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Farmers' participatory selection for early bulking cassava genotypes in semi-arid Eastern Kenya

Joseph Kamau[1]*, Rob Melis[2], Mark Laing[2], John Derera[2], Paul Shanahan[2] and Eliud C. K. Ngugi[3]

[1]Kenya Agricultural Research Institute- Katumani, Kenya.
[2]University of KwazuluNatal- Petermaritzburg, Kenya.
[3]University of Nairobi, Kabete campus, Kenya.

Cassava is an important food security crop in semi-arid, Eastern Kenya, but production is constrained by planting late bulking landraces. Therefore, farmer participatory variety selection was initiated with the aim of identifying early bulking varieties with preferred root qualities. Four popular local varieties were crossed with six early-bulking varieties selected from IITA germplasm in a North Carolina II mating scheme. The resultant 225 cloned F_1 progenies were evaluated for early bulking in a 15 x 15 simple lattice design with two replications at KARI-Kiboko farm in Eastern Kenya. Sixty-five farmers participated in the selection of early bulking genotypes with preferred root qualities during the second and third harvests at 7 and 8 months after planting. At 7 months, there was a significant variation among genotypes for root bulking, cyanide content, dry matter content, harvest index and root number. Farmers subjected all the genotypes to a preference test and selected 30 genotypes (13%), which combined early-bulking and high root quality. A selection index based on farmers' ranking of agronomic traits was then imposed on the selected 30 genotypes to identify those that were superior in both agronomic and end-user traits for possible release and advancement. The selected genotypes were all significantly superior to the parents. The top 10 genotypes displayed above average performance for all agronomic traits. Involving farmers in selection helped to identify early bulking genotypes with end-user root qualities that could/should ultimately accelerate their adoption.

Key words: Cassava, participatory, early bulking.

INTRODUCTION

One of the major limiting factors for cassava production in the semi-arid areas is lack of appropriate varieties. PRA studies in the past, revealed that drought was the most limiting production constraint followed, in the order of importance, by lack of planting materials, pests and diseases. Early bulking varieties with end-user root qualities could enhance cassava production in the semi-arid areas if they could be harvested between 6 to 8 months after planting. Farmers that participated in PRA studies requested that the cassava breeder involve them during the selection process to ensure that genotypes with the required root qualities were identified at an early stage.

Early studies on root bulking in cassava were started by physiologists wanting to know when storage root development started in different genotypes (Doku, 1969). In the early 1970s, when CIAT and IITA were established, root bulking was used in germplasm characterisation to group accessions into early and late bulking. The different groups were to be used in the breeding programme to develop germplasm adapted to different agro-ecological zones (Wholey and Cock, 1974). This germplasm was used later to develop early bulking germplasm at the two institutions for the semi-arid areas (Hershey, 1984). Among the national programmes to benefit from this early work was Brazil, which used the early bulking germplasm from CIAT to develop early bulking varieties for their semi-arid areas (Fukuda et al.,

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*Corresponding author. E-mail: jkamauw@yahoo.com.

2002).

There is no above ground morphological trait that can be associated with root bulking. In the absence of such traits, Kawano et al. (1978) recommended the use of root yield at harvest to assess for early bulking. However, IITA (1993) reported that performance of genotypes at the early stage of the growth cycle might not necessarily predict their performance in later stages. CIAT demonstrated that harvest index (HI), observed at the F_1 seedling and first clonal trials, remained constant in subsequent advanced field trials in a wide range of environmental conditions (Kawano, 1990). Therefore, harvest index is a better trait to select for than root yield.

Storage root development starts when the plants are 1 month old. Differences in the rate of bulking account for differences in root yield after 6 month (CIAT, 1972). In grain crops, variability in rate of grain filling accounted for 70 to 80% of the differences in yield potential of hybrids (Daynard, 1969). Wholey and Cock (1974) observed differences in the rate of bulking in three cassava varieties which was attributed to the differences in root yield.

Early bulking is important in the semi-arid areas to allow harvesting after only one cycle of rain or immediately after the second rain season. Studies at CIAT and in Brazil found that it was not difficult to identify early bulking genotypes for the semi-arid environments. The major difficulties were, in achieving acceptable dry matter content and the end-user root quality requirements (CIAT, 1994). Acceptable root qualities can only be defined by the end-users. In order to identify the genotypes with the preferred root qualities, breeders should involve the end-users in the selection process at the early stage of breeding, so that selection is applied on a broad range of genotypes. This is termed participatory plant breeding (PPB), which ensures that only the genotypes with the right root qualities for the target agro-ecological zone are released as commercial varieties (Fukuda et al., 2000; Fukuda and Saad, 2001; Ceccarelli and Grando, 2007).

In the semi-arid areas, subsistence farmers are generally resource-poor and must deal with poor and erratic rainfall. They plant a range of crops and varieties suited to different land, soil and moisture conditions that guarantees some harvest, even when rains are late or end early. The wide range of crops and varieties counter the uncertainty of the weather. In such environments, PPB has proved useful. In Mexico for instance, PPB was used to improve maize productivity with small-scale farmers (Fujisaka et al., 1997). It has been found to increase adoption rate of new varieties, which farmers have participated in selecting (Mikkelsen, 1995). Thus, in the current study, a participatory variety selection was applied in breeding early bulking and adoptable cassava genotypes in Eastern Kenya. Good breeding progress will be realised by applying high selection intensity, which

depends on the proportion selected). Breeding progress is realised by applying high selection pressure on diverse germplasm with new and valuable alleles (Falconer and Mackay, 1996; Banziger et al., 2000). In the current study, farmers selected cassava genotypes from a large population created by crossing popular local varieties with early-bulking and elite genotypes from IITA.

MATERIALS AND METHODS

Parental genotypes

Four popular local varieties (820001, 820058, 990010 and 990014) and six IITA varieties 960249, 990056, 9900676, 990072, 990127 and 990183 were crossed in a North Carolina II design mating scheme to produce F_1 genotypes. F_1 seedlings were planted in a trial at KARI-Kiboko in December, 2004. The best genotypes were selected, primarily on the basis of resistance to cassava mosaic, and planted in the first clonal trial. This trial was planted at Kiboko in June, 2005. The trial experienced a high incidence of red and green spider mites. The best performing clones were selected for evaluation in the second clonal trial.

Field trials

The second clonal performance trial was planted on December, 2005 at Kiboko farm with 225 F_1 genotypes selected from the earlier clonal trial. The 10 parents were planted in plots of two rows of 12 plants, repeated twice, adjacent to the trial. The trial was planted in a 15 x 15 lattice design with two replications. Each clone was planted in two rows of 12 plants each at the commercial spacing for cassava (1 x 1 m). The stakes planted were cut from stems that were 6 month old, not the recommended age of 8 to 18 month (Lozano et al., 1977). At planting, three plants were intended to be harvested on each plot at 6, 7 and 8 month after planting. Harvesting was done by pulling plants out by hand and digging out any roots left in the ground with a hoe.

Shoot weight was determined by weighing the aerial parts (stems and leaves) and the rootstock. The number of tuberous roots per plant were counted and weighed. The root cyanide content was determined by the alkaline picrate method (Williams and Edward, 1980) and scored on a scale from 1 (<10 mg kg^{-1}) to 9 (>150 mg kg^{-1}). Root dry matter content was estimated from the specific gravity method (Kawano, 1987) using the formula: DM % = 158.3 x [weight in air / (weight in air – weight in water)] – 142, while dry matter yield was estimated as follows:

Dry matter yield = root yield x dry matter content

Biomass, harvest index, and root yield per hectare were estimated using the data as follows:

(i) Root yield (t ha^{-1}) = root weight (kg m^{-2}) x 10000 / 1000 kg
(ii) Biomass (kg plant^{-1}) = shoot weight + root weight
(iii) Harvest index = (root weight / biomass) x 100%

Farmer-participatory selection

Using the Ministry of Agriculture extension officers, 65 cassava farmers were invited from Kiboko, Mulala, Nguu and Makindu divisions to participate in the selection of early bulking genotypes at

Table 1. The grouping of scores that were used by farmers to select the best genotypes.

Raw roots		Cooked roots		Aggregate score (raw + cooked)	
Total score across groups	Preference	Total score across groups	Preference	Total score across groups	Preference
4	Very acceptable	3	Very acceptable	7	Very acceptable
5 –8	Fairly acceptable	4 - 6	Fairly acceptable	8-15	Fairly acceptable
12	Not acceptable	9	Not acceptable	16 -21	Not acceptable

the second and third harvesting (at 7 and 8 month after planting). Sixty-five of the farmers were over 30 years, 92% had primary and secondary education and 52% were women. Farmers were selected from different villages in the divisions on the basis of being cassava growers and members of the local farmer groups. The role of the farmers was to ensure identification of genotypes that combine early bulking and preferred root qualities. They were accompanied by their local extension officers. Farmers assembled at the trial and were briefed on the importance of their invitation. Together with the breeder and the social economist, the group, led by one of the farmers, brainstormed on the important qualities they would use to select the genotypes with preferred qualities. To be consistent, they agreed to use root size, appearance, taste and fibre content of both raw and cooked roots as selection criteria. Genotypes, that had marketable roots at 7 month, were considered early. Assessment was based on a 'Yes' or 'No' vote by the majority of the farmers. Size was used to select only those genotypes that had roots big enough to be cooked. All the roots harvested from each plant were presented to the farmers to make their decision based on root size.

Farmers, in groups of 13, chewed small pieces of the roots and rated each genotype as follows:

(i) Appearance   (1= very acceptable; 2= acceptable; 3= not acceptable).
(ii) Taste/ texture (1= sweet/mealy, 2=medium, 3= bitter/waxy).
(iii) Fibre (1= few fibres; 2=medium fibrous; 3= very fibrous).
(iv) Size (1= large/marketable; 2= medium; 3= not marketable) (rated for raw roots only)

Overall acceptability of each genotype was based on the aggregate sum of raw and cooked tubers, scores as indicated below:

(i) Aggregate score of 7 = very acceptable;
(ii) Aggregate score of 8 to 15 = fairly acceptable;
(iii) Aggregate score of 16 to 21 = not acceptable).

This rating procedure was adopted with modification from Kiarie et al. (1991). Preference data from the five groups of 13 farmers was pooled (summed) and the average score tabulated (Table 3). Texture was combined with taste of the cooked root to give a single score. Roots of genotypes that had acceptable size were peeled and chopped into small cubes and placed on labelled plates. Any genotype that had an aggregate score of more than 4 for raw roots or 3 for cooked root was excluded (Table 1).

The roots were peeled and washed with clean water. Roots of each genotype were put in separate polythene bags with a manila label indicating the genotype. They were placed in pots with water. The pots were placed over a fire, covered and allowed to boil for 10 min until the roots were cooked. Once cooked, the pots were removed from the fire, the water drained and they were left to cool. The roots were removed and placed on labelled plates arranged on tables. Using the small groups of 13 farmers, all the cooked roots were evaluated for palatability, one genotype at a time.

The selection index was applied to discriminate between the genotypes that were selected on the basis of the aggregate score of farmers' preferences. The criteria used in calculating the selection index was based on the importance farmers put on the various agronomic traits. Farmers were requested, as a group, to give the importance of each of the following traits: root yield, dry matter yield, ratio of roots to the other plant parts (harvest index %), root cyanide, root number and aerial parts (shoot weight). Farmers agreed on a scale (1 = least important and 5 = most important) that the breeder was to impose on selected genotypes, to identify those that combined high farmers' preferences with high agronomic performance. The weight for each trait used in calculating selection index was as follows: (the letter is the code of each trait u,v,w,x,y and z are used in the model below):

Root yield	(u)	5
Dry matter yield	(v)	4
Harvest index %	(w)	3
Root cyanide	(x)	-3
Root number	(y)	2
Shoot weight	(z)	1

Negative number indicates that the trait was not desired. Standardisation of the phenotype means (P_i) measured in the separate trials was incorporated into the selection index to enable comparisons to be made as follows: $P_i = (x_{ij} − m_i)/s_i$, Where, x_{ij} is the value of the trait i measured on genotype j, while m_i and s_i are the mean and standard deviation, respectively, of trait i in a population. The selection index of each genotype was calculated as follows using the weights of the agronomic traits:

Selection index = $[((u_{ij} − m_i)/s_i)*5 + ((v_{ij} − m_i)/s_i)*4 + ((w_{ij} − m_i)/s_i)*3 + ((x_{ij} − m_i)/s_i)*-3 + ((y_{ij} − m_i)/s_i)*2 + ((z_{ij} − m_i)/s_i)*1]$ (Banziger et al., 2000)

Where the numbers (5,4,3,-3,2,1) represent the weights of importance to each agronomic trait as indicated above.

Analysis of data for agronomic traits

Agronomic data were analysed using the GenStat Version 9 statistical software package. Time of harvesting, families and the crosses nested within families were considered fixed effects, while replications, blocks within replications and error were considered random effects in the model, as follows:

$Y_{ijklm} = U + r_i + r(b)_{ij} + f_k + f(c)_{kl} + t_m + (t.f)_{km} + f(c).t_{kml} + e_{ijklm}$, (Ott, 1993), Where;

Table 2. REML Analysis of various agronomic traits measured per plant across the families, and crosses within the families at 3, 6, 7 and 8 mo after planting.

Source	d.f.	SHWT	sign	RTN	sign	RTW	sign	Biomass	sign	HI%	sign	DM%	sign	RCNP	sign
								Mean square values							
Time	2	119.20	***	21.62	***	262.10	***	190.55	***	45.76	***	146.95	***	33.31	***
Family	3	1.78	ns	4.13	**	14.46	***	3.65	*	3.34	*	3.12	*	0.77	ns
Time x family	6	1.95	ns	0.11	ns	0.34	ns	1.35	ns	1.44	ns	0.16	ns	1.80	ns
Family/cross	219	1.27	**	1.43	***	3.91	***	1.79	***	1.99	***	1.58	***	1.04	ns
Time x family/ cross	438	0.99	*	0.97	*	1.00	ns	0.97	ns	0.95	*	1.15	*	0.79	ns

*, ** and *** is significant at 5%, 1% and 0.1% ; SHWT – shoot weight (kg plant^{-1}), RTN – root numbers per plant, RWT – root weight (kg plant^{-1}), HI% – harvest index, DM% - dry matter content, RCNP – root cyanide content.

Table 3. Mean values, standard error (S.E) of the new genotypes and the average range of each trait over the three harvests (6, 7 and 8 months after planting).

Trait	Mean	S.E.	Minimum	Maximum
Root weight (kg plant^{-1})	2.50	0.24	0.78	6.03
Dry matter content (%)	34.50	0.37	17.85	45.00
Harvest index (%)	45.00	0.01	10.00	69.00
Root cyanide content (score)	4.00	0.13	2.00	5.00
Root number per plant	9.00	0.27	3.00	15.00
Shoot weight (kg plant^{-1})	3.98	0.52	0.68	9.91
Total biomass (kg plant^{-1})	6.42	0.77	1.49	13.45

Y_{ijkm} = trait measured in the jth block in the ith replication corresponding to the ith cross of the kth family measured ant the mth time, U = overall mean, r_i = i^{th} *replication effects*, $r(b)_{ij}$ = j^{th} block within i^{th} replication effects, f_k = k^{th} family effects, f_k (c_l) = i^{th} cross within k^{th} family effects, t_m = m^{th} time effects, $(f.t)_{km}$ = km^{th} family by time interaction effects, $f(c).t_{kml}$ = interaction between families f_k and crosses within a family $f(c)_k$ and time t_m, e_{ijklm} k= random error effects.

RESULTS

Agronomic traits

Families were significantly different for root weight per plant, root number per plant, biomass per plant, percentage harvest index and dry matter (Table 2). The new genotypes were significantly different for all traits except root cyanide content (Table 2). The crosses also exhibited wide variation for the various traits with root weight ranging from 0.8 to more than 6 kg/plant (Table 3).

The second harvest at 7 month was used as the primary selection date for early bulking genotypes which combined end-user preferences by farmers. At 7 month the parents were significantly different for all traits except harvest index and shoot weight. The new genotypes were

significantly different for all traits except root cyanide content and shoot weight (Table 4).

Root weight of the parents ranged from 0.7 to 1.9 kg/plant, while that of the new genotypes varied from 0.6 to 5.6 kg/plant, indicative of the progress made in developing early bulking varieties (Table 2). The new genotypes had significantly improved harvest indices (max. 58.5%), compared to that of the parents (max. 37.8%) (Table 2).

Participatory selection

At 7 and 8 months after planting (Figure 1), farmers identified three classes of genotypes based on their aggregate scores (Table 1). At 7 month after planting, farmers selected 30 genotypes that were early bulking with what they considered to be very acceptable attributes. At 8 month after planting an additional 21 genotypes were selected, which were considered medium in bulking.

The grouping according to the farmers' preference aggregate score of the parents and the new genotypes at 7 and 8 month are presented below (Figure 2). Using aggregate preference scores at 7 month after planting,

Table 4. REML analysis of variance of parents and new genotypes at 7 month after planting.

	Parents			New genotypes		
Source	df	ms		df	ms	
Root weight (kg plant^{-1})	9	4.46	***	222	2.46	***
Harvest index (%)	9	1.77	ns	222	1.87	***
Dry matter content (%)	9	2.10	*	222	1.24	**
Root cyanide content (score)	9	18.23	***	222	0.99	Ns
Root number (count)	9	2.43	**	222	1.42	***
Shoot weight (kg plant^{-1})	9	0.25	ns	222	1.01	Ns

*, ** and *** is significant at 5, 1 and 0.1%, ns - not significant.
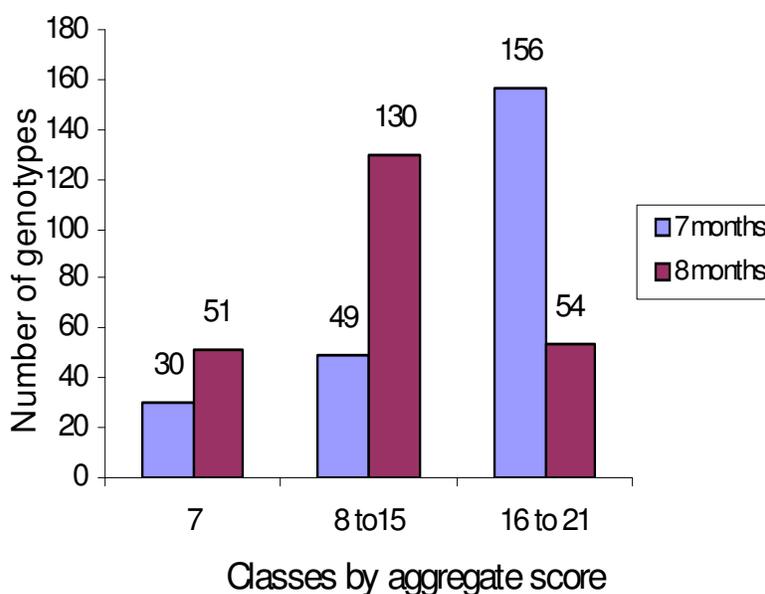
Figure 1. Classification of genotypes according to farmers' preference scores.

the farmers selected 30 crosses out of a total of 225 new genotypes, which amounted to a selection pressure of 13%. At 8 mo after planting (Figure 3), there were additional genotypes that had edible roots, resulting in the selection of a total of 51 of the best early to medium bulking genotypes from a total of 225, equalling a final selection pressure of 22%.

Selection index

The selection index was used to rank the 30 new genotypes, selected by the farmers, in order to identify the best ten. A comparison of the 10 best genotypes with the original parents clearly shows the progress achieved

in the breeding (Table 5). The average root weight of the 10 best new genotypes was more than three times higher than the mean root yield of the parents. The harvest index of the new genotypes was 1.95 times higher than the index of the parents, while the dry matter content was 7.4% higher than that of the parents. These data are indicative of considerable genetic gain.

It appears that involvement of farmers increased the selection intensity compared to selection based on root yield alone at 7 months after planting. Farmers' selection of 30 out of 225 genotypes (13%) is equivalent to a high selection intensity of 1.76 assuming normal distribution as described by Falconer and Mackay (1996). However, if the breeder could have used root yield, as the sole criterion to select early bulking genotypes, more than 100
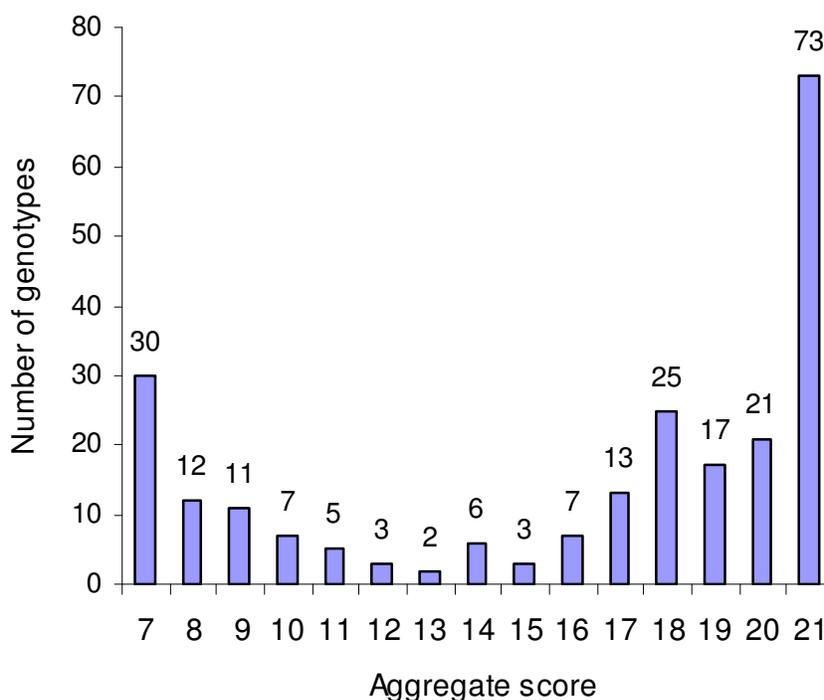
Figure 2. Frequency distribution of the 235 genotypes including 10 parents for preference score at 7 months after planting.
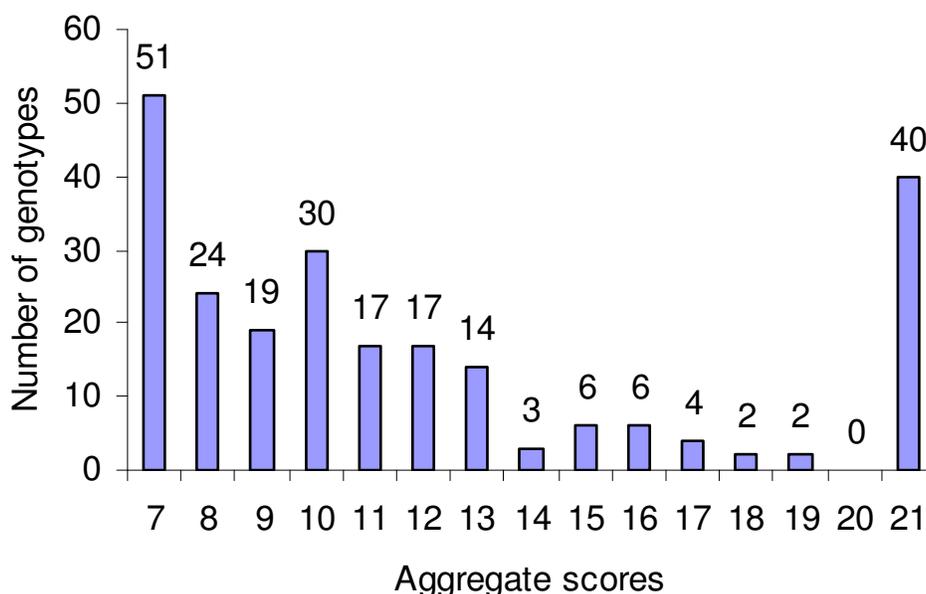
Figure 3. Frequency distribution of 225 genotypes for preference at 8 months after planting.

genotypes or 42% would have been selected, which results in a low selection intensity of 0.97. Comparison of root weight of each of the 10 best new genotypes with the root weight of each of their parents demonstrates the possible response to selection in root weight (Figure 4).

DISCUSSION AND CONCLUSION

The aim of this study was to identify genotypes that combined early bulking and end-user preferences from the progenies of crosses between six early bulking IITA

Table 5. Mean of agronomic data, preference aggregate score and selection index of 10 best new genotypes and 10 parents.

Crosses	Family	Pedigree	Means from REML analysis						Preference aggregate score	Selection index
			SHWT	RTN	RTW	HI%	DM	RCNP		
Cross 139	990010	990010 x 990183 P4R1B1	6.49	14	5.56	48.19	39.57	5	7	26.04
Cross 53	990014	990067 x 990014 P1R1B1	3.65	11	4.39	53.09	38.97	3	7	22.8
Cross 146	820001	990056 x 820001 P4R2B6	5.56	11	4.35	46.49	38.55	4	7	19.06
Cross 214	820001	990067 x 820001 P8R2B3	2.99	10	3.84	54.54	39.25	4	7	16.47
Cross 168	820001	820001 x 960249 P1R1B7	5.83	12	3.93	43.49	37.07	3	7	15.69
Cross 92	820001	820001 x 990183 P1R1B5	5.9	11	4.4	45.37	34.3	4	7	15.55
Cross 188	990014	990067 x 990014 P8R2B5	5.87	11	3.57	42.33	36.92	3	7	14.47
Cross 104	990010	990010 x 990127 P9R1B6	4.31	11	3.79	46.8	40.28	4	7	14.06
Cross 98	820058	990067 x 820058 P1R1B5	3.53	10	3.5	48.89	36.45	3	7	13.44
Cross 14	990010	990010 x 990127 P8R1B6	2.38	8	2.65	53.46	39.01	3	7	11.06
Mean			4.651	11	3.998	48.265	38.037	3.6		
Parents										
990127	IITA		3.75	12	1.75	37.83	35.6	5	18	18.68
990072	IITA		3.75	10	1.87	32.78	35.01	4	17	15.86
990183	IITA		4.05	11	1.65	29.87	35.75	5	18	10.87
990067	IITA		3.85	9	1.51	27.76	34.83	4	17	6.3
990056	IITA		2.92	11	1.38	31.98	37.68	4	18	2.82
990014	Local		4.5	10	0.73	14.07	36.24	5	18	-17.35
990010	Local		3.85	9	0.68	15.09	36.76	8	19	-19.68
960249	IITA		4.02	10	1.51	27.37	31.66	5	17	13.59
820058	Local		4.1	9	0.75	15.48	34.68	5	19	-14.31
820001	Local		4.38	9	0.73	14.3	35.68	3	19	-16.73
Mean			3.917	10	1.256	24.653	35.389	4.8		

SHWT – shoot weight (kg plant^{-1}), RTN – root number, RTW – root weight (kg plant^{-1}), HI – harvest index, DM% - percentage dry matter content, RCNP – root cyanide content. Preference score - genotypes with an aggregate score of seven were the best, 8 to15 acceptable and 16 to 21 not acceptable. Farmers weights on the different traits shoot weight – 1, root yield – 5, dry matter yield – 4, harvest index – 3 and root cyanide - (-3).

cassava varieties and four local landraces. The progenies were initially evaluated in a seedling trial, cloned and advanced to the first clonal trial which, was harvested at 6, 7 and 8 months after planting and agronomic data and farmers' aggregate scores recorded. The agronomic data was used to estimate the selection indices that were used to rank the farmers' selected genotypes. Finally, after using the selection index, the ten best genotypes, with superior end-user preferences and yield, were identified.

Large variation in shoot weight, root weight, root yield, and dry matter content was an indication of the wide genetic variation for these traits present in the population of 225 crosses. Kawano et al. (1978) reported that root yield was the best criteria for selecting early bulking cassava genotypes. However, in this study, farmers' criteria for selecting early bulking genotypes were used in combination with measured, agronomic data. From the yield data at 7 months, several new genotypes yielded more than 4.1 kg/plant, with one new genotype, number 139 yielding 5.5 kg/plant. These high root yields, observed in the crosses at 7 months, were comparable with those observed by Williams (1974) at 8 months after planting. In future studies it would be advisable to start selecting as early as 5 and 6 months after planting in order to be able to identify the very early bulking genotypes.

Harvest index in cassava is little affected by the environment and is a good indicator of the potential performance of a genotype across agro-ecological zones (Kawano, 1990). The 10 new genotypes all had harvest indices over 40% and some were even over 50%, which is very high according to the CIAT classification (Kawano, 1990). A few genotypes, which were not part of the genotypes selected by the farmers, had harvest indices ranging from 57 to 64%, which is very high according to the optimum 50 to 60% for cassava (Williams, 1974; Iglesias et al., 1994).

Average dry matter content for the 10 best genotypes
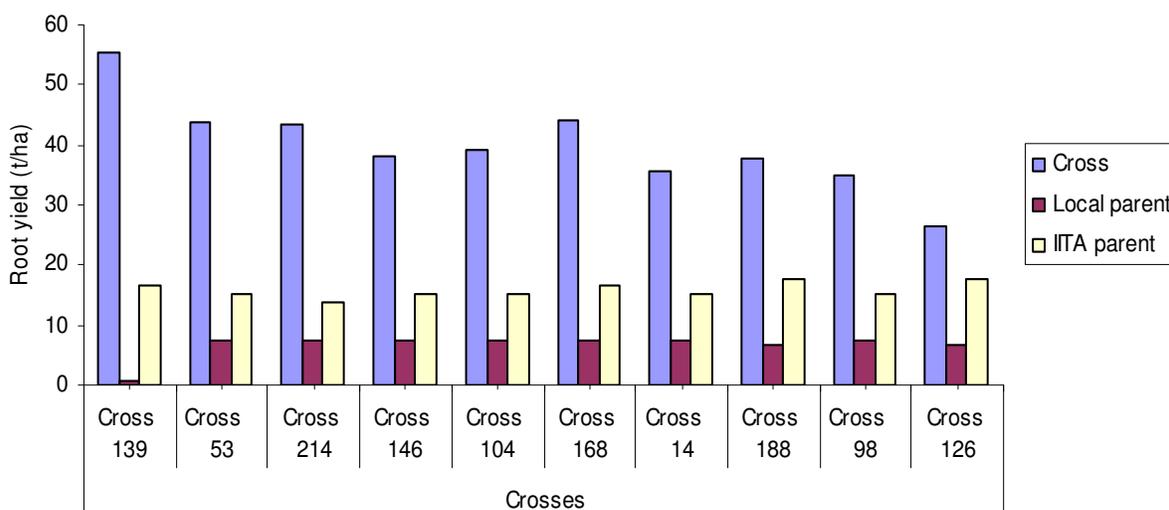
Figure 4. Comparison of the best 10 crosses from the 30 selected by farmers identified through selection index with their parents.

was 34%, which compared well with 30 to 35% of the popular local parents. A number of new genotypes had dry matter contents between 41 and 45%, but these roots were often fibrous and therefore rejected by the farmers. The high dry matter content exhibited by the new genotypes was clearly superior to all the parents, indicating that some significant improvement was achieved and contradicted previous reports from CIAT (1994) that it is very difficult to attain high dry matter content and the preferred root qualities. The PPB selection by the farmers proved to be a fast and simple method to identify superior genotypes. The farmers in most cases appeared to use the same criteria as a breeder would. The farmers' selection process was holistic, combining several agronomic and storage root quality traits at the same time. The selection was based on consensus building process, where farmers discussed until the majority voted for or against.

Using preference scores, a total of 30 early bulking and 21 medium bulking genotypes were selected by the farmers. The 30 early bulking genotypes selected, represented a 13% selection pressure, resulting in a high selection intensity of 1.76 (Falconer and Mackay, 1996). If root yield was the sole criterion for selection, over 100 genotypes that had more than 3.0 kg/plant would have been selected that is, 42%, equivalent to a lower selection intensity of 0.97. The PPB enabled incorporation of a preference aggregate score, thereby ensuring a higher selection intensity (i), and together with a large population (n = 225) of the new genotypes would increase response to selection. The study has shown that farmers clearly do not select varieties on the basis of root yield alone, but consider other quality traits, which breeders often ignore. Similar sentiments have been

reported from Colombia (CIAT, 1994), where it was found to be essential that farmers participate in selection, and which may assist in the future adoption of the varieties selected. In Tanzania, Kapinga et al. (1997) reported better adoption when farmers were involved in selection.

Farmers' selection helped to bring down the final number of superior genotypes, based primarily on root yield and root qualities (taste, appearance, fibre content etc). Several selected genotypes, such as numbers 53,139, and 146, were highly superior to the best parental genotype (990127), in root yield as well as dry matter content, showing strong progress in breeding and an indication of transgressive segregation and hybrid vigour. Merging the farmers' preference aggregate score and the selection index based on the agronomic data, assisted in the final identification of the best genotypes developed in the breeding programme.

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