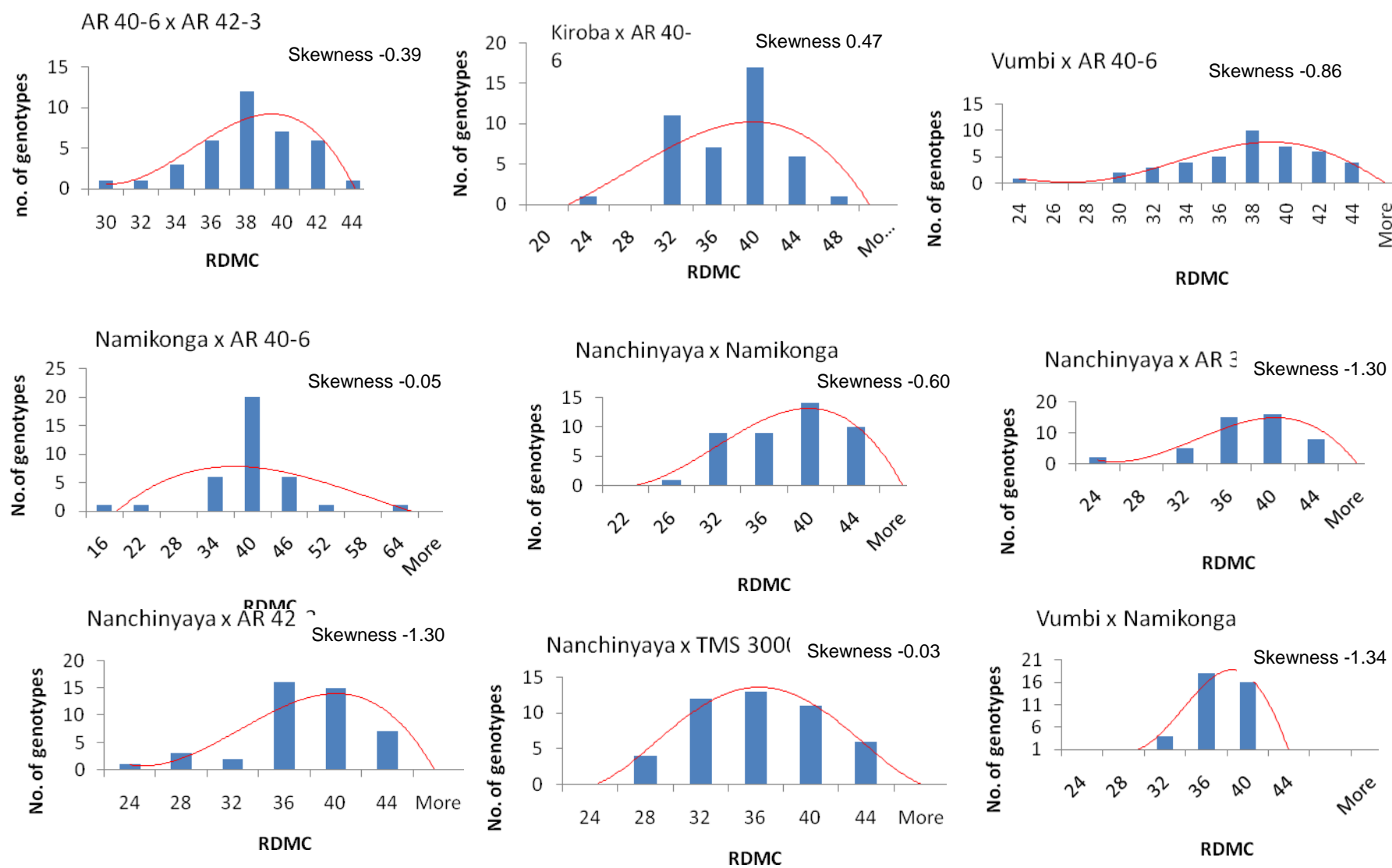
Figure 4.2 Frequency distribution of progeny within the top nine families for root dry matter (%) evaluated at the seedling evaluation trial
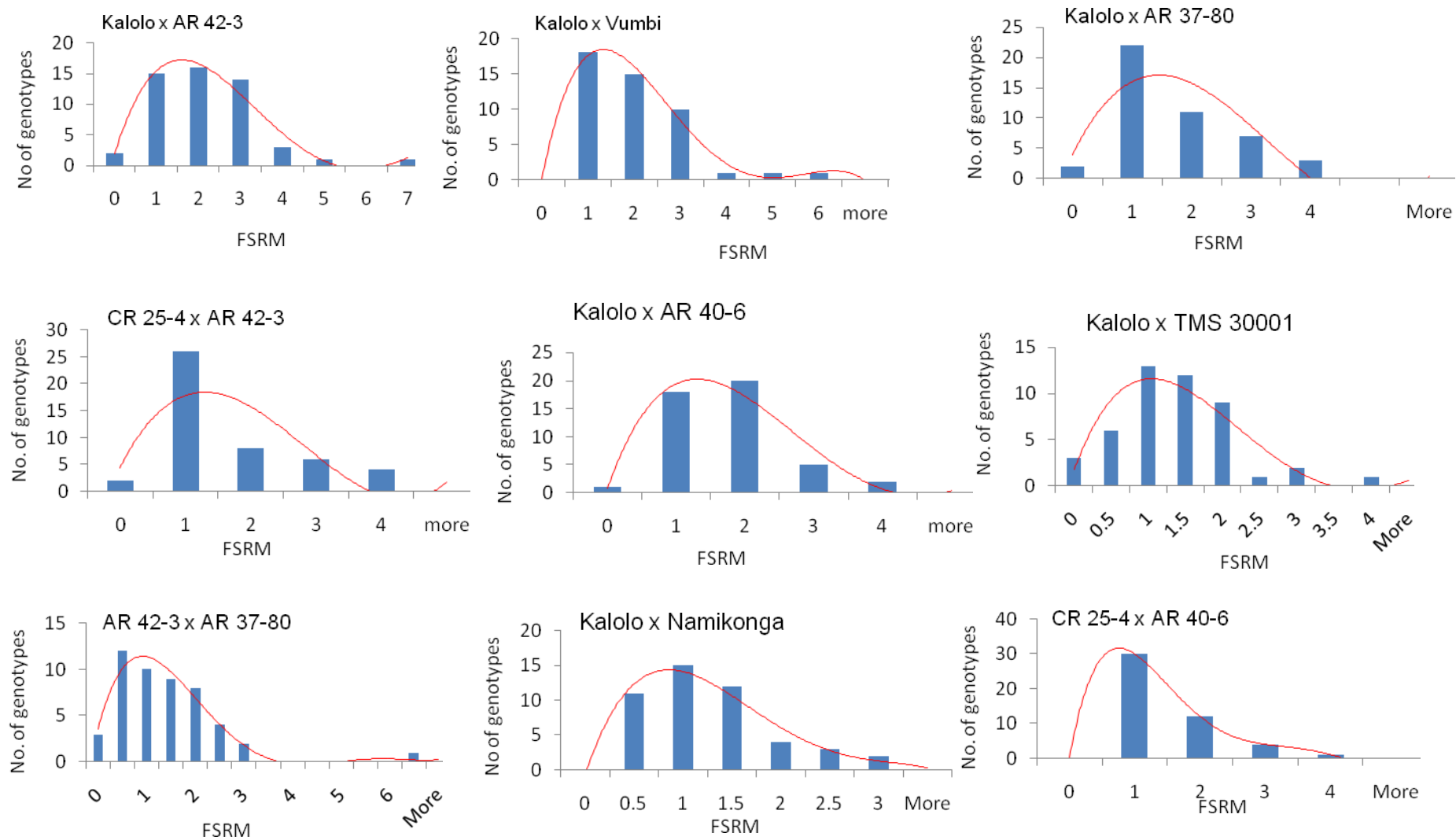
Figure 4.3 Frequency distribution of progeny within the top nine families for fresh storage root mass (kg plant^{-1}) evaluated at the seedling evaluation trial

4.5   Discussion and conclusion

The study was conducted with the objective of generating and evaluating genotypes for yield, yield components, and diseases tolerance. The average seed set obtained in this study was reasonable, about one third of the theoretical maximum (34.9%), assuming that every fruit has three ovules (Ceballos et al., 2004; Jennings and Iglesias, 2002; Byrne, 1984) which means that on average one seed per fruit had developed. These findings are in line with previous studies (Alves, 2002; Jennings and Hershey, 1985; Jennings, 1963). Ceballos et al. (2004) indicated that one to two viable seeds are obtained from hand pollination. However, Mbahe et al. (1994) obtained a mean of 2.57 seed per fruit from hand pollination. Unnikrishnan et al. (2004) in India reported seed set ranging from 17 to 74% per cross. Seed set per cross depends on the female parent (Jennings and Iglesias, 2002) and in this study CR 25-4 and Nanchinyaya proved to be prolific seed parents. In general, pollination was very successful for the majority of the parent clones and a good number of seeds were obtained, indicating that controlled pollination is a reliable method of generating F_1 progeny, with the advantage of knowing both parents involved in the production of full-sib progeny. The high percentage of seed germination obtained in this study could be attributed to the favourable environment prevailing at the time. The temperatures were relatively high around November and December which provided favourable environment for seed germination. Unnikrishnan et al. (2004) reported seed germination ranging between 46 and 87% evaluated from seedbed. Temperatures below 24ºC delay seed germination (Jennings and Hershey, 1985).

The number of storage roots was highly variable, with some genotypes with no roots at all and some with a good number of roots per plant. However, data obtained in this study were within the reported range (Munga, 2008; Alves, 2002). Storage root number is influenced by genotype and growing condition (Hunt et al., 1977). In addition, the good SRN obtained could have been influenced by the technique used in raising seedlings on seedbed and transplanting. A tap root of the seedling is often damaged while pulling it from the soil for transplanting, which enhances storage root development (Nair and Unikrishnan, 2008). Significantly high FSRM plant^{-1} within each F_1 family was observed indicating potential new clonal lines and ultimately, cultivars.

Root dry matter content varied significantly from 30.3 to 37.5% on family basis. However for individual progeny RDMC ranged between 6.4 and 60.5%. Root dry matter content ranging between 23-43% has been reported by other workers (Okechukwu and Dixon, 2009;

Unnikrishnan et al., 2004; Kawano et al., 1987).   The mean branching height of genotypes within families (118.2 cm) was good and acceptable. Hahn et al. (1979) commented that low branching genotypes were associated with heavy branching which tended to lower the HI and yield. All 36 families expressed CMD symptoms at different levels, indicating the presence of sufficient inoculum around the trial field. However, the CMD average scores for each family were low; some families had maximum scores of up to class 4. Although a spreader cultivar was planted around the field, the expression of CBSD symptoms was not so pronounced at the seedling stage. Munga et al. (2008) recorded low and non-significant severity of CBSD at the seedling stage. Absence of CBSV from seedlings grown from seeds obtained from infected plants has been reported (Maruthi et al., 2005). Bringing in CMD and CBSD at the earliest possible stage of the breeding population is important, to ensure enough build up of virus titre. Dry storage root yield correlated significantly and positively with HI, RDMC, SRN, and FSRM indicating that they are a function of dry storage root yield. These findings are in line with those of Okechukwu and Dixon (2009). A negative association between RDMC and FSRM was observed which has also been reported elsewhere (Iglesias et al., 1994). The RDMC and FSRM are independent characters therefore can be improved simultaneously. The positive transgressive segregation observed in the F_1 progeny for different traits evaluated in the seedling trial provides for potential genetic advance.   The high genetic heterogeneity and associated variation in the seedling trial is the major basis for selection.

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Appendix

Appendix 1 Field layout for the seedling evaluation trial
REPLICATION 1

B1		SPREADER ROW		2 m alley		SPREADER ROW		B6
		Kalolo x Vumbi						
						CR 25-4 x AR 37-80		
		Kalolo x Namikonga						
						CR 25-4 x AR 40-6		
		Kalolo x AR 40-6						
						CR 25-4 x AR 42-3		
		Kalolo x TMS 30001						
						AR 42-3 x AR 37-80		
		Kalolo x AR 42-3						
						AR 40-6 x AR 37-80		
	S	Kalolo x AR 37-80	S		S		S	
	P		P		P	AR 40-6 x AR 42-3	P	
B2	R	Kiroba x Namikonga	R		R		R	B5
	E		E		E	AR 40-6 x TMS 30001	E	
	A	Kiroba x Vumbi	A		A		A	
	D		D		D	Namikonga x AR 37-80	D	
	E	Nanchinyaya x Vumbi	E		E		E	
	R		R		R	Namikonga x AR 42-3	R	
		Kiroba x AR 40-6						
	R		R		R	TMS 30001 x AR 42-3	R	
	O	Kiroba x TMS 30001	O		O		O	
	W		W		W	Namikonga x TMS 30001	W	
		Kiroba x AR 42-3						
						Namikonga x AR 40-6		
B3		Kiroba x AR 37-80						B4
						TMS 30001 x AR 37-80		
		Nanchinyaya x Namikonga						
						Vumbi x AR 37-80		
		Nanchinyaya x AR 40-6						
						Vumbi x AR 42-3		
		Nanchinyaya x TMS 30001						
						Vumbi x TMS 30001		
		Nanchinyaya x AR 42-3						
						Vumbi x AR 40-6		
		Nanchinyaya x AR 37-80						
						Vumbi x Namikonga		
		SPREADER ROW				SPREADER ROW		

|← 27 m →| |← 27 m →|

Each plot (family) had 50 genotypes planted in two rows of 25 m long

REPLICATION 2

B2		SPREADER ROW		2 m alley		SPREADER ROW		B5
		Kiroba x Namikonga						
						Namikonga x AR 37-80		
		Kiroba x Vumbi						
						TMS 30001 x AR 42-3		
		Kiroba x TMS 30001						
						Namikonga x AR 42-3		
		Kiroba x AR 42-3						
						Namikonga x AR 40-6		
		Nanchinyaya x Vumbi						
						Namikonga x TMS 30001		
		Kiroba x AR 40-6						
						AR 40-6 x TMS 30001		
B3	S	Nanchinyaya x AR 40-6	S		S		S	B6
	P		P		P	CR 25-4 x AR 37-80	P	
	R	Nanchinyaya x Namikonga	R		R		R	
	E		E		E	AR 40-6 x AR 37-80	E	
	A	Nanchinyaya x TMS 30001	A		A		A	
	D		D		D	CR 25-4 x AR 40-6	D	
	E	Nanchinyaya x AR 37-80	E		E		E	
	R		R		R	AR 42-3 x AR 37-80	R	
		Nanchinyaya x AR 42-3						
	R		R		R	CR 25-4 x AR 42-3	R	
	O	Kiroba x AR 37-80	O		O		O	
	W		W		W	AR 40-6 x TMS 30001	W	
B1		Kalolo x TMS 30001						B4
						Vumbi x AR 37-80		
		Kalolo x AR 40-6						
						Vumbi x AR 42-3		
		Kalolo x Namikonga						
						AR 37-80 x TMS 30001		
		Kalolo x AR 37-80						
						Vumbi x TMS 30001		
		Kalolo x AR 42-3						
						Vumbi x AR 40-6		
		Kalolo x Vumbi						
						Vumbi x Namikonga		
		SPREADER ROW				SPREADER ROW		

| ← 27 m → | | ← 27 m → |

Each plot (family) had 50 genotypes planted in two rows of 25 m long

REPLICATION 3

B5		SPREADER ROW		2 m alley		SPREADER ROW		B1
		Namikonga x TMS 30001						
						Kiroba x AR 40-6		
		AR 40-6 x TMS 30001						
						Kalolo x TMS 30001		
		Namikonga x AR 37-80						
						Kalolo x Vumbi		
		Namikonga x AR 40-6						
						Kalolo x AR 40-6		
		TMS 30001 x AR 42-3						
						Kalolo x AR 42-3		
		Namikonga x AR 42-3						
						Kalolo x AR 37-80		
B6	S	CR 25-4 x AR 40-6	S		S		S	B3
	P		P		P	Kiroba x AR 37-80	P	
	R	AR 42-3 x AR 37-80	R		R		R	
	E		E		E	Nanchinyaya x Namikonga	E	
	A	AR 40-6 x AR 42-3	A		A		A	
	D		D		D	Nanchinyaya x AR 42-3	D	
	E	CR 25-4 x AR 42-3	E		E		E	
	R		R		R	Nanchinyaya x AR 40-6	R	
		AR 40-6 x AR 37-80						
	R		R		R	Nanchinyaya x TMS 30001	R	
	O	CR 25-4 x AR 37-80	O		O		O	
	W		W		W	Nanchinyaya x AR 37-80	W	
B4		Vumbi x AR 42-3						B2
						Kiroba x AR 40-6		
		AR 37-80 x TMS 30001						
						Kiroba x TMS 30001		
		Vumbi x Namikonga						
						Kiroba x Vumbi		
		Vumbi x TMS 30001						
						Nanchinyaya x Vumbi		
		Vumbi x AR 40-6						
						Kiroba x Namikonga		
		Vumbi x AR 37-80						
						Kiroba x AR 42-3		
		SPREADER ROW				SPREADER ROW		

27 m   27 m

Each plot (family) had 50 genotypes planted in two rows of 25 m long

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CROSSING BLOCK (10 PARENTS)

Block1	Block 2	Block 3
Kalolo	Kalolo	Kalolo
AR 40-6	AR 42-3	AR 37-80
Kalolo	Kalolo	Kalolo
Vumbi	Vumbi	Vumbi
AR 40-6	AR 42-3	AR 37-80
Vumbi	Vumbi	Vumbi
Kiroba	Kiroba	Kiroba
AR 40-6	AR 42-3	AR 37-80
Kiroba	Kiroba	Kiroba
Namikonga	Namikonga	Namikonga
AR 40-6	AR 42-3	AR 37-80
Namikonga	Namikonga	Namikonga
Nanchinyaya	Nanchinyaya	Nanchinyaya
AR 40-6	AR 42-3	AR 37-80
Nanchiyaya	Nanchinyaya	Nanchinyaya
Block 4	**Block 5**	**Block 6**
Kalolo	Kalolo	AR 40-6
CR 25-4	TMS 30001	CR 25-4
Kalolo	Kalolo	AR 40-6
Vumbi	Vumbi	AR 42-3
CR 25-4	TMS 30001	CR 25-4
Vumbi	Vumbi	AR 42-3
Kiroba	Kiroba	AR 37-80
CR 25-4	TMS 30001	CR 25-4
Kiroba	Kiroba	AR 37-80
Namikonga	Namikonga	AR 40-6
CR 25-4	TMS 30001	AR 37-80
Namikonga	Namikonga	AR 42-3
Nanchinyaya	Nanchinyaya	
CR 25-4	TMS 30001	
Nanchinyaya	Nanchinyaya	
15 m	**15m**	**15m**

Chapter 5

Diallel analysis of cassava genotypes evaluated at clonal stage

Abstract

Cassava genotypes selected from a 10X10 half diallel were evaluated at ARI-Chambezi, Coast region, Tanzania, in 2008/09 season. The objective of the study was to determine the combining abilities of the parents, and evaluate the performance of the F_1 progeny for yield, starch content, and starch yield. The study also aimed to identify genotypes that are high in starch content (StC) and starch yield (StY) and determine the heterosis of the best genotypes for StC and StY relative to the mid-parent and best parent values. A total of 1440 genotypes were evaluated using 4 row x 10 column design superimposed on an α- lattice design, with three replications and six blocks for each replication. Data were collected on yield, yield traits, diseases, StC, and StY. Significant differences in fresh storage root yield (FSRY), fresh biomass (FBM), storage root number (SRN), root dry matter (RDMC), StC, and StY, and cassava brown streak disease root necrosis (CBSRN) were observed between families and progeny. The FSRY for the families ranged from 15.0 to 36.3 t ha^{-1} with a mean of 20.9 t ha^{-1}. The StC ranged from 23 to 29.9% with the mean of 27%; mean RDMC was 36.6% and ranged from 31.4 to 40.1%. Starch yield ranged from 3.3 to 8.3 t ha^{-1} with a mean of 5.2 t ha^{-1}. The cassava mosaic disease (CMD) severity ranged from 1.7 to 2.7 with the mean of 2.2, while cassava brown streak disease (CBSD) severity for above ground symptoms ranged from 1.0 to 1.9 and averaged at 1.6. Additive genetic effects were predominant over non-additive genetic effects for RDMC, StC, and CBSRN, while for FSRY, FBM, SRN, and StY non-additive genetic effects predominated. Mid-parent heterosis for StC ranged from 41.6 to 134.1%, while best parent heterosis ranged from 30.4 to 119.6%. Genotype KBH/08/6807 from family Vumbi x TMS 30001 had the highest mid- and best parent heterosis percentage for StC. For StY, mid-parent and best parent heterosis ranged from 168.0 to 1391%, and from 140.4 to 1079%, respectively, with the genotype 6879 (Vumbi x AR 42-3) exhibiting the highest mid- and best parent heterosis percentage for StY. Improvement for StC, RDMC, and CBSRN may be realized by selecting parents with the highest GCA effects for the traits and hybridize with that combine well to maximize the positive SCA effects for the StC, RDMC and CBSRN. The hybridization programme should include complementary desirable traits such as resistance to CBSD and CMD, and pyramid the genes through convergent breeding. The predominance of non-additive genetic effects in the

expression of StY, FSRY, SRN, and FBM suggest the use of different approach. Cassava clones might be grouped into heterotic pools and specific hybrid combinations implemented to select potential genotypes to exploit non-additive gene action.

5.1 Introduction

Cassava, introduced as food security crop in Africa in the 16th century by the Portugese (Nweke et al., 2002; Jennings, 1970), has recently (1990s) attained the status of a commercial crop, generating income to farmers and processors in Africa. In addition to simply cooking fresh cassava roots and processing them into flour and granules, they can be used as chips or pellets for animal feed and in the production of starch (Westby, 2002). Since roots tend to perish rapidly after harvest (Van Oirschot et al., 2000), the roots have to be used immediately or processed into dry products (Westby, 2002; Bokanga, 1994). In Tanzania, the cassava starch industry is still young; however, there is potential for its growth due to the local and international demand for starch. Therefore, cassava cultivars that are high yielding and high in starch content are required.

The main traits determining cassava root quantity and quality includes starch, dry matter content, cyanogenic potential, post harvest physiological deterioration, protein and carotene contents, and minerals (Chavez et al., 2005; Ceballos et al., 2004; Byrne, 1984). However, for industrial or even small scale processing of cassava, high dry mass and starch content are the main quantity criteria for the roots, whereas for human consumption cooking quality and/or starch characteristics (waxyness, mealiness, texture) are the determining criteria (Ceballos et al., 2004). Other quality characteristics include root shape, size, colour, ease of peeling, and taste (bitter or sweet).

Diallel designs have been implemented in cassava to evaluate combining ability and to provide information on the quantitative inheritance of important traits (Cach et al., 2006; Jaramillo et al., 2005; Perez et al., 2005; Easwari Amma et al., 1995). Combining ability analysis can be very useful in the selection of parents and in the designing of a crossing plan for a plant breeding programme (Easwari Amma et al., 1995; Rajendran, 1989; Tai et al., 1976). Information on the

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relative magnitude of general (GCA) and specific (SCA) combining ability is also helpful in the analysis and interpretation of the genetic basis of important traits such as yield in root crops.

The major challenge in early breeding stages is the limited number of cuttings available for evaluation because the vegetative multiplication rate of cassava is low. From a single plant five to 10 cuttings can typically be obtained at the end of the growing season. This is the case for both seed and cutting propagated generations, so enough cuttings for replicated trials across several locations can only be produced over an extended period of three to four years. Previous experience with cassava breeding at early stages has been mainly based on mass phenotypic selection with little data recorded; this has resulted in a lack of organized information on the breeding values of the parental lines used in breeding programme (Ceballos et al., 2004). To address this issue, this research was conducted using a modified scheme proposed by CIAT (CIAT, 2003). In this system replication and blocking in the clonal evaluation trial are employed and data on yield and yield components from all genotypes are collected. A similar system has been mentioned by Ceballos et al. (2004). The generated information which is obtained from each genotype and family can be used to derive the relative breeding values of the parental lines The objective of the study was to evaluate the F_1 progeny and: 1) determine combining ability and gene action controlling starch content, yield, and yield components; 2) identify parents and their progeny with high starch content, high yield and high root dry matter content for the processing industry in Tanzania; 3) determine heterosis percentage based on starch content and starch yield; and 4) identify superior genotypes in terms of starch content and starch yield.

5.2 Materials and methods

The study was conducted at Agricultural Research Institute (ARI)-Chambezi, in Bagamoyo district, Coast region, Tanzania in the 2008/09 cropping season. The area has two rain seasons: October to December, and March to May, with the annual rainfall ranging between 750 to 900 mm. The annual mean temperature ranging between 22 to 32 ºC; the altitude is 39 masl; and the coordinates are 38º 54´ E and 06º 34´ S. The site is characterized by deep, well drained, sandy soils (ustic soil moisture regime) with flat to almost flat topography, in the humid lowland agro-ecology (soil analysis attached; Appendix 1; Map Appendix 2).

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5.2.1 Germplasm source

Ten parents from two genetically diverse germplasm groups were crossed in a half-diallel (excluding selfs) and their respective full-sib families were generated in 2006 (Table 4.1). Genotypes from 36 families selected from the 45 and constituting a 10x10 half-diallel were evaluated at the seedling stage at the Sugarcane Research Institute (SRI)-Kibaha in 2007 (Chapter 4). Among the many F_1 progeny of a given cross, 40 were randomly selected based on their capacity to produce at least six vegetative cuttings from a plant. On that basis a total of 1440 genotypes were randomly selected from the seedling trial for evaluation at the clonal stage.

5.2.2 Experimental design

Two of the cuttings from the selected genotypes were planted in one of the three replications in a 4 x 10 α-lattice design at ARI-Chambezi in the 2008/09 season. Planting was done in the first week of April 2008. The 40 clones from each F_1 cross were planted together in the respective plots of each replication. The families were observed for several traits including yield and yield components, and starch content. In the seedling trial, spreader rows had been used to facilitate cassava brown streak disease infection of the genotypes. However, in the clonal trial cultivar Kifumulo was planted in two border rows around each replication to facilitate the spread of cassava mosaic and cassava brown streak disease infection. In addition, Chambezi site is considered as a 'hot spot' area for both cassava brown streak (CBSD) and cassava mosaic diseases (CMD). In this trial, therefore disease spread depended on: 1) infection gathered at seedling stage; 2) spreader rows; and 3) natural inoculum because of the abundance of the vector, whitefly (*Bemisia tabaci* Gennadius) during the rainfall season. Plants were spaced at 1 x 1 m between and within rows, resulting in a population of 10 000 plants ha^{-1}. No fertilizer or herbicide was applied during the course of the trial. Hand weeding was done whenever necessary. Harvesting was done 12 months after planting.

5.2.3 Data collection

Data on yield, yield components and starch content (StC) for each progeny were recorded. The progeny were numbered according to the National Root and Tuber Crops Research Programme system in Tanzania (MALD, 1991), therefore the numbers started from KBH/08/6001 up to the last genotype 7440. For brevity only the last four numbers are used for presentation purposes (e.g. 6001) (the numbers from KBH/08/01 to KBH/08/5999 were given to other genotypes generated by the programme at SRI-Kibaha in 2008). The number of storage roots (SRN) from each plot was counted. Fresh yield of storage roots (FSRY) and stems plus foliage were weighed (FSM). Harvest index (HI) was measured as a percentage of fresh root mass relative to total biomass. Root dry matter content (RDMC) was estimated using a forced draught oven (Dixon and Nukenine, 2000) as follows: cassava roots were washed and cut into thin slices. Duplicate samples of 100 g each were taken and dried at 70°C for 72 h. The dried samples were weighed to obtain the dry mass, and the dry matter content as percentage were obtained as a proportion of the fresh mass. Dry storage root yield (DSRY) in t ha^{-1} was calculated as a product of FSRY and RDMC.

The StC was determined by a modified method of Asaoka et al. (1992). About 300 g of wet roots were disintegrated using a laboratory Waring blender with excess water. The slurry was double filtered through a sieve mesh and muslin cloth. The residue was rinsed twice with 500 ml of water each time to remove remnants of starch. The filtrate was allowed to settle for 2 h before decanting the liquid. The starch was suspended three times in 3 L water and non-starch materials removed by decanting the supernatant. The starch was then dried in a ventilated oven at 30 to 33°C for 72 h, sieved with 200 μm mesh sieve, then placed in polythene bag and stored until required. When a large number of samples were collected and time did not allow prompt analyses, representative samples of roots were put in polythene bags and stored in a deep freezer at -20°C within 6 h. The dried starch was calculated as a percentage of fresh root mass. Starch yield (StY) in t ha^{-1} was calculated as a product of fresh storage root yield multiplied by the percentage starch of the root. Destructive sampling was done by cutting the roots transversely into several pieces at harvest to check for CBSD root necrosis symptoms and its severity was recorded as follows:
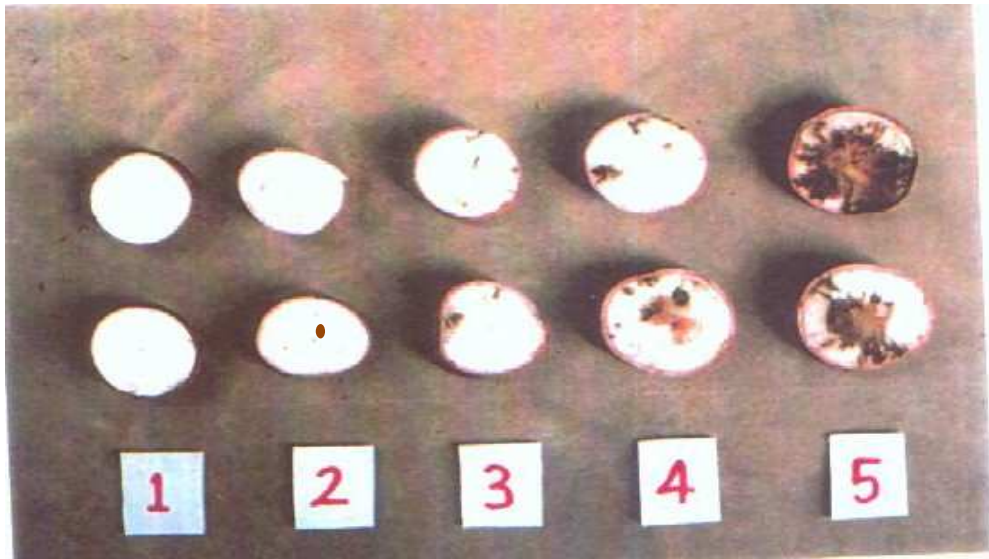
Figure 5.1 Scoring system for cassava brown streak root necrosis (source: IITA, Tanzania, 2008)

Cassava mosaic and cassava brown streak diseases above ground symptoms were rated as follows:

    i.   Cassava mosaic disease (CMD) severity was assessed subjectively at 6 MAP on a scale of 1 to 5 according to Mahungu and Kanju (1997) as follows:

        1= No symptoms observed;

        2= Mild chlorotic pattern on entire leaflets or mild distortion at base of leaflets, the rest of leaflets appearing green and healthy;

        3= Strong mosaic pattern on entire leaf, and narrowing and distortion of lower one-third of leaflets;

        4= Severe mosaic with distortion of two-thirds of leaflets and general reduction of leaf size; and

        5= Severe mosaic, distortion of four-fifths or more of leaflets, twisted and misshapen leaves.

    ii.   Cassava brown streak disease (CBSD) severity was assessed subjectively at 6 MAP on above ground parts, on a scale of 1 to 5 (Mahungu and Kanju, 1997), where;

1= No visible symptoms;

2= Slight foliar chlorosis between leaf vein, no stem lesions;

3= Foliar chlorosis between leaf veins, with mild stem lesions, no die-back;

4= Foliar chlorosis between leaf veins, and pronounced stem lesions with
   beginning of die-back; and

5=Defoliation with pronounced die-back and stem lesions

Figure 5.2 Cassava brown streak disease symptoms in (A) leaf, (B) stem, and (C) roots

5.2.4 Statistical analyses

The residual maximum likelihood (REML) spatial analysis procedure in Genstat version 12 (Payne et al., 2008) was used to analyse clonal stage data at both the family and progeny level. Either family or progeny, and the linear trend across rows and columns were declared as fixed effects, while replications, blocks within replications and interaction between rows and columns were considered random. At the family level of the statistical analysis, mean SRN, FSRY, FBM, HI, CBSRN, RDMC, StC, and StY for the 40 progeny of each family across three replications, were computed by the REML spatial analysis procedure. Similarly, at the progeny level of statistical analysis, means across replications for the same traits were computed for each of the

1440 progeny. If there were missing values within families and genotypes REML computed chi-square (χ^2) probability, while the F probability was computed if there were no missing values. The analysis of variance (ANOVA) for combining ability effects conducted using SAS version 9.2 (Zhang et al., 2005) for traits for which there were significant differences (p≤0.05) between families at the clonal stage. Griffing's (1956) diallel method IV model I for a fixed model was fitted for the GCA and SCA analysis as follows:

$Y_{ijk} = \mu + g_i + g_j + s_{ij} + (\Sigma_k \Sigma_l \text{Є}_{ijkl})/b$; where:

Y_{ijk}= observed value of the cross between parent i and j and replication k;

μ= the overall mean;

gi= the GCA of the parent i;

gj= the GCA of the parent j;

sij= SCA of the cross between parents i and j;

Єijkl= experimental error;

b= replications.

In determining the performance of the hybrids generated, the relative importance of GCA and SCA for each trait was measured by expressing the GCA and SCA sum of squares (SS) as a percentage of family SS. Pearson's phenotypic correlations between traits were performed using Genstat version 12, for the family means. Mid-parent and best parent heterosis of the 30 best performing F_1 progeny was calculated for StC, StY, RDMC and FSRY.

5.3 Results

5.3.1 Agronomic characteristics at the progeny level

Significant differences (p≤0.001) in FSM, FBM, SRN, FSRY, CBSRN and HI were observed between progeny (Table 5.1). Linear effects across columns were significant (p≤0.05) for FBM, FSRY, SRN, FSM, and CBSRN, while the linear effects across rows were not significant with the exception of HI (p≤0.01) and CBSRN (p≤0.05). The mean FSRY over three replications was 20.8 with a range of 0.0 to 124.2 t ha^{-1}. Genotype 6086 (Kalolo x AR 40-6) had the highest mean FSRY (124.2 t ha^{-1}), followed by genotype 6090 (100.1 t ha^{-1}; Kalolo x AR 40-6). The

DSRY ranged from 0.0 to 43.1 t ha^{-1} with the mean of 7.6 t ha^{-1}. The genotype 6086 (43.05 t ha^{-1}; Kalolo x AR 40-6) had the highest DSRY, followed by genotype 6879 (40.9 t ha^{-1}; Vumbi x AR 42-3). The mean FBM over three replications ranged between 1.9 and 268.3 t ha^{-1} with the mean value of 57.8 t ha^{-1}. Genotype 6086 had the highest FBM (268.3 t ha^{-1}) followed by genotype 6841 (209.2 t ha^{-1}; Vumbi x AR 42-3). The SRN ranged from 0.0 to 14.4 roots plant^{-1} with a mean of 4.6 roots plant^{-1}. Genotype 6629 (14.4; Nachinyaya x TMS 30001) had the highest SRN, followed by the genotype 6682 (13.5; Nanchinyaya x AR 37-80). The CBSRN ranged between 1.0 and 5.0, with the mean of 1.6. Four genotypes (6781, 7424, 7304, and 7316) recorded the maximum root necrosis severity of class 5.0. The frequency distribution of the other genotypes according to class of severity was as follows: mean score for class 1.0 (35.4%), class 2 (46.0%), class 3 (14.4%), class 4 (3.2%) and class 4 and above (0.9%).

Table 5.1 Residual maximum likelihood Wald's chi-square statistic of significance and summary statistics for eight traits of the progeny at clonal stage

Variable	Degrees of freedom			Chi-square (χ^2) statistic			Min	Max	Mean	SEM	SED
	Lin_R	Lin_C	Progeny	Lin_R	Lin_C	Progeny					
FBM	1	1	1436	0.82	6.99**	4549.1***	1.86	268.3	57.83	4.45	26.56
FSRY	1	1	1439	0.51	8.51**	5045.1***	0.00	124.22	20.82	8.59	12.02
SRN	1	1	1434	1.89	3.98*	4442.1***	0.00	14.36	4.55	1.39	1.95
DSRY	1	1	1437	2.02	4.04*	4658.5***	0.00	43.05	7.63	0.28	2.42
CBSRN	1	1	1394	4.18*	6.22*	2049.4***	1.00	5.00	1.58	0.57	0.82
HI	1	1	1392	7.10**	0.78	3939.2***	0.01	0.80	0.35	0.07	0.10
RDMC	1	1	1381	2.52	6.63*	2561.5***	13.92	56.67	36.53	3.48	4.93
StC	1	1	1321	0.53	0.70	2048.7***	6.69	40.92	26.97	0.33	5.02
StY	1	1	1321	1.07	1.95	3788.2***	0.00	34.90	5.10	0.36	3.78

FSRY (fresh storage root yield in t ha^{-1}); FBM (fresh biomass weight in kg plant^{-1}); HI (harvest index); DSRY (dry storage root yield); RDMC (root dry matter in %); StC (starch content in %); StY (starch yield in t ha^{-1}); CBSRN (cassava brown streak disease root necrosis severity); Lin_R (Linear row); Lin _C (Linear column); Min (minimum); Max (maximum); SEM (standard error); SED (standard error of the mean); significance levels: * 0.05; ** 0.01; *** 0.001

5.3.2 Root dry matter content, starch content and yield at the progeny level

Significant differences in RDMC, StC and StY (p≤0.001) were observed between progeny (Table 5.1). Linear effects across rows as well as columns for the same traits were not significant with the exception of RDMC which had significant (p≤0.05) linear effects across columns. The overall performance of the progeny in RDMC ranged from 13.9 (7433; CR 25-4 x AR 37-80) to 56.7% with a mean of 36.5%. Genotype 7085 had the highest RDMC (56.7%) (Table 5.1) followed by genotype 6769 (50.5%). The StC ranged from 6.7 to 40.9%, with a mean of 27.0%, while StY ranged from 0.0 to 34.9 t ha^{-1} with a mean of 5.2 t ha^{-1} (Table 5.1). Genotype 6256 from cross Kiroba x Namikonga had the highest StC (40.9%), and genotype 6879 from cross Vumbi x AR 42-3 had the highest StY (34.9 t ha^{-1}). The lowest StC was recorded from genotype 6828 (6.7%; Vumbi x TMS 30001). The majority of the progeny (>80%) had StC ranging between 25 and 35% (figure 5.3). For StY, more than 90% of the genotypes achieved between 0 and 10 t ha^{-1} (figure 5.4)
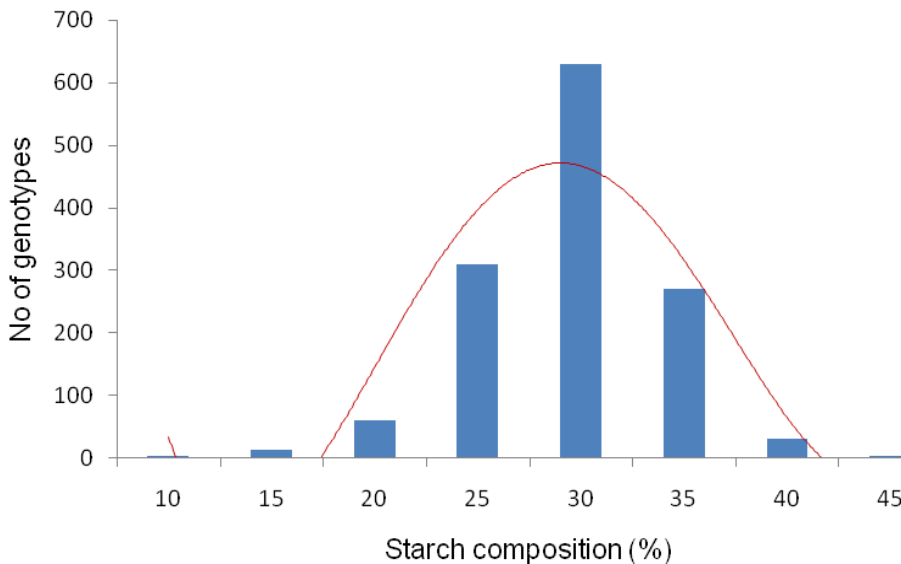
Figure 5.3 Frequency distribution of the genotypes in starch composition at the progeny level
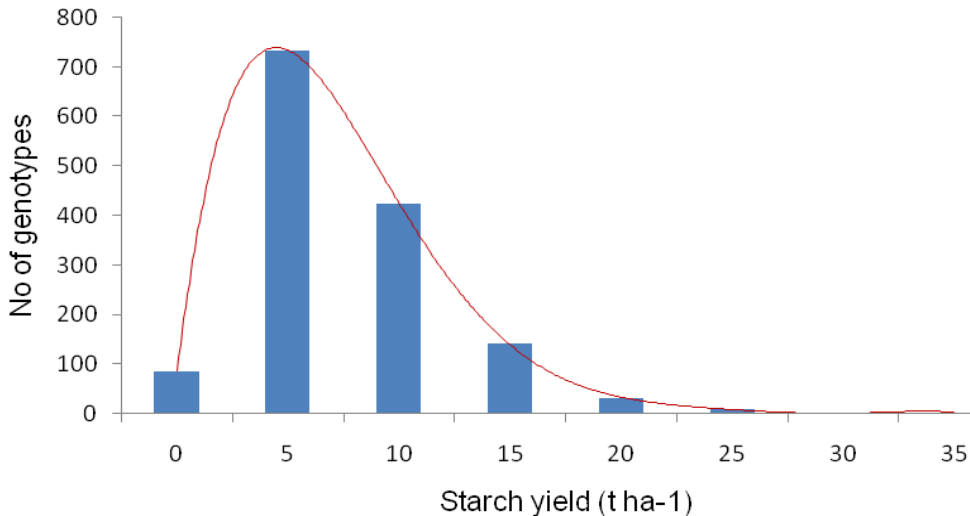
Figure 5.4 Frequency distribution of genotypes in starch yield (t ha^{-1}) at progeny level

5.3.3 Yield and yield components at the family level

The family variances for FSRY, FBM, SRN, CBSRN and HI were highly significant (p≤0.001) (Table 5.2). The linear effects across the rows and columns were not significant, except for the linear effects across rows for HI (p≤0.05). The mean value for FSRY was 21 t ha^{-1} and varied from 15.0 to 36.3 t ha^{-1}, from families Kiroba x Namikonga and Kalolo x AR 40-6, respectively. The SRN ranged from 3.1 (Vumbi x Namikonga) to 6.3 roots plant^{-1} (Nanchinyaya x AR 37-80) with the mean of 4.6 roots plant^{-1}. Mean FBM was 58.6 t ha^{-1} and varied from 41.9 (Vumbi x TMS 30001) to 82.3 t ha^{-1} (Kalolo x AR 40-6) (Table 5.3). Mean HI was 0.35 and varied from 0.27 (Vumbi x Namikonga) to 0.45 (TMS x AR42-3). Dry storage root yield ranged from 5.2 to 13 t ha^{-1}, with the mean of 7.7 t ha^{-1}

5.3.4 Root dry matter content, starch content and yield at the family level

The family variance for RDMC, StC and StY were highly significant (p≤0.001) (Table 5.2). The linear effects across rows and columns were not significant. The RDMC for families ranged from a low of 31.4 (Kalolo x TMS 30001) to a high of 40.1% (Nanchinyaya x Namikonga) with a mean of 36.6%. The mean StC across families was 27% (Tables 5.2 and 5.3), with the lowest StC of 23% measured in family Kalolo x TMS 30001, and the highest of 29.9% in two families Nanchinyaya x Namikonga and AR 40-6 x AR 42-3 (Table 5.3). Overall mean StY for families was 5.16 t ha^{-1} and varied from 3.7 (TMS 30001 x AR 37-80) to 8.5 t ha^{-1} (Kalolo x AR 40-6) (Table 5.3).

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Table 5.2 Residual maximum likelihood Wald's F statistic of significance and summary statistics for eight traits of the families at clonal stage

	Degrees of freedom			F statistic							
Variable	Lin_R	Lin_C	Families	Lin_R	Lin_C	Families	Min	Max	Mean	SE	SED
FBM	1	1	35	0.00	0.18	4.20***	41.9	82.32	58.6	4.89	0.66
FSRY	1	1	35	1.86	1.50	4.04***	14.95	36.27	20.96	2.55	3.17
SRN	1	1	35	2.84	0.00	6.23***	3.07	6.34	4.6	0.37	0.43
DSRY	1	1	35	4.40	0.54	4.40***	5.23	12.98	7.67	0.38	1.11
HI	1	1	35	7.82*	0.02	5.76***	0.27	0.45	0.35	0.02	0.03
RDMC	1	1	35	3.24	2.69	6.21***	31.47	40.14	36.59	0.91	1.14
StC	1	1	35	0.02	0.58	3.98***	22.79	29.9	26.98	0.93	1.23
StY	1	1	35	3.45	1.15	3.59***	2.73	8.45	5.16	0.89	1.17

FSRY (fresh storage root yield in t ha^{-1}); FBM (fresh biomass in t ha^{-1}); HI (harvest index); DSRY (dry storage root yield in t ha^{-1}); RDMC (root dry matter in %); StC (starch content in %); StY (starch yield in t ha^{-1}); Lin_R (Linear row); Lin _C (linear column); Min (minimum); Max (maximum); SEM (standard error of the mean) and SD (standard deviation); significance levels: * 0.05; ** 0.01; *** 0.001.

Table 5.3 Family means for fresh storage root yield, root dry matter content, starch content and starch yield at clonal stage.

Cross	FSRY	RDMC	StC	StY
Kalolo x Vumbi	18.68	34.95	26.54	4.19
Kalolo x Namikonga	23.59	34.63	26.00	5.17
Kalolo x AR 40-6	35.94	33.39	23.67	8.31
Kalolo x TMS 30001	23.04	31.42	23.01	4.28
Kalolo x AR 42-3	26.56	35.96	26.81	6.03
Kalolo x AR 37-8	23.14	33.30	26.07	4.51
Kiroba x Namikonga	14.08	37.34	27.54	3.95
Kiroba x Vumbi	18.00	38.43	28.16	5.36
Nanchinyaya x Vumbi	20.49	39.74	28.76	5.14
Kiroba x AR 40-6	20.15	39.30	28.82	5.83
Kiroba x TMS 30001	23.58	36.20	27.63	6.10
Kiroba x AR 42-3	25.56	39.99	28.11	5.66
Kiroba x AR 37-80	20.50	37.36	28.25	5.71
Nanchinyaya x Namikonga	20.20	40.10	29.78	5.32
Nanchinyaya x AR 40-6	20.83	36.98	25.46	4.72
Nanchinyaya x TMS 30001	20.08	38.72	28.94	4.81
Nanchinyaya x AR 42-3	18.07	38.26	27.64	4.29
Nanchinyaya x AR 37-80	20.78	36.84	26.54	5.06
Vumbi x Namikonga	17.00	38.03	26.42	3.84
Vumbi x AR 40-6	16.76	37.38	25.74	4.05
Vumbi x TMS 30001	15.38	35.71	24.92	3.42
Vumbi x AR 42-3	27.00	38.11	26.55	7.07
Vumbi x AR 37-80	18.51	37.20	25.87	4.62
TMS 30001 x AR 37-80	16.42	33.28	24.62	3.23
Namikonga x AR 40-6	18.97	38.99	28.72	4.72
Namikonga x TMS 30001	19.35	38.20	28.64	5.06
TMS 30001 x AR 42-3	26.04	36.14	27.15	6.72
Namikonga x AR 42-3	20.46	37.90	29.34	5.72
Namikonga x AR 37-80	22.34	36.41	27.40	5.66
AR 40-6 x TMS 30001	20.27	36.32	27.73	5.21
AR 40-6 x AR 42-3	23.88	37.54	29.78	6.62
AR 40-6 x AR 37-80	17.42	36.52	27.66	5.00
AR 42-3 x AR 37-80	19.14	34.57	25.13	4.54
CR 25-4 x AR 42-3	22.21	34.68	26.13	6.00
CR 25-4 x AR 40-6	24.03	35.75	27.24	6.22
CR 25-4 x AR 37-80	16.22	31.51	24.55	3.68
Mean	**20.96**	**36.59**	**26.98**	**5.16**
SEM	0.904	0.29	0.49	0.30
LSD	6.428	2.30	2.56	2.84

FSRY (fresh storage root yield in t ha^{-1}); RDMC (root dry matter in %); StC (starch content in %);

StY (starch yield in t ha^{-1}); SEM (standard error of the mean); LSD (least significant difference)

Table 5.4 Family means for storage root number, harvest index and

fresh biomass at clonal stage

Cross	SRN	HI	FBM
Kalolo x Vumbi	3.73	0.33	55.3
Kalolo x Namikonga	4.85	0.37	61.6
Kalolo x AR 40-6	6.19	0.43	82.3
Kalolo x TMS 30001	4.53	0.41	53.3
Kalolo x AR 42-3	5.16	0.41	61.7
Kalolo x AR 37-8	4.57	0.35	62.9
Kiroba x Namikonga	3.65	0.29	49.9
Kiroba x Vumbi	3.15	0.33	58.0
Nanchinyaya x Vumbi	5.17	0.30	66.5
Kiroba x AR 40-6	4.05	0.34	63.6
Kiroba x TMS 30001	5.08	0.41	54.9
Kiroba x AR 42-3	4.76	0.33	80.8
Kiroba x AR 37-80	5.04	0.35	63.9
Nanchinyaya x	5.56	0.29	67.2
Nanchinyaya x AR 40-6	6.02	0.35	60.2
Nanchinyaya x TMS	5.91	0.35	54.7
Nanchinyaya x AR 42-3	5.11	0.32	53.6
Nanchinyaya x AR 37-	6.40	0.34	58.7
Vumbi x Namikonga	3.11	0.27	58.7
Vumbi x AR 40-6	3.89	0.29	57.0
Vumbi x TMS 30001	4.18	0.34	41.9
Vumbi x AR 42-3	4.50	0.35	77.7
Vumbi x AR 37-80	3.91	0.33	59.2
TMS 30001 x AR 37-80	3.90	0.35	46.9
Namikonga x AR 40-6	4.14	0.32	59.1
Namikonga x TMS	4.75	0.38	50.4
TMS 30001 x AR 42-3	4.74	0.45	57.5
Namikonga x AR 42-3	4.08	0.33	61.1
Namikonga x AR 37-80	4.97	0.38	54.8
AR 40-6 x TMS 30001	5.03	0.41	47.4
AR 40-6 x AR 42-3	4.70	0.39	60.1
AR 40-6 x AR 37-80	4.08	0.36	49.4
AR 42-3 x AR 37-80	4.11	0.35	59.1
CR 25-4 x AR 42-3	4.53	0.39	55.6
CR 25-4 x AR 40-6	4.82	0.39	58.7
CR 25-4 x AR 37-80	3.38	0.35	45.5
Mean	**4.6**	**0.35**	**58.6**
SEM	0.24	0.005	4.9
LSD	0.84	0.04	14.2

SRN (storage root number plant^{-1}); HI (harvest index) FBM (fresh biomass in t ha^{-1});

SEM (standard error of the mean); LSD (least significant difference)

Figure 5.5 (A) Plants at 9 MAP and (B) harvested roots at 12 MAP

5.3.5 Virus diseases at family level

Families differed significantly (p≤0.001) in the expression of CMD and CBSD above ground symptoms (Table 5.5). The CMD severity for the above ground symptoms ranged from 1.7 (Vumbi x AR 42-3) to 2.7 (Vumbi x Namikonga) with the mean of 2.2 (Table 5.6). The CBSD severity for the above ground symptoms averaged at 1.2 and ranged from 1.0 (Namikonga x AR 40-6) to 1.9 (CR 25-4 x AR 40-6). For the CBSRN, the below ground symptoms ranged from 1.2 (Namikonga x AR 37-80) to 2.2 (TMS 30001 x AR 37-80) with the mean of 1.6 (Tables 5.5; 5.6).

Table 5.5 Residual maximum likelihood Wald's F statistic and summary statistics for two cassava diseases of the family at clonal stage

	Degrees of freedom	F statistic					
Source	df	Family	Min	Max	Mean	SEM	SED
CMDS	35	9.75***	1.71	2.68	2.15	0.09	0.12
CBSDS	35	28.19***	1.00	1.87	1.15	0.02	0.05
CBSRN	35	4.38***	1.18	2.24	1.58	0.14	0.17

CMDS (cassava mosaic disease severity); CBSD (cassava brown streak disease severity); CBSRN (cassava brown streak disease root necrosis); Min (minimum); Max (maximum); SEM (standard error of the mean); SED (standard error of the difference)

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Table 5.6 Family means for cassava mosaic and cassava brown streak disease severity scores for the above ground symptoms and root necrosis at clonal stage

Cross	CMDS	CBSDS	CBSDNCR
Kalolo x Vumbi	2.58	1.15	1.70
Kalolo x Namikonga	2.51	1.13	1.46
Kalolo x AR 40-6	2.43	1.11	1.53
Kalolo x TMS 30001	2.46	1.02	1.54
Kalolo x AR 42-3	2.24	1.05	1.39
Kalolo x AR 37-8	2.42	1.03	1.77
Kiroba x Namikonga	2.52	1.05	1.37
Kiroba x Vumbi	2.22	1.05	1.38
Nanchinyaya x Vumbi	2.43	1.18	1.79
Kiroba x AR 40-6	2.15	1.09	1.23
Kiroba x TMS 30001	2.08	1.08	1.34
Kiroba x AR 42-3	1.89	1.04	1.46
Kiroba x AR 37-80	2.24	1.10	1.47
Nanchinyaya x Namikonga	2.35	1.10	1.56
Nanchinyaya x AR 40-6	1.93	1.08	1.43
Nanchinyaya x TMS 30001	2.45	1.04	1.83
Nanchinyaya x AR 42-3	2.30	1.20	1.71
Nanchinyaya x AR 37-80	1.98	1.35	1.99
Vumbi x Namikonga	2.68	1.05	1.47
Vumbi x AR 40-6	2.25	1.12	1.58
Vumbi x TMS 30001	2.31	1.10	1.75
Vumbi x AR 42-3	1.71	1.03	1.65
Vumbi x AR 37-80	2.08	1.19	1.58
TMS 30001 x AR 37-80	2.18	1.08	2.16
Namikonga x AR 40-6	2.27	1.00	1.53
Namikonga x TMS 30001	2.22	1.07	1.37
TMS 30001 x AR 42-3	2.03	1.03	1.57
Namikonga x AR 42-3	2.12	1.07	1.24
Namikonga x AR 37-80	1.98	1.03	1.17
AR 40-6 x TMS 30001	1.75	1.04	1.30
AR 40-6 x AR 42-3	1.71	1.12	1.44
AR 40-6 x AR 37-80	1.72	1.11	1.46
AR 42-3 x AR 37-80	1.78	1.25	2.12
CR 25-4 x AR 42-3	2.03	1.58	1.96
CR 25-4 x AR 40-6	1.72	1.87	1.41
CR 25-4 x AR 37-80	1.81	1.74	2.12
Mean	**2.15**	**1.15**	**1.58**
SE	0.09	0.02	0.05
LSD	0.24	0.10	0.34

CMDS (cassava mosaic disease severity); CBSD (cassava brown streak disease severity); CBSRN (cassava

brown streak root necrosis); SE (standard error of the mean); LSD (least significant difference)

Figure 5.6 (A), (B), (C) plants with no symptoms of cassava mosaic disease; and (D) plant with cassava mosaic disease symptoms

5.3.6 Combining ability effects

The GCA and SCA effects were highly significant (p≤0.001) for StC, StY, RDMC, FSRY, FBM, SRN and CBSRN. The SCA effects for StC (p≤0.05) and CBSRN (p≤0.01) were also significant (Table 5.7). The GCA SS as a percentage of family SS ranged from 35 to 56% for the seven traits under consideration (Table 5.5). The SCA SS as a percentage of family SS ranged from 44 to 65%. The SCA SS % was higher than the GCA SS % for FSRY, StY, SRN, and FBM (Table 5.7). However, for RDMC, StC, and CBSRN the GCA SS % was greater than SCA%.

Table 5.7 Combining ability ANOVA for seven traits of ten cassava parents and 10 x 10 half diallel at clonal stage

Source	df	FSRY	RDMC	StC	StY	CBSRN	SRN	FBM
Family	44	63.5***	11.96***	9.85***	4.76***	0.19***	1.72***	233.7***
GCA	9	125.3***	32.87***	26.82***	8.20***	0.48***	3.79***	403.6***
SCA	35	47.6***	6.58***	1.59*	3.87***	0.11**	1.19***	190.1***
Error	88	12.4	2.63	3.44	1.22	0.06	0.29	79.5
%Family SS								
GCA (%)		40.38	56.24	55.71	35.28	52.36	52.36	35.32
SCA (%)		59.62	43.76	44.29	64.72	47.64	55.00	64.68

FSRY (fresh storage root t ha^{-1}); RDMC (root dry mass in %); StC (starch content in %); StY (starch yield in t ha^{-1}); CBSRN (cassava brown steak disease root necrosis); SRN (storage root number); FBM (fresh biomass t ha^{-1}); GCA (general combining ability); SCA (specific combining ability); SS (sum of squares); significance levels: * 0.05; ** 0.01; *** 0.001

The GCA effects for RDMC were positive and significant for the parents Vumbi ($p \leq 0.001$), Kiroba ($p \leq 0.01$), Namikonga ($p \leq 0.01$), and Nanchinyaya ($p \leq 0.001$), but negative and significant ($p \leq 0.001$) for parents Kalolo, AR 37-80, CR 25-4, and TMS 30001 ($p \leq 0.05$). The GCA effects for StC were high, positive and significant for parents Namikonga ($p \leq 0.001$) and Kiroba ($p \leq 0.05$), while for parents Kalolo and CR 25-4, the GCA effects were high, negative and significant ($p \leq 0.001$) (Table 5.8). Significant and positive GCA effects for StY were observed for parents Kalolo and AR 42-3, while parents AR 37-80 and CR 25-4 had negative significant GCA effects. Parent Kalolo indicated significant GCA effects for seven of eight traits: RDMC ($p \leq .001$), FSRY ($p \leq 0.001$), StC ($p \leq 0.001$), StY ($p \leq 0.001$), SRN ($p \leq 0.01$), FBM ($p \leq 0.01$), and CBSRN ($p \leq 0.001$) (Table 5.8). Parent AR 42-3 had positive GCA effects for all the traits; however, only FSRY ($p \leq 0.001$), StC ($p \leq 0.01$), FBM, and HI were significant ($p \leq 0.05$). Parent AR 37-80 indicated negative significant effects for RDMC, FSRY, StarchY, SRN, and FBWT. However, it showed positive significant effects for CBSRN ($p \leq 0.001$).

Table 5.8 General combining ability effects for eight traits of ten cassava parents and 10 x10 half diallel at the clonal stage

Parent	RDMC	FSRY	StC	StY	SRN	CBSRN	FBM	HI
Kalolo	-1.52***	5.14***	-1.44***	1.08***	0.33**	-0.04	5.06**	0.04***
Vumbi	1.06***	-1.33**	-0.11	-0.24	-0.63***	0.03	3.64*	0.03***
Kiroba	0.96**	-0.19	0.92*	0.19	-0.23*	-0.18***	1.59	-0.006
Namikonga	0.94**	-1.62*	1.83***	-0.13	-0.21*	-0.20***	-0.92	-0.024***
Nanchinyaya	1.38***	-1.02	0.21	-0.34	0.82**	0.08	0.81	-0.25***
AR 40-6	0.31	0.93	0.31	0.38	0.19	-0.15**	1.45	0.01
TMS 30001	-0.73*	-0.91	-0.11	-0.35	0.13	0.03	-7.39***	0.033***
AR 42-3	0.49	2.44***	0.62	0.72**	0.04	0.07	4.08*	0.01*
AR 37-80	-1.71***	-2.59***	-0.50	-0.79***	-0.23*	0.23***	-4.65**	-0.009
CR 25-4	-1.19***	-0.83	-1.73***	-0.52*	-0.21*	0.13**	-3.66*	0.004
SEM	0.312	0.09	0.39	0.22	0.11	0.05	0.18	0.006
CV (%)	4.44	20.7	6.93	20.8	11.5	15.1	14.8	9.5
R^2	0.71	0.61	0.6	0.69	0.77	0.65	0.66	0.68
LSD 0.05	0.63	0.18	0.72	0.42	0.21	0.09	0.34	0.01
LSD 0.01	0.83	0.24	0.95	0.56	0.27	0.12	0.45	0.02

FSRY (fresh storage root yield in t ha^{-1}); RDMC (root dry matter content in %); StC (starch content in %); HI (harvest index); StY (starch yield in t ha^{-1}); CBSRN (cassava brown steak disease root necrosis); SRN (storage root number); FBWT (fresh biomass weight in t ha^{-1}); SEM (standard error of the mean); significance levels: * 0.05; ** 0.01; *** 0.001; g=general combining ability (LSD for g

The deviations of the individual crosses from the average performance of the parents were compared on the basis of SCA effects (Table 5.9). Among the families, three families: Kiroba x AR 40-6, Kiroba x AR42-3, and Kiroba x AR 37-80 had positive and significant (p≤0.05) SCA effects for RDMC. Family Kiroba x AR 42-3 had the highest, positive SCA effect (2.11; p≤0.05) of all the families for RDMC. However, families Kalolo x TMS 30001, Kiroba x Namikonga, and AR 37-80 x CR 25-4 had negative and significant (p≤0.01) effects for the RDMC. Four families had significant SCA effects (p≤0.05) for StC. Among the four, Nanchinyaya x TMS 30001 and Namikonga x AR 37-80 had positive significant SCA effects, while the other two Kalolo x TMS 30001 and AR 42-3 x AR37-80 had negative significant SCA effects for StC. Family Nanchinyaya x TMS 30001 recorded highest positive (2.3) and significant (p≤0.01) SCA effect for StC (Table 5.9). The families Kalolo x TMS 30001 and AR 42-3 x AR 37-80 had negative and significant effects (p≤0.01) for StC. For StY, family Kalolo x AR 40-6 recorded the highest, positive (3.12) significant (p≤0.001) SCA effects. Other families with positive and significant

effects include: Vumbi x AR 42-3 (1.96; p≤0.01), Kiroba x TMS 30001 (1.37; p≤0.05), Kiroba x AR 37-80 (1.39; p≤0.05) and Namikonga x AR 37-80 (1.66; p≤0.01). However, the majority of the families did not record significant SCA effects for StY. For FSRY, Kalolo x AR 40-6 recorded the highest, positive (13.39) significant (p≤0.001) SCA effects, whereas most of the other families had non-significant SCA effects.

Three families, Kalolo x AR 42-3, Vumbi x AR 37-80, and Namikonga x AR 37-80 had negative (-0.27, -0.26, -0.41) and significant (p≤0.05; p≤0.05; p≤0.001 respectively) SCA effects for CBSRN (Table 5.9). Family Namikonga x AR 37-80 had the lowest, negative (-0.41) highly significant (p≤0.001) SCA effects for CBSRN. Only eight of the 36 families had significant SCA effects for SRN. Family Kalolo x AR 40-6 had the highest, positive (1.25) and significant (p≤0.001) SCA effects for SRN. For HI, families Kalolo x Vumbi, Kalolo x Namikonga, Kalolo x AR 40-6 and Namikonga x AR 37-80 had positive and significant (p≤0.001; p≤0.001; p≤0.01, and p≤0.01 respectively) SCA effects, while for FBM, Kalolo x AR 40-6, Vumbi x AR 42-3, Kiroba X AR 42-3 recorded positive (19.5; 15.2; 14.1) and significant (p≤0.001; p≤0.01; p≤0.01 respectively) SCA effects. The family Namikonga x AR 37-80 recorded positive (1.98; 1.66; 4.59) and significant (p≤0.05; p≤0.01; p≤0.05 respectively) SCA effects for the StC, StY, and FSRY while the family AR 42-3 x AR 37-80 recorded negative (-2.58; -1.23) and significant (p≤0.01; p≤0.05 respectively) SCA effects for the StC and StY.

Table 5.9 Specific combining ability effects for eight traits of ten cassava parents and 10 x 10 half diallel at the clonal stage

Family	RDMC	StC	StY	FSRY	CBSRN	SRN	HI	FBM
Kalolo x Vumbi	-0.48	1.51	-0.72	-3.36*	0.22	-0.34	0.001***	-9.55*
Kalolo x Namikonga	-0.66	-0.91	0.49	1.65	0.03	0.30	0.03***	1.68
Kalolo x AR 40-6	-1.36	-1.67	3.12***	13.39***	0.11	1.25***	0.04**	19.53***
Kalolo x TMS 30001	-2.28**	-2.07*	-0.48	-0.05	-0.12	-0.42	0.005	-0.75
Kalolo x AR 42-3	1.02	1.16	0.58	0.48	-0.27*	0.54	0.02	-3.69
Kalolo x AR 37-80	0.36	1.47	0.29	1.27	-0.06	0.04	-0.01	6.71
Vumbi x Kiroba	0.04	0.83	0.08	-0.45	-0.08	-0.54	0.02	-6.41
Vumbi x Namikonga	-0.53	-1.74	-0.66	-1.30	-0.005	-0.73**	-0.04*	-0.83
Vumbi x Nanchinyaya	1.03	1.08	0.72	2.98	0.03	0.64*	0.01	2.49
Vumbi x AR 40-6	-0.57	-0.91	-1.06	-3.45	0.11	-0.34	-0.04*	4.86
Vumbi x TMS 30001	-1.12	-1.07	-1.39*	-4.64*	0.17	-0.03	-0.02	-9.73*
Vumbi x AR 42-3	0.31	-0.04	1.96**	6.35***	-0.03	0.46	0.02	15.19**
Vumbi x AR 37-80	1.18	-0.03	0.54	1.69	-0.26*	0.05	0.01	3.96
Kiroba x Namikonga	-3.50***	0.93	-1.53	-5.42**	0.09	-0.47	-0.03	-11.08*
Kiroba x AR 40-6	1.76*	1.00	0.08	-0.48	-0.07	-0.44	-0.01	0.84
Kiroba x TMS 30001	-0.49	0.48	1.37*	3.48	-0.05	0.47	0.03	2.15
Kiroba x AR 42-3	2.11*	0.12	0.12	3.40	-0.04	0.36	-0.03	14.14**
Kiroba x AR 37-80	1.64*	0.86	1.39*	2.16	-0.20	0.87**	0.01	7.34
Namikonga x Nanchinyaya	1.19	0.99	0.57	1.32	0.06	0.31	-0.02	8.45
Namikonga x AR 40-6	1.12	-0.39	-0.97	-2.17	0.36**	-0.48	-0.02	-2.01
Namikonga x TMS 30001	1.56	0.26	-0.03	-0.19	-0.006	0.21	0.02	-1.53
Namikonga x AR 42-3	0.07	0.44	0.05	-0.93	-0.19	-0.35	-0.02	-0.54
Namikonga x AR 37-80	0.50	1.98*	1.66**	4.59*	-0.41***	0.79**	0.06***	1.28
Nanchinyaya x AR 40-6	-1.28	-1.72	-0.47	-0.52	-0.16	0.40	0.003	-1.48
Nanchinyaya x TMS 30001	1.43	2.30*	0.41	0.59	0.08	0.31	-0.02	2.46
Nanchinyaya x AR 42-3	-0.33	0.03	-1.51*	-5.52**	0.02	-0.42	-0.03	-11.82**
Nanchi nyaya x AR 37-80	0.37	0.10	0.72	2.19	0.14	1.11***	0.01	5.32
AR 40-6 x TMS 30001	-0.01	0.80	-0.19	-2.26	-0.11	0.06	0.01	-7.21
AR 40-6 x AR 42-3	-0.10	1.36	-0.50	-2.84	-0.02	-0.17	0.01	-5.15
AR 40-6 x AR 37-80	0.93	0.29	-0.49	-3.29	-0.14	-0.54	-0.01	-9.42*
AR 40-6 x CR 25-4	-0.49	1.24	0.49	1.62	-0.08	0.27	0.01	0.02
TMS 30001 x AR 42-3	-0.02	-0.13	0.76	3.27	-0.09	-0.03	0.05	2.49
TMS 30001 x AR 37-80	-0.99	-0.94	-1.10	-1.95	0.29*	-0.65*	-0.03	1.06
AR 42-3 x AR 37-80	-1.25	-2.58**	-1.23*	-2.16	0.35**	-0.38	-0.03	-3.85
AR 42-3 x CR 25-4	-1.80*	-0.35	-0.22	-2.04	0.27*	-0.01	0.01	-6.77
AR 37-80 x CR 25-4	-2.74**	-1.16	-1.78**	-4.50*	0.30*	-1.30***	-0.02	-12.41**
SCA SE	**0.821**	**0.954**	**0.59**	**0.235**	**0.121**	**0.276**	**0.02**	**0.469**

FSRY (fresh storage root yield in t ha^{-1}); FBM (fresh biomass in t ha^{-1}); HI (harvest index); RDMC (root dry matter content in %); StC (starch content in %); StY (starch yield in t ha^{-1}); CBSRN (cassava brown streak disease root necrosis severity)

5.3.7 Correlation between traits at the clonal stage

High, positive (r≥0.5) and significant (p≤0.05) phenotypic correlations were obtained between the following traits (Table 5.10):

- The StY and DSRY, FSRY, FBM, HI and SRN;

- The StC and RDM;

- The FSRY and DSRY, SRN, HI, and FBM;

- The SRN and DSRY, FSRY and FBM.

Low, negative (r≤-0.3) and non-significant correlations were obtained between the following traits (Table 5.10)

- The CBSRN and StY, StC and RDM;

- The StC and FSRY, and HI.

5.3.8 Correlation of traits between the seedling and clonal stages

The RDMC and FSRY values at seedling and clonal stages were positive and significantly (p≤0.01) correlated (r=0.67; r=0.50, respectively) (Table 5.11). The HI and SRN were also positive and significantly correlated (r=0.69; r=0.52 respectively) between the two stages. However, FBM was not significantly correlated between the two stages (Table 5.11).

Table 5.10 Phenotypic correlations between ten traits at clonal stage

	DSRY	FSRY	FSM	FBM	HI	CBSRN	SRN	RDMC	StC	StY
DSRY	-									
FSRY	0.96***	-								
FSM	0.55***	0.54***	-							
FBM	0.82***	0.83***	0.92***	-						
HI	0.51***	0.55***	-0.23	0.11***	-					
CBSRN	0.006	0.03	0.04*	0.04*	0.01	-				
SRN	0.62***	0.64***	0.36***	0.54***	0.46***	0.03				
RDMC	0.21***	0.01	0.09***	0.07***	-0.06	-0.11	0.06**			
StC	0.10***	-0.01	0.04*	0.02ns	-0.04	-0.11	0.024	0.55***	-	
StY	0.95***	0.94***	0.52***	0.79***	0.51***	-0.01	0.62***	0.16***	0.26***	-
	DSRY	FSRY	FSM	FBM	HI	CBSRN	SRN	RDMC	StC	StY

FSRY (fresh storage root yield in t ha^{-1}); FSM (fresh shoot mass in kg plant^{-1}); FBM (fresh biomass in t ha^{-1}); HI (harvest index); DSRY (dry storage root yield in t ha^{-1}); RDMC (root dry matter in %); StC (starch content %); StY (starch yield in t ha^{-1}); CBSRN (cassava brown streak disease root necrosis severity); SRN (storage root yield); significance levels: * 0.05; ** 0.01; *** 0.001

Table 5.11 Correlation between four traits in the seedling and clonal stages

Variable	df	t-statistic	correlation (r)
Root dry matter	70	4.40***	0.67***
Fresh storage root yield	70	13.86***	0.50**
Harvest index	70	0.20ns	0.69***
Fresh biomass	69	21.34***	0.33ns
Storage root number	70	0.71ns	0.52**

Significance levels: * 0.05; ** 0.01; *** 0.001; ns=not significant

5.3.9 Starch content, starch yield and six other traits and heterosis of the 30 top progeny at clonal stage (ranking based on starch content)

The StC of the top 30 families ranged from 35.1 to 40.9% (Table 5.12). The highest value of StC was recorded from progeny 6256 (40.9%) from the family Kiroba x Namikonga, followed by progeny 6731 from the family Vumbi x Namikonga (40.6%). The best progeny (6256) from family Kiroba x Namikonga had 51% more StC than the overall progeny mean, while the best family (Nanchinyaya x Namikonga and AR 40-6 x AR 42-3) had 10.4% more StC than the overall family mean. The StY of the top 30 progeny ranged from 0.52 to 16.8 t ha^{-1}, while RDMC ranged from 28.5 to 49.0%. The SRN ranged from 0.6 to 9.1 roots plant^{-1}. For FSRY, the range was from 1.3 to 47.2 t ha^{-1}. Progeny 6537 from family Nanchinyaya x Namikonga was the best in FSRY among the 30 best performers based on StC. However, if the progeny are individually ranked on StY then not surprisingly a different order of performance is obtained (Tables 5.12 and 5.14).

Table 5.12 Starch content and yield, and other six traits of the 30 top progeny at clonal stage (ranking based on starch content)

Cross	Clone	StC	StY	FSRY	RDMC	SRN	FBM	HI	CBSRN
Kiroba x Namikonga	6256	40.93	1.12	2.80	40.92	1.23	17.38	0.36	1.00
Vumbi x Namikonga	6731	40.56	6.33	13.44	43.89	2.56	40.65	0.46	1.00
TMS 30001 x AR 42-3	7078	40.31	6.45	10.85	44.25	1.98	40.50	0.34	1.05
Namikonga x AR40-6	6991	39.33	6.47	20.21	44.81	3.68	49.67	0.38	1.57
Nanchinyaya x Namikonga	6535	39.23	10.44	27.24	49.02	9.09	97.00	0.28	1.00
Namikonga x TMS 30001	7036	38.80	6.75	27.06	39.03	6.79	101.17	0.27	1.00
Namikonga x AR40-6	6984	38.30	2.41	9.59	35.48	2.44	20.50	0.60	1.00
Namikonga x TMS 30001	7039	38.03	3.92	16.93	43.56	4.39	37.67	0.48	1.30
Namikonga x TMS 30001	7030	37.78	3.54	9.50	42.20	2.78	33.00	0.33	1.00
Nanchinyaya x AR 37-80	6688	37.59	2.46	11.69	28.50	3.69	42.00	0.34	2.32
AR 40-6 x AR 42-3	7218	37.22	1.31	8.64	36.85	3.31	49.33	0.23	1.30
Vumbi x TMS 30001	6807	37.06	0.99	8.46	37.92	3.51	30.60	0.28	3.62
Namikonga x AR 40-6	6996	37.06	10.63	18.85	37.37	2.12	34.67	0.57	1.05
AR 40-6 x AR 42-3	7203	36.89	6.93	19.62	39.84	4.74	64.33	0.28	1.03
Kiroba x Namikonga	6265	36.69	12.23	32.42	42.02	6.31	72.62	0.44	1.05
Nanchinyaya x TMS 30001	6635	36.32	10.15	3.76	39.87	1.97	22.71	0.26	3.59
Kalolo x Namikonga	6045	36.85	16.82	47.17	39.75	5.70	92.07	0.51	1.38
Namikonga x AR 42-3	7102	36.14	0.52	1.33	43.53	0.60	23.50	0.09	1.06
Namikonga x AR 42-3	7084	35.94	7.38	19.19	46.28	5.63	65.50	0.27	1.01
TMS 30001 x AR 42-3	7070	35.87	8.96	37.59	36.82	4.99	63.50	0.61	1.89
Namikonga x AR 40-6	7000	35.76	4.46	24.78	37.93	6.14	112.67	0.23	1.57
Kiroba AR 40-6	6372	35.64	4.68	7.02	40.84	3.55	41.74	0.28	1.02
Nanchinyaya x AR40-6	6585	35.52	0.85	2.65	46.44	2.40	19.10	0.19	1.00
TMS 30001 x AR 42-3	7066	35.43	11.13	32.92	45.06	5.80	60.50	0.56	1.00
Namikonga x AR 40-6	6988	35.42	3.18	10.59	39.55	3.63	24.83	0.51	2.45
TMS 30001 x AR 42-3	7166	35.34	6.49	14.81	40.04	4.13	60.00	0.53	1.00
AR 40-6 x TMS 30001	7074	35.33	15.67	17.68	35.15	7.82	49.33	0.65	1.00
Nanchinyaya x Namikonga	6537	35.27	14.98	43.92	46.48	5.20	132.20	0.34	1.00
Kiroba x AR 40-6	6369	35.18	3.90	10.43	42.71	2.35	27.20	0.41	1.00
Vumbi x AR 42-3	6856	35.09	10.31	28.52	47.56	3.51	88.38	0.35	1.29
Parents									
Kalolo		16.56	4.04	21.21	27.67	3.00	50.81	0.42	2.00
Vumbi		16.86	1.72	15.00	27.33	2.75	32.00	0.49	3.00
Kiroba		26.97	5.77	25.00	35.00	6.75	40.02	0.55	1.00
Namikonga		24.22	2.87	11.52	36.33	2.50	30.04	0.38	1.00
Nanchinyaya		25.53	2.39	12.50	35.33	5.75	48.52	0.28	1.50
AR 40-6		23.38	7.26	34.00	33.00	5.75	104.01	0.34	1.50
TMS 30001		14.76	2.18	15.50	24.33	5.75	25.02	0.62	1.50
AR 43-2		22.78	2.96	13.04	33.00	2.00	22.50	0.57	1.80
AR 37-80		22.14	1.08	5.53	28.33	3.25	16.73	0.31	3.00
CR 25-4		19.33	4.36	22.21	34.33	4.25	22.51	0.45	1.00

FSRY (fresh storage root yield in t ha^{-1}); FBM (fresh biomass in t ha^{-1}); HI (harvest index); RDMC (root dry matter content in %); StC (starch content in %); StY (starch yield in t ha^{-1}); CBSRN (cassava brown streak disease root necrosis severity)

Mid-parent heterosis for StC ranged from 41.6 and 134.1% for progeny 6372 (Kiroba x AR 40-6) and progeny 6807 (Vumbi x TMS 30001) respectively, while the best parent heterosis ranged from 30.4 to 119.6 for progeny 6369 from Kiroba x AR 40-6 and progeny 6807 from Vumbi x TMS 30001, respectively (Table 5.13).   Among the top 30 progeny, the highest value of both mid-parent (134.1%) and best parent heterosis (119.6%) for StC was recorded by progeny 6807 (Vumbi x TMS 30001). For StY, the highest mid-parent (469.6%) and best parent (422%) heterosis was recorded by progeny 6537 (Nanchinyaya x Namikonga). These values are based on best performance in StC (Table 5.13). The highest mid-parent heterosis (57.7%) for RDMC was recorded by progeny 6856 (Vumbi x AR 42-3), and the highest best parent heterosis (44.1%) was recorded by progeny 6807 (Vumbi x AR 42-3) (Appendix 3). The mid-parent heterosis for FSRY ranged from -88.9 (6585; Nanchinyaya x AR 40-6) to 267.3% (6537; Nanchinyaya x Namikonga) (Appendix 3). The best parent heterosis ranged from -92.4 (6585; Nanchinyaya x AR 40-6) to 252.6 (Nanchinyaya x Namikonga). However, more than half of the top 30 progeny had negative mid-parent and best parent heterosis for FSRY.

Table 5.13 Starch content and yield, and estimates of heterosis of the 30 top progeny at clonal stage (ranking based on starch content)

Family	Clone	StC (%)			StY t ha^{-1}		
		StC	StC†	StC‡	StY	StY†	StY‡
Kiroba x Namikonga	6256	40.93	59.91	51.76	1.12	-74.07	-80.59
Vumbi x Namikonga	6731	40.56	97.47	67.46	6.33	175.82	120.56
TMS 30001 x AR 42-3	7078	40.31	115.93	77.92	6.45	150.97	117.91
Namikonga x AR40-6	6991	39.33	66.18	63.29	6.47	27.74	-10.88
Nanchinyaya x Namikonga	6535	39.23	61.23	60.21	10.44	296.96	256.31
Namikonga x TMS 30001	7036	38.80	96.10	57.80	6.75	167.33	135.19
Namikonga x AR40-6	6984	38.30	60.42	57.64	2.41	-52.42	-66.80
Namikonga x TMS 30001	7039	38.03	94.46	56.48	3.92	55.25	36.59
Namikonga x TMS 30001	7030	37.78	92.51	54.91	3.54	40.20	23.34
Nanchinyaya x AR 37-80	6688	37.59	60.57	52.75	2.46	41.79	2.93
AR 40-6 x AR 42-3	7218	37.22	70.69	64.35	1.31	-74.36	-81.96
Vumbi x TMS 30001	6807	37.06	134.41	119.81	1.00	-49.23	-54.59
Namikonga x AR 40-6	6996	37.06	55.71	53.01	10.63	109.87	46.42
AR 40-6 x AR 42-3	7203	36.89	60.49	58.43	6.91	35.23	-4.82
Kiroba x Namikonga	6265	36.69	43.35	36.04	12.23	141.46	111.96
Nanchinyaya x TMS 30001	6635	36.32	86.77	49.57	10.15	344.20	324.69
Kalolo x Namikonga	6045	36.85	80.74	52.32	16.82	386.83	316.34
Namikonga x AR 42-3	7102	36.14	53.79	49.22	0.52	-82.16	-82.43
Namikonga x AR 42-3	7084	35.94	52.94	48.39	7.38	153.17	149.32
TMS 30001 x AR 42-3	7070	35.87	92.80	57.46	8.96	248.64	202.70
Namikonga x AR 40-6	7000	35.76	50.25	47.65	4.46	-11.94	-38.57
Kiroba x AR 40-6	6372	35.64	41.57	32.15	4.68	-28.17	-35.54
Nanchinyaya x AR40-6	6585	35.52	48.28	44.80	0.85	-82.38	-88.29
TMS 30001 x AR 42-3	7066	35.43	88.76	55.53	11.13	333.07	276.01
Namikonga x AR 40-6	6988	35.42	48.82	46.24	3.18	-37.22	-56.20
TMS 30001 x AR 42-3	7166	35.34	88.28	55.14	6.49	152.53	119.26
AR 40-6 x TMS 30001	7074	35.33	85.26	51.11	15.67	231.99	115.84
Nanchinyaya x Namikonga	6537	35.27	44.70	43.78	14.98	469.58	421.95
Kiroba x AR 40-6	6369	35.18	39.74	30.44	3.90	-40.14	-46.28
Vumbi x AR 42-3	6856	35.09	77.04	54.04	10.31	340.60	248.31

StC (mean starch content in %); StY (mean starch yield in t ha^{-1}); StC† (mid-parent heterosis %); StC‡ (best parent heterosis %); StY† (mid-parent heterosis %); StY‡ (best-parent heterosis %).

5.3.10 Starch yield, starch content and other six traits and heterosis of the 30 top progeny at clonal stage (ranking based on starch yield)

The StY for the top 30 progeny ranged from 16.7 (6407 to 6431 both from Kalolo x AR 42-3) and 34.80 t ha^{-1} (6879 from Vumbi x AR 42-3). The highest StY was recorded by genotype 6879 (Vumbi x AR 42-3) followed by genotype 6086 (30.4 t ha^{-1}; Kalolo x AR 40-6). In contrast, the same set of 30 top progeny based on StY, its StC ranged from 21.6 (6111 from Kalolo x AR 40-6) to 36.9% (6045 from Kalolo x Namikonga). The top 30 genotypes in terms of StC presented in Table 5.12 do not appear in the Table 5.14 except for genotype 6045. Importantly, the best genotype in FSRY (6086; 30.4 t ha^{-1}) was second best in terms of StY (Table 5.14). These results also indicate clearly that FSRY is highly associated with StY (r=0.94; p≤0.001; Table

5.10). Other genotypes exhibiting the same relationship are 6879 (34.9 t ha^{-1}; Vumbi x AR 42-3), 6090 (23.2 t ha^{-1}; Kalolo x AR 40-6), 6081 (22.9 t ha^{-1}; Kalolo x AR 40-6). In general almost all 30 top progeny exhibit this kind of relationship.

The mid-parent heterosis for StY ranged from 168.0 (progeny 6400 from Kiroba x AR 40-6) to 1391.0% (progeny 6879 from Vumbi x AR 42-3), while best parent heterosis ranged from 131.4 (progeny 6103 from Kalolo x AR 40-6) to 1079.0% (progeny 6879 from Vumbi x AR 42-3). The highest mid-parent and best parent heterosis was recorded by genotype 6879, followed by genotype 6845 (955.6) from Vumbi x AR42-3 (Table 5.15). However, the extremely high mid-parent and best parent heterosis observed from genotype 6879 (1391%; 1079%) could have been attributed by the poor performance of the parent Vumbi in terms of StY (1.72 t ha^{-1}) and high levels of CBSRN (class 3) recorded (Table 5.12).

Table 5.14 Starch yield, starch content and other six traits of the top 30 progeny at clonal stage (ranking based on starch yield)

Cross	Clone	StY	StC	RDMC	FSRY	SRN	FBM	HI	CBSRN
Vumbi x AR42-3	6879	34.85	32.81	41.78	98.11	6.96	190.94	0.51	1.00
Kalolo x AR 40-6	6086	30.43	23.19	32.42	124.22	11.53	268.33	0.45	1.38
Vumbi x AR42-3	6845	24.72	34.59	41.15	70.63	6.42	130.32	0.55	1.31
Kalolo x AR 40-6	6090	23.24	23.92	35.43	100.01	11.40	174.50	0.56	1.34
Kalolo x AR 40-6	6081	22.88	24.43	35.43	93.12	10.59	189.33	0.48	1.16
Kalolo x AR 40-6	6114	22.07	24.19	36.64	92.88	10.89	152.87	0.60	2.73
Namikonga x AR 42-3	7092	21.20	28.41	44.15	73.28	8.78	152.50	0.51	1.03
CR 25-4 x AR 40-6	7391	20.57	25.56	34.95	82.38	9.75	170.65	0.52	1.04
Kalolo x AR 40-6	6119	19.86	31.32	45.31	63.76	8.33	114.78	0.56	1.01
AR 40-6 x AR 43-2	7239	19.97	26.35	36.26	72.14	6.24	104.50	0.57	1.00
Kalolo x AR 40-6	6116	19.89	29.25	40.44	68.47	8.06	132.20	0.52	2.04
Kalolo x AR 42-3	6183	19.72	26.40	35.96	80.53	9.42	173.33	0.47	1.07
Kalolo x AR 40-6	6111	19.71	21.61	34.75	91.81	10.94	188.90	0.47	1.08
Kalolo x AR 42-3	6180	18.79	26.40	37.70	71.07	5.77	139.70	0.05	1.63
Kalolo x AR 42-3	6167	18.66	25.21	36.22	74.64	8.49	115.27	0.65	1.36
AR 40-6 x AR 37-80	7267	18.83	29.60	34.83	63.76	9.73	122.33	0.55	1.00
Kalolo x Namikonga	6077	18.50	31.50	40.56	56.61	6.56	134.38	0.41	1.36
Nanchinyaya x Vumbi	6328	18.09	29.02	35.95	57.84	9.09	99.85	0.56	1.34
Kalolo x AR 37-80	6214	18.15	28.58	35.06	59.88	7.06	114.38	0.51	1.05
Namikonga x AR 42-3	7093	18.39	29.81	41.22	60.91	5.71	150.33	0.40	1.02
Kiroba x AR 42-3	6461	18.26	26.74	38.24	75.76	10.00	134.88	0.50	1.05
Kalolo x TMS 30001	6143	17.78	28.68	29.56	53.49	7.17	112.18	0.48	1.00
Kiroba x AR 40-6	6400	17.16	26.50	36.18	67.11	9.90	168.35	0.39	1.00
Kalolo x AR 40-6	6104	17.37	33.37	42.30	49.94	8.05	107.93	0.43	1.07
Kalolo x Namikonga	6042	17.12	30.52	40.20	72.03	8.91	170.17	0.41	1.08
Vumbi x Namikonga	6725	17.12	28.68	38.38	61.97	7.67	146.33	0.42	1.66
Kalolo x Namikonga	6045	16.82	36.85	39.75	47.17	5.70	92.07	0.51	1.38
Kiroba x TMS 30001	6407	16.73	31.04	34.96	49.98	7.18	92.95	0.50	1.34
Kalolo x AR 40-6	6103	16.79	31.17	41.23	54.63	8.96	95.25	0.56	1.08
Kiroba x TMS 30001	6431	16.69	33.99	40.58	48.96	9.78	99.33	0.48	1.09
Parents									
Kalolo		4.04	16.56	26.67	21.21	3.00	50.81	0.42	2.00
Vumbi		1.72	16.86	27.33	15.00	2.75	32.00	0.49	3.00
Kiroba		5.77	26.97	35.00	25.00	6.75	40.02	0.55	1.00
Namikonga		2.87	24.22	36.33	11.52	2.50	30.04	0.38	1.00
Nanchinyaya		2.39	25.53	35.33	12.50	5.75	48.52	0.28	1.50
AR 40-6		7.26	23.38	33.00	34.00	5.75	104.01	0.34	1.50
TMS 30001		2.18	14.76	24.33	15.50	5.75	25.02	0.62	1.50
AR 42-3		2.96	22.78	33.00	13.04	2.00	22.50	0.57	1.80
AR 37-80		1.08	22.14	28.33	5.53	3.25	16.73	0.31	3.00
CR 25-4		4.36	19.33	34.33	22.21	4.25	22.51	0.45	1.00

StY (starch yield t ha^{-1}); StC (starch content in %); RDMC (root dry matter in %); FSRY (fresh storage root yield in t ha^{-1}); SRN (storage root number); FBM (fresh biomass weight in t ha^{-1}); HI (harvest index); CBSRN (cassava brown streak root necrosis)

Table 5.15 Starch yield and content, and estimates of heterosis of the 30 top progeny at clonal stage (ranking based on starch yield)

Cross	Clone	StC	StC†	StC‡	StY	StY†	StY‡
Vumbi x AR42-3	6879	32.85	72.53	54.81	34.85	1391.45	1079.05
Kalolo x AR 40-6	6086	23.02	22.28	9.15	30.43	438.05	318.73
Vumbi x AR42-3	6845	34.72	82.35	63.62	24.72	955.56	734.46
Kalolo x AR 40-6	6090	23.56	25.15	11.71	23.24	310.62	219.56
Kalolo x AR 40-6	6081	24.44	29.83	15.88	22.88	305.31	215.43
Kalolo x AR 40-6	6114	24.08	27.92	14.18	22.15	291.15	204.41
Namikonga x AR 42-3	7092	28.55	25.66	17.88	21.20	627.27	616.22
CR 25-4 x AR 40-6	7391	25.73	27.31	22.00	20.47	252.84	182.37
Kalolo x AR 40-6	6119	31.05	64.94	47.23	19.86	252.21	174.10
AR 40-6 x AR 43-2	7239	26.26	24.13	23.75	19.97	291.39	175.48
Kalolo x AR 40-6	6116	29.07	54.42	37.84	19.89	252.21	174.10
Kalolo x AR 42-3	6183	26.26	39.02	23.75	19.72	462.86	387.62
Kalolo x AR 40-6	6111	21.62	14.85	2.51	19.71	248.67	171.35
Kalolo x AR 42-3	6180	26.11	38.22	23.04	18.79	437.14	365.35
Kalolo x AR 42-3	6167	24.94	32.03	17.53	18.66	434.29	362.87
AR 40-6 x AR 37-80	7267	29.59	36.90	33.65	18.83	302.57	158.95
Kalolo x Namikonga	6077	31.22	53.11	28.90	18.50	435.46	357.92
Nanchinyaya x Vumbi	6328	28.80	35.88	12.81	18.09	780.78	657.32
Kalolo x AR 37-80	6214	28.44	46.98	28.46	18.15	610.94	313.64
Namikonga x AR 42-3	7093	29.92	31.69	23.53	18.39	531.22	521.62
Kiroba x AR 42-3	6461	26.77	11.10	-0.74	18.26	319.24	217.16
Kalolo x TMS 30001	6143	28.34	80.97	71.14	17.78	472.35	340.59
Kiroba x AR 40-6	6400	26.26	9.28	-2.63	17.16	164.01	136.91
Kalolo x AR 40-6	6104	33.25	76.63	57.66	17.37	207.96	139.67
Kalolo x Namikonga	6042	30.40	49.09	25.52	17.12	394.93	323.27
Vumbi x Namikonga	6725	28.66	39.53	18.33	17.12	479.12	495.82
Kalolo x Namikonga	6045	36.85	80.74	52.32	16.82	386.83	316.34
Kiroba x TMS 30001	6407	30.90	48.09	14.57	16.73	320.13	189.43
Kalolo x AR 40-6	6103	31.08	65.10	47.37	16.79	197.35	131.40
Kiroba x TMS 30001	6431	34.11	63.48	26.47	16.69	320.13	189.43

StC (mean starch content in %); StY (mean starch yield in t ha^{-1}); StC† (mid parent heterosis); StC‡ (best parent heterosis); StY† (mid parent heterosis); StY‡ (best parent heterosis);

5.4   Discussion and conclusion

The diallel analysis was conducted to study the combining ability and the gene action determining StC, StY, RDMC, FSRY, FBM, and CBSRN. In addition, the study aimed to identify

parents and genotypes with high RDMC, StC and StY for the processing industry in Tanzania. Since parents were not randomly selected from the population the families and progeny were declared as fixed effects and consequently these results only apply to the germplasm in this study.

Progeny and families varied significantly in all the traits studied i.e. StC, StY, FSRY, SRN, FBM, RDMC, HI and CBSRN. The quantification of StC (%) and StY (t ha^{-1}) in this study has provided an insight into the performance under Tanzanian conditions of more than 1000 progeny generated from the crosses. The StC recorded in this study ranged from as low as 6.7 to as high as 41%. Other workers (Sriroth et al., 1999) reported starch content varying between 18.6 and 27% from Thai improved cultivars harvested at 12 MAP. Similarly, Easwari Amma et al. (1995) reported mean StC ranging from 17.0 to 37.3% obtained from hybrids that were crossed from inbred lines in India. Average value of 24% for StC has also been reported (ISI-Denmark, 2008). The range in StC obtained in the present study provides potential opportunity for selection. The best progeny in StC was 6256 (40.9%) from the family Kiroba x Namikonga, followed by progeny 6731 (40.6%) from family Vumbi x Namikonga. The StY also varied significantly between progeny and families. The highest StY was recorded from progeny 6879 (34.8 t ha^{-1}; Vumbi x AR 42-3), followed by progeny 6086 (34.7 t ha^{-1}; Kalolo x AR 40-6).

The variances for families for the traits (FSRY, FBM, HI, SRN, CBSRN) were highly significant. The GCA and SCA effects were also significant, indicating that both additive and non-additive genetic effects were important in the expression of the traits. However, SCA effects were relatively more important than GCA effects for FSRY, SRN, and FBM suggesting the predominance of non-additive over additive genetic effects. Similar findings were reported for FSRY (Jaramillo et al., 2005; Perez et al., 2005). Studies by Abraham et al. (2001) reported that root yield and most of the yield components in cassava were governed by dominant gene action. The contribution of GCA SS to family SS% was relatively higher than SCA SS for CBSRN severity suggesting prevalence of additive genetic effects. However, the ratio between GCA SS% and SCA SS% was narrow (>2) suggesting that both additive and non-additive genetic effects had a role in controlling the expression of CBSRN. Munga (2008) reported that GCA effects for the severity of root necrosis due to CBSD were more important that SCA

effects. Differences due to GCA of the parent are due to additive genetic variances whereas SCA is a reflection of non-additive genetic variances (Chahal and Gosal, 2002).

Both GCA and SCA effects were significant for RDMC, StC and StY, suggesting that both additive and non-additive genetic effects played a role in expressing the StC, RDMC, and StY. However, the contribution to the family SS% denote that GCA effects were relatively more important in determining StC and RDMC, while for the StY, SCA effects were more important than GCA effects, suggesting that additive genetic effects had a predominant role in controlling RDMC and StC. Cach et al. (2006) reported that RDMC was controlled by additive genetic effects. In contrast, Easwari-Amma et al. (1995) observed that StC was controlled by non-additive genetic effects. Application of selection pressure would improve the RDMC and StC, but for StY, a different approach would be required. Parents Vumbi, Kiroba, Namikonga, Nanchinyaya were found to be good combiners for RDMC, whereas, parents Kalolo, TMS 30001, AR 37-80 and CR 25-4 had significant negative general combining ability. Parent Kiroba and Namikonga were found to be the best combiners in terms of GCA for StC. For StY, Kalolo and AR 42-3 had significant positive general combining ability, while AR 37-80 and CR 25-4 indicated significant negative general combining ability.

High, positive and significant correlations were obtained between StC and RDMC. Similar findings were observed from yield trials which evaluated 205 clones (IITA, 1974). This implies that indirect selection can be done for starch content at clonal stage. Starch yield correlated significantly with DRY, FSRY, FBWT, HI, and SRN at clonal stage. However, the correlation between starch yield and FSRY was stronger (r=0.94***) than with starch content (r=0.26***), suggesting that FSRY has a positive effect in determining starch yield. The CBSRN correlated negatively with StC, StY and RDMC. Hillocks et al. (2001) reported that CBSD affected root quality in cassava roots. Collectively, these results indicate that when breeding for high starch content, selection should also consider CBSD resistance. A negative non-significant correlation was also obtained between StC and FSRY, suggesting that the two characters seem to be negatively associated. Fresh storage root yield positively and significantly correlated with DRY, FBM, HI, and SRN. Reports have indicated similar results (Okechukwu and Dixon, 2009; Kamau, 2006).

High and significant correlation between the seedling and clonal stage in FSRM, RDMC, HI, and SRM were observed, suggesting that indirect selection could start at seedling stage for FSRM, RDMC, HI, and SRN. Byrne (1984) reported significant correlation (r = 0.48**) between dry matter content in both seedling and clonal stage trials, therefore selection for dry matter at the F_1 seedling stage is feasible. However, other breeding programmes i.e. IITA, have been screening genotypes at seedling stage for diseases tolerance, root conformation (neck length, uniformity, and compact roots), branching and cyanogenic potentials, while RDMC was not considered at the seedling stage (Jennings and Hershey, 1985; Hahn et al., 1979). The significant positive correlation between seedling and clonal stage for RDMC obtained in this study suggests the potential of screening for the trait at seedling stage.

From the study, it is clear that the progress in improving starch content has been achieved in the F_1 population as all the top 30 genotypes based on StC indicated positive mid- and best parent heterosis values. Different combinations between local and introduced clones produced these best progeny. When StY was considered, the mid-parent or best parent heterosis estimates of the top 30 genotypes were also positive and very high. When genotypes were ranked individually according to the StY a different order of performance was obtained with the exception of genotype 6045 which appeared in both StC and StY ranking and had StC of 36.9% and StY of 16.8 t ha^{-1}. The superiority of the progeny compared to either of the two parents for StC, StY, and FSRY suggest the presence of both additive and non-additive gene action, however it depends on the relative magnitudes of GCA and SCA. This form of heterosis is due to the masking of unfavourable recessive alleles in a heterozygote (Bernado, 2002). Empirical evidence strongly indicated that heterosis is mostly due to partial or complete dominance.

It is obvious from the present study that both additive and non-additive gene actions were involved in the expression of the characters evaluated at the clonal stage. For those traits (StC, RDMC and CBSRN) where additive genetic effects accounted for most of the variation, a hybridization scheme followed by phenotypic mass selection may be effective in creating desirable recombinants. Improvement for StC and RDMC may be realized by selecting parents with the highest GCA effects for the StC and RDMC and hybridize with that combine well to

maximize the positive SCA effects for the StC and RDMC. The hybridization programme should include complementary desirable traits such as resistance to CBSD and CMD, and pyramid the genes through convergent breeding. The predominance of non-additive genetic effects in the expression of StY, FSRY, SRN, and FBM suggest the use of different approach. Cassava clones might be grouped into heterotic pools and specific hybrid combinations implemented to select potential genotypes to exploit non-additive gene action. Since cassava is a vegetatively propagated species, in selecting outstanding clones all genetic effects (additive, dominant and epistatic effects) are exploited. As a way forward, selected genotypes from the clonal stage will be evaluated in preliminary yield trial and advanced further to multi-locational trials while implementing participatory approaches involving farmers and processors in selection.

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APPENDIX

Appendix 1 CHAMBEZI SOIL PROFILE DESCRIPTION AND ANALYTICAL DATA

Profile No. Chambezi 01

General information on site and soil

Location:

Region: Coastal   **District**: Bagamoyo district   **Site/Village:** Chambezi Exper.Station

Co-ordinates: 06^0 33' 32"S,   38^0 54' 37"E

Landforms: Coastal Plain   **Topography**: Flat to almost flat   **Position:** summit

Slope of site: 1-2%   **Microtopgraphy:** Termite mounds   **Elevation:** 48 masl

Soil Temperature Regime: Isohyperthemic   **Soil Moisture** Regime: Ustic

Land use and vegetation: Annual and perennial field cropping (cassava, coconuts, cashew, cowpeas, pigeon peas and sweet potatoes).   **Human influence:** natural vegetation disturbed due to cultivation and wild fires.

Drainage: somewhat excessively drained.   **Internal drainage:** moderately rapid

Moist conditions: dry up to 28 cm, below moist   **Ground water table:** not observed

Parent material: Marine deposits   **Effective soil depth**: Very deep (>150 cm).   **Erosion:** no evidence of erosion

Authors: Njapuka A and Mugogo S.E.   **Date of description**: 30th June 2007

Soil profile description

Ap: Brownish black (10YR 3/2) moist, dully yellowish brown (10YR 5/3) dry; 0-12 cm: loamy sand; fine, granular and weak subangular blocky; slightly hard when dry, friable when moist, non-sticky and no-plastic when wet; many pores; many very fine and fine roots; clear and wavy boundary.

AB: Dully yellowish brown (10YR 4/3) moist, dully yellowish brown (10YR 5/3) dry; 12-28 cm: Loamy sand; fine granular and weak subangular blocky; slightly hard when dry, friable when moist, non-sticky and no-plastic when wet; many pores; many very fine and fine and few medium roots; clear and smooth boundary

Bs1:   Brown (10 YR 4/4) moist; sandy loam; weak, fine and medium sub-angular 28-56 cm: blocky, friable when moist, non-sticky and non-plastic when wet; many pores; moderate fine roots; gradual and smooth boundary

Bs2:   Brown (10 YR 4/6) moist; sandy loam; weak, fine and medium sub-angular 56-100 cm: blocky, friable when moist, non-sticky and non-plastic when wet; many pores; few fine roots; gradual and smooth boundary

Bs3:   Brown (10 YR 4/4) moist; sandy loam; weak, fine and medium subangular 100-158+ cm: blocky, friable when moist, non-sticky and non-plastic when wet; many pores; moderate fine roots; gradual and smooth boundary

Analytical data

Horizon Depth (cm)	Ap 0- 12	AB 12- 28	Bs1 28- 56	Bs2 56- 100	Bs3 100- 158+
Texture Clay % Silt % Sand % Textural class	8 4 88 S	8 4 88 S	14 6 80 LS	18 4 78 SL	18 4 78 SL
pH water 1:2.5 pH KCL 1:2.5 EC mmho 1:2.5	5.6 4.4 0.7	4.7 4.1 1.2	4.5 3.7 1.3	4.1 3.7 1.5	4.5 3.7 1.3
Organic C % TN % Available P Bray 1 mg/kg	2.3 0.1 9.8	0.4 0.1 6.9	0.4 0.1 4.2	0.3 0.1 2.95	0.2 0.1 1.9
CEC NH4OAc Exch. Ca me/100g Exch. Mg me/100g Exch. K me/100g Exch. Na me/100g Base saturation %	3.8 3.6 0.0 0.1 0.1 98	3.2 1.2 0.0 0.1 0.1 42	4.0 1.2 0.1 0.1 0.5 34	3.0 1.0 0.1 0.2 0.0 39	3.9 0.8 0.6 0.1 0.0 40

Brief description of the soil**:**

Very deep sandy top soil over loamy sand to sandy loamy subsoil, very acidic and of very low fertility status as shown by very low organic matter content, CEC and base saturation.

APPENDIX 2 Map of Tanzania
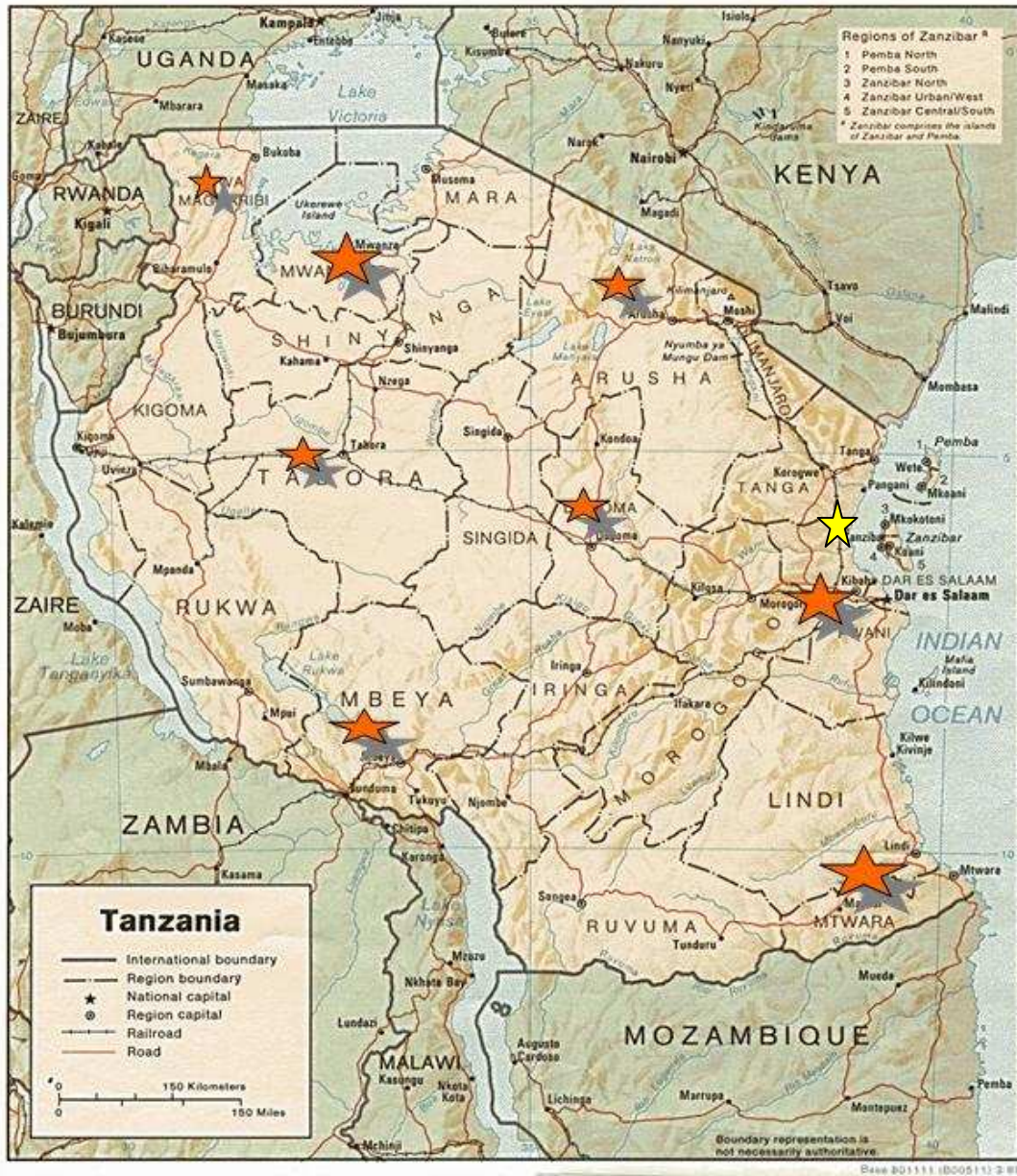
 Root and Tuber Crop Research team in Tanzania

 ARI CHambezi, Bagamoyo, Coast region, where clonal evaluation trial was conducted

Appendix 3 Per se performance and heterosis percentage of the F_1 progeny for the root dry matter content and fresh storage root yield

Cross	Clone	Root dry matter content			Fresh storage root yield		
		RDMC	RDMC†	RDMC‡	FSRY	FSRY†	FSRY‡
Kiroba x Namikonga	6256	40.92	14.73	12.63	2.80	-83.73	-88.12
Vumbi x Namikonga	6731	43.89	37.89	20.81	13.44	0.00	-11.67
TMS 30001 x AR 42-3	7078	44.25	54.37	34.09	10.85	-24.00	-30.13
Namikonga x AR40-6	6991	44.81	29.27	23.34	20.21	-10.99	-40.44
Nanchinyaya x Namikonga	6535	49.02	36.81	34.93	27.24	126.75	117.68
Namikonga x TMS 30001	7036	39.03	28.68	7.43	27.06	100.44	74.58
Namikonga x AR40-6	6984	35.48	2.35	-2.34	9.59	-57.80	-71.76
Namikonga x TMS 30001	7039	43.56	43.62	19.90	16.93	25.48	9.29
Namikonga x TMS 30001	7030	42.20	39.14	16.16	9.50	-29.04	-38.19
Nanchinyaya x AR 37-80	6688	28.50	-10.46	-19.33	11.69	28.67	-7.36
AR 40-6 x AR 42-3	7218	36.85	11.67	11.67	8.64	-63.23	-74.59
Vumbi x TMS 30001	6807	37.92	46.81	38.75	8.46	-45.11	-46.00
Namikonga x AR 40-6	6996	37.37	7.80	2.86	18.85	-17.05	-44.50
AR 40-6 x AR 42-3	7203	39.84	20.73	20.73	19.62	-16.55	-42.32
Kiroba x Namikonga	6265	42.02	17.82	15.66	32.42	78.52	30.32
Nanchinyaya x TMS 30001	6635	39.87	33.66	12.85	3.76	-48.21	-53.23
Kalolo x Namikonga	6045	39.75	24.22	9.41	47.17	189.54	123.30
Namikonga x AR 42-3	7102	43.53	25.57	19.82	1.33	-87.92	-88.62
Namikonga x AR 42-3	7084	46.28	33.51	27.39	19.19	56.49	47.46
TMS 30001 x AR 42-3	7070	36.82	28.45	11.58	37.59	163.72	189.08
Namikonga x AR 40-6	7000	37.93	9.42	4.40	24.78	8.44	-27.44
Kiroba x AR 40-6	6372	40.84	20.12	16.69	7.02	-75.86	-79.06
Nanchinyaya x AR40-6	6585	46.44	35.93	31.45	2.65	-88.86	-92.38
TMS 30001 x AR 42-3	7066	45.06	57.20	36.55	32.92	130.95	112.32
Namikonga x AR 40-6	6988	39.55	14.09	8.86	10.59	-53.32	-68.76
TMS 30001 x AR 42-3	7166	40.04	39.68	21.33	14.81	173.40	151.35
AR 40-6 x TMS 30001	7074	35.15	22.62	6.52	17.68	-28.65	-48.06
Nanchinyaya x Namikonga	6537	46.48	29.72	27.94	43.92	267.33	252.64
Kiroba x AR 40-6	6369	42.71	25.62	22.03	10.43	-64.24	-68.97
Vumbi x AR 42-3	6856	47.56	57.67	44.12	28.52	102.71	89.20

RDMC (root dry matter content in %); FSRY (fresh storage root yield t ha^{-1}); † (mid-parent heterosis); ‡ (better parent heterosis).

Appendix 4 Per se performance and heterosis percentage of the F_1 progeny for the root dry matter content and fresh storage root yield

Cross	Clone	RDMC	RDMC†	RDMC‡	FSRY	FSRY†	FSRY‡
Vumbi x AR 42-3	6879	41.42	37.31	25.52	98.24	601.71	554.93
Kalolo x AR 40-6	6086	32.67	7.70	-1.00	125	352.90	267.65
Vumbi x AR 42-3	6845	41.00	35.92	24.24	70.32	402.29	368.80
Kalolo x AR 40-6	6090	35.33	16.47	7.06	101.17	266.56	197.56
Kalolo x AR 40-6	6081	36.00	18.67	9.09	92.67	235.76	172.56
Kalolo x AR 40-6	6114	37.00	21.97	12.12	92.87	236.49	173.15
Namikonga x AR 42-3	7092	44.33	27.88	22.02	72.5	491.84	457.69
CR 25-4 x AR 40-6	7391	35.24	4.68	2.65	81.86	191.32	140.76
Kalolo x AR 40-6	6119	45.33	50.27	37.36	64.78	134.71	90.53
AR 40-6 x AR 43-2	7239	36.00	9.09	9.09	72.83	209.91	114.21
Kalolo x AR 40-6	6116	40.67	34.07	23.24	68.87	149.53	102.56
Kalolo x AR 42-3	6183	36.18	19.27	9.64	80.68	371.81	280.57
Kalolo x AR 40-6	6111	35.33	16.47	7.06	91.4	231.16	168.82
Kalolo x AR 42-3	6180	37.67	24.18	14.15	72.2	322.22	240.57
Kalolo x AR 42-3	6167	36.33	19.76	10.09	75.47	341.35	255.99
AR 40-6 x AR 37-80	7267	34.67	13.06	5.06	64.00	224.05	88.24
Kalolo x Namikonga	6077	40.67	27.09	11.95	57.72	253.03	172.26
Nanchinyaya x Vumbi	6328	36.00	14.91	1.90	58.60	326.18	290.67
Kalolo x AR 37-80	6214	35.16	25.57	24.11	60.15	350.56	179.77
Namikonga x AR 42-3	7093	41.33	19.23	13.76	60.33	392.49	364.08
Kiroba x AR 42-3	6461	38.67	13.74	10.49	74.88	294.11	199.52
Kalolo x TMS 30001	6143	29.14	12.08	5.31	53.85	193.46	154.01
Kiroba x AR 40-6	6400	36.00	5.88	2.86	68.35	131.69	101.03
Kalolo x AR 40-6	6104	42.67	40.66	29.30	49.93	80.91	46.85
Kalolo x Namikonga	6042	40.67	27.09	11.95	71.83	339.33	238.82
Vumbi x Namikonga	6725	37.33	17.28	2.75	62.17	369.21	314.47
Kalolo x Namikonga	6045	40.00	25.00	10.10	47.9	192.97	125.94
Kiroba x TMS 30001	6407	35.00	17.98	0.00	50.45	149.14	101.80
Kalolo x AR 40-6	6103	41.67	37.37	26.27	54.42	97.17	60.06
Kiroba x TMS 30001	6431	41.00	38.21	17.14	48.5	139.51	94.00

RDMC (mean root dry matter content %); RDMC† (mid-parent heterosis); RDMC‡ (better parent value heterosis); FSRY† (mid-parent heterosis); FSRY‡ (best parent heterosis)

Chapter 6

General overview

Cassava is a potential industrial crop for Tanzania, but no cassava cultivars have up to now been developed or recommended for such an enterprise. This research was conducted with the aim of evaluating crosses developing new varieties that are high yielding, with high dry matter, and high starch content. The objectives were studied in two parts: 1) preliminary studies were carried out through a participatory rural appraisal in three representative districts, and screening of germplasm was done at four sites to determine the variability of root dry matter (RDMC), starch content (StC) and starch yield (StY) over time; 2) the second part involved the generation and evaluation of F_1 clones to determine the combining ability of the parents and the performance of the new genotypes in terms of fresh storage root yield (FSRY), StC, StY and virus diseases mainly cassava mosaic (CMD) and cassava brown streak disease (CBSD) resistance, and to identify superior genotypes. This overview summarizes the main findings of the study and discusses the implication for cassava breeding.

The participatory rural appraisal was conducted in Bagamoyo and Rufiji districts in Coast region and Mkinga district in Tanga region with the aim of understanding farmers' cultivar preferences and selection criteria. The main findings of the study were:

- The cassava crop, which is grown as a sole crop or intercropped with other crops such as cereals, legumes, and young tree crops (cashew, coconut), had relatively low yield (4 t ha^{-1})
- Recycling of cassava planting materials is a common practise by the majority of farmers, and less than 10% of farmers received planting material of improved varieties
- Major production constraints include; pests, diseases, and root rotting caused by CBSD. Other constraints are low farm gate prices for fresh roots, issues related to infrastructure such as inadequate transport, unreliable markets for fresh cassava, and drought. Post harvest constraints include poor drying technologies.
- Sweet cultivars are predominant over bitter cultivars in the coastal area, reflecting that most of the cultivars are for fresh use. However both sweet and bitter are processed into stable products (flour and chips).

- Attributes desired by farmers were high yielding cultivars, earliness, tolerance to pests and diseases. The complementing attributes associated with culinary qualities were sweetness, good cookability, high dry matter content or mealyness and marketability.
- High RDMC ranging from 32.5 and 46% was observed in landraces, signifying that farmers are also practicing selection pressure to landraces.

A preliminary study was carried out to evaluate the variability in FSRY, RDMC, StC, and StY over different harvesting times of ten cassava cultivars. The study involved three harvesting dates (7, 11, and 14 MAP), and four sites; Kibaha, Chambezi, Hombolo in Tanzania mainland and Kizimbani in Zanzibar Island and the following were the findings:

- Cultivars varied significantly in RDMC, and the highest RDMC was recorded at 7 MAP rather than 11 and 14 MAP. The RDMC ranged from 29 to 40%. Cultivar Namikonga had the highest RDMC content and the lowest was recorded from cultivar Kalolo.
- The StC varied significantly with cultivars and harvesting dates. Values of StC ranged from 20 to 25%. Cultivar Namikonga had the highest StC value. The differences observed might be due to the genetic composition of cultivars, cultural practices, and environmental factors. Sites also differed significantly in StC.
- An increase in StC was observed up to 7 MAP, followed by a decline between 7 and 11 MAP, and finally an increase again between 11 and 14 MAP. However, for most of the cultivars at Kibaha an increase in StC between 11 and 14 MAP could not surpass values recorded at 7 MAP. At Kizimbani, cultivar Kalolo and Vumbi did not increase StC after 11 MAP. At Chambezi and Hombolo, a dramatic gain in StC was observed for most of the cultivars between 11 and 14 MAP.
- At Hombolo, a substantial decline in StC was observed between 7 and 11 MAP. It is important to note that probably starch from roots was used to support tissue maintenance during the long dry season. Further drawing of starch from roots was also expected at the beginning of the new rain season.
- Significant differences in StY were observed between cultivars, harvesting dates and sites. In general, a marginal increase was noted between 7 and 11 MAP for most of the cultivars and sites, and a considerable increase was observed between 11 and 14 MAP especially at Chambezi and Hombolo sites.
- High levels of disease (CMD, CBSD) severity were recorded for some of the cultivars such as Vumbi, TMS 30001, AR 42-3, and AR 37-80.

Diallel analysis of cassava genotypes was implemented at seedling and clonal stages. At seedling stage the performance of the F_1 seedling population was determined for yield characteristics and at clonal stage the aim was to determine: combining abilities of the parents, performance of F_1 progeny for FSRY, StC, StY, RDMC, and other agronomic traits. The study also aimed to identify genotypes that are high in StC, and StY, and determine the mid- and best parent heterosis of the best genotypes.

- The fresh storage root mass (FSRM), storage root number (SRN), harvest index (HI), fresh biomass (FBM), and RDMC varied significantly in the F_1 segregating population. High genetic heterogeneity and variation in the seedling trial and clonal stage for the traits provides potential for selection.

- Although spreader rows were employed at the seedling trial, genotypes did not express high levels of disease (CBSD) symptoms. However, application of spreader rows at seedling stage is important to ensure that genotypes are screened at early stages of the breeding programme.

- High values of FSRY were obtained in this study and genotype 6086 (124.2 t ha^{-1}) and 6090 (100.1 t ha^{-1}) were the best in FSRY and were both from family Kalolo x AR 40-6. The parent clones Kalolo and AR 42-3 were identified to have positive GCA effects for the trait.

- Good levels of RDMC were obtained both at seedling and clonal stage. At seedling stage, the progeny RDMC ranged from 6.4 (Kiroba x Namikonga) to 60.5% (Namikonga x AR 40-6), while at family level the range was from 30.3 (Kalolo x TMS 30001) to 37.5% (Namikonga x AR 42-3). In the clonal trial, progeny RDMC ranged from 13.9 (CR 25-4 x AR 37-80) to 56.7% (Namikonga x AR 42-3), and family RDMC ranged from 31.4 (Kalolo x TMS 30001) to 40.1% (Nanchinyaya x Namikonga).

- The StC varied significantly and high values were obtained for the trait at the clonal stage. The StC at progeny level ranged from 6.7 (Vumbi x TMS 30001) to 40.9% (Kiroba x Namikonga), while at family level StC ranged from 22.8 (Kalolo x TMS 30001) to 29.9% (Nanchinyaya x Namikonga and AR 40-6 x AR 42-3). The best overall genotype was 6256 (40.9%) from family Kiroba x Namikonga followed by genotype 6731 (40.6%; Vumbi x Namikonga). Among the parents, Kiroba and Namikonga were identified as best combiners in terms of GCA effects for StC.

- High values of StY were obtained at the clonal stage, and at progeny level the range was as low as 0.0 to as high as 34.9 t ha^{-1} (Vumbi x AR 42-3). At family level, StY ranged

from 2.7 (TMS 30001 x AR 37-80) to 8.5 t ha^{-1} (Kalolo x AR 42-3). Genotype 6879 from family Vumbi x AR 42-3 had the highest StY value of 34.8 t ha^{-1} followed by genotype 6086 (30.4 t ha^{-1}; Kalolo x AR 40-6). Among the parents, Kalolo and AR 42-3 were identified as good combiners for the trait.

- Negative and non-significant correlation between RDMC and FSRY was observed at the seedling stage (r=-0.018), while at clonal stage the correlation was positive and non-significant (r=0.01). The RDMC and StC were positive and significantly correlated (r=0.55***) at clonal stage, therefore, indirect selection for starch can start at the seedling stage by selecting for high RDMC. However, the StC negatively and non-significantly correlated with FSRY (r=-0.01), implying that the two traits were independent.

- High, positive and significant correlation (r=0.94; p≤0.001) was found between the StY and FSRY at clonal stage. Since StC and FSRY were negatively correlated it is therefore recommended to breed and select for reasonably high FSRY with high StC to achieve high levels of StY.

- High, positive and significant correlations between the seedling and clonal stage for FSRM (r=0.50; p≤0.01), RDMC (r=0.67; p≤0.001), HI (r=0.69; p≤0.001), and SRN (r=0.52; p≤0.01) were observed, suggesting that indirect selection could start at seedling stage for FSRM, RDMC, HI, and SRN.

- Although both additive and non-additive gene action were involved in the expression of the characters considered in the diallel study, additive genetic effects were predominant over non-genetic effects for the RDMC, StC and CBSRN. Similarly, non-additive genetic effects were predominant over additive genetic effects for StY, FSRY, FBM, and SRN, hence exploitation of dominance and epistasis genetic effects for further improvement, and selection can be done among crosses

- Heterosis values for StC and StY were high, and major progress has been achieved to improve the two traits. The genotype with the highest mid- and best parent heterosis for StC was 6807 (134.1%; 119.6%) from family Vumbi x TMS 30001. For StY, genotype 6879 from family Vumbi x AR 42-3 had the highest mid- and best parent heterosis values (1391%; 1079%). However, the very high mid- and best parent heterosis exhibited by genotype 6879 for StY may have been exaggerated by the poor performance of the parents and susceptibility to CBSRN.

Implications for cassava breeding

Clones with high yielding potential have been generated in this research project. Genotypes with high FSRY, RDMC, StC, and StY have been identified. Involvement of farmers through participatory plant breeding in the next evaluation cycle (preliminary yield trial; PYT) will provide an opportunity for them to select clones that are high yielding, tolerant to pests and diseases, high in RDMC, mealy, with good cooking quality according to farmers' preferences. Asaoka et al. (1992) and Safo-Kantanka and Owusu-Nipah (1992) commented that good cooking quality and mealiness is associated with high RDMC and StC. The process of farmer participation will also facilitate adoption of improved cultivars.

The preliminary study conducted to determine variability in RDMC, StC and yield has established the periods to expect high RDMC. Hence, breeders could apply selection for RDMC around 7 MAP. The study has also revealed the critical periods for StC in cassava growth cycle and its variation over time and between sites. It is therefore recommended that, genotypes meant for the processing industry, should be evaluated for RDMC, StC, and StY over time and in different sites to establish the optimum harvest date before recommending for release. Since StC and FSRY are negatively correlated, breeders should find a balance between StC and FSRY for the maximum returns. Earliness is an important trait in cassava; however earliness can be associated with yield penalty. Kamau (2006) focused on earliness and obtained good yields at 6 MAP. Breeding for earliness should be accompanied with screening for high StC and StY to provide farmers with early maturing varieties, to serve a cassava processing industry. Starch physico-chemical properties are influenced by the amylose to amylopectin ratio. Variations in the ratio of amylose to amylopectin could create new markets for cassava starch. Therefore, it is recommended to conduct further analyses on starch quality (amylose: amylopectin ratio, starch particle size, etc) in order to provide relevant information on the use of the starch from different cassava clones developed in this research.

It is obvious from the diallel analysis that both additive and non-additive gene actions were involved in the expression of the characters evaluated at the clonal stage. For those traits (StC, RDMC and CBSRN) where additive genetic effects accounted for most of the variation, a hybridization scheme followed by phenotypic mass selection may be effective in creating desirable recombinants. Improvement for StC, RDMC, and CBSRN may be realized by selecting parents with the highest GCA effects for StC and RDMC and hybridize with that combine well to maximize the positive SCA effects for the StC and RDMC. The hybridization

programme should include complementary desirable traits such as resistance to CBSD and CMD, and pyramid the genes through convergent breeding. The prevalence of non-additive genetic effects in the expression of StY, FSRY, SRN, and FBM suggest the use of another approach. Cassava clones might be grouped into heterotic pools and specific hybrid combinations implemented to select potential genotypes to exploit non-additive gene action. Since cassava is a vegetatively propagated species, in selecting outstanding clones all genetic effects (additive, dominant and epistatic effects) are exploited. As a way forward, selected genotypes from the clonal stage will be evaluated in preliminary yield trial (PYT) and advanced further to multi-locational trials (AYT) while implementing participatory approaches involving farmers and processors in selection. The PYT will also be conducted over several sites to determine the performance and stability of different traits of interest under diverse environment. The new promising cultivars should be tested at different sites and the best harvesting dates should be established.

References

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