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Full Length Research Paper

A breeding scheme for local adoption of cassava (*Manihot esculenta* Crantz)

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In many rural communities, cassava mosaic disease (CMD) resistant varieties are being rejected by farmers owing to their inferior root qualities when compared to locally adapted varieties. In response to this challenge, we implemented a breeding scheme whose objective was to combine CMD resistance with farmer preferred root qualities, whose genes were respectively sourced for elite and local varieties. We targeted to achieve this goal within five years that comprised of: i) hybridization of complementary parental lines, ii) seedling evaluation trial (SET); iii) clonal evaluation trial (CET); iv) modified preliminary yield trial (MPYT) and v) modified uniform yield trial (MUYT). At SET and CET, emphasis was placed on traits of moderate to high heritability while for MPYT and MUYT emphasis was on traits of low heritability. Generated F_1 progeny (4080 half sibs) were established in SET of which 1014 seedlings were selected and advanced to the CET. At CET, only 143 clones were selected and advanced. Under MPYT, slightly less than 50% of the clones were selected, while under MUYT, (8 to 40 clones per site) were selected. Clones selected per site were characterized by: DMC (28 to 38%); ii) HI (0.26 to 0.62); iii) yield (14 to 59 t/ha), resistance to CMD and desirable farmer root qualities. Given this outcome, we have demonstrated the utility of this scheme in accelerating development of locally adapted cassava varieties and thus propose the scheme be referred to as "speed cassava breeding".

Key words: Cassava breeding, half sibs, local varieties, selection index.

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a popular and widely grown crop in tropical Africa (Nweke et al., 2002). Thus, interventions aimed at increasing its productivity would significantly improve its contribution towards food and nutrition security and income of communities heavily dependent on this crop. This premise is based on previous findings that technologies generated through plant breeding have played a significant role in providing basic human needs (Frey, 1992). Indeed, plant breeding has been broadly viewed as a powerful driver for achieving both economic and social advances as clearly demonstrated by the Green Revolution in Asia and meso-American countries that benefited from the high-yielding wheat and rice varieties that were developed then.

For cassava, the domestication process, which in part involved selections by subsistence farmers, began the era of cassava breeding. Involvement of trained breeders only began in the early twentieth century, with the pioneer breeding programmes that were established in India, Brazil, Madagascar, Tanzania, Nigeria, Indonesia, Senegal, Democratic Republic of Congo and Côte d'Ivoire (Hershey, 2011). Years later, in the late 1960s, two international centres, International Institute of Tropical Agriculture (IITA) and International Centre for Tropical Agriculture (CIAT) were established and furthered cassava breeding in partnership with the national agricultural research systems (NARS) of Africa, Asia and Latin America (Kawano, 2003; Ceballos et al., 2004; Hershey, 2011). These research centres (IITA and CIAT) had vibrant cassava breeding programmes with varying objectives depending on the prevailing local needs, regional and or global mandates.

For example in Africa, emphasis was initially placed on breeding for CMD resistance and bacterial blight (Jennings,

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Table 1. Parental lines used in the polycross to generate half-sib F_1 families at Namulonge during growing season 2003/2004.

Parental genotype	Clone name	Source	CMD reaction
Bamunanika	Local variety	Central Uganda	Susceptible
Kakwale	Local variety	Central Uganda	Susceptible
Bao	Local variety	Northern Uganda	Susceptible
Nyaraboke	Local variety	North-western Uganda	Susceptible
TME5	Local variety	IITA	Resistant
TME14	Local variety	IITA	Resistant
95/SE-00036	95/SE-00036	IITA	Resistant
NASE12	MH95/0414	IITA	Resistant
NASE10	95/NA-00063	IITA	Resistant

1957; Hahn et al., 1980; IITA, 1990), while CIAT largely focused on improvement of yield through selection for harvest index (Kawano, 2003). However, over the years, both IITA and CIAT, the major cassava breeding centres, have transformed to nearly have the same breeding objectives (Ceballos et al., 2004; Hershey, 2011). The principal output of most of these cassava breeding programmes has been genetically improved germplasm and information (that is, evaluation and selection schemes for cassava) that is intended for use by farmers and NARS breeders (Ceballos et al., 2004; Ojulong et al., 2008; Hershey, 2011).

In the case of Uganda, up to 12 high-yielding and CMD resistant varieties were released during the period 1990 to 2000. However, as CMD incidence and severity decreased, farmers reluctantly cultivated these improved varieties, and resorted back to their locally adapted varieties, for which, they have had a long historic association with (Gorrettie Nankinga Personal Communication). This was partly attributed to the notion that many of the released varieties lacked desirable root quality attributes (taste, mealiness, texture and aroma) that the locally adapted varieties had. This reversion by farmers to local CMD-susceptible varieties after the control of the CMD pandemic required a timely and concerted breeding intervention, which was the focus of this work. It suffices to note that for most NARS breeding programmes, release of a new cassava variety can take between eight to ten years depending on whether the IITA or the CIAT cassava breeding scheme is adopted (IITA, 1990; Ceballos et al., 2004).

Both the IITA and CIAT cassava selection schemes are characterised with:

(1) Reduced number of clones per advanced evaluation stage.
(2) Farmer participation in the final stages.
(3) Selection of clones with broad adaptability and not location-specific selection.
(4) Different experiment layout, that is, use of unreplicated trials in earlier stages at single locations and then replicated trials in latter stages at different locations.

To increase cassava variety adoption by farmers and also to reduce costs, we modified the CIAT and IITA schemes with the objective of developing a cassava improvement scheme appropriate for our local needs, that takes up to five years only that include: F_1 seed generation, seedling evaluation trial (SET), clonal evaluation trial (CET), modified preliminary yield trial (MPYT) and modified uniform yield trial (MUYT), with farmers participating in the location specific-selection process at both MPYT and MUYT. This modified scheme is uniquely characterised with:

(1) Omission of the preliminary yield trial which is often conducted at a single location.
(2) Location-specific selection and hence the term “breeding scheme for local adoption of cassava”.
(3) Participation of farmers in evaluation and selection at both MPYT and MUYT.

Our quest for farmer involvement in the selection process was to increase chances of adoption of the developed varieties. This paper discusses how we used this modified scheme to develop and disseminate improved cassava varieties that combined CMD resistance and desirable farmer preferred root qualities.

MATERIALS AND METHODS

Parental selection, hybridization and seedling evaluation

Five CMD resistant parental lines (SE/95-00036, NASE10, NASE12, TME14 and TME5) from IITA and four local varieties with farmer preferred culinary root qualities, but susceptible to CMD (Kakwale, Bamunanika, Nyaraboke and Bao) were selected and established in a polycross mating design during 2003/2004. Our interest was not to evaluate the breeding value of parental lines, but rather to generate a base population for selection and we thus used a polycross. Pedigree information on the parental lines is provided in Table 1. At harvest, seeds were collected from each parental line and bulked to form nine half-sib families. In April 2005, seeds from each family were planted in a seedling nursery at Namulonge, central Uganda. At the height of 20 to 25 cm, the seedlings were transplanted to the field at spacing of 1 × 1 m for evaluation. CMD was evaluated using a scale of 1 to 5; where 1 = highly resistant

and 5 = highly susceptible (IITA, 1990). Only seedlings with CMD severity score in the rating of between 1 and 2 were advanced for the CET.

Clonal evaluation trial (CET)

The CET was established at Namulonge as single-row unreplicated plots of eight plants each. Progeny from each family were separated into three groups randomly allocated to one of the three blocks. During evaluation of the CET, emphasis was placed on traits of moderate to high heritability: plant type, CMD resistance, and HI. Three data sets at three, six and nine (MAP) were collected on CMD, whose pressure is high at Namulonge. This was done using a scale of 1 to 5 (IITA, 1990). Plant type was scored using a scale of 1 to 3, were 1 = poor plant type; 2 = average plant type and 3 = good plant type.

Plant type considers the overall architectural outlook of the plant including branching height, branching angles, and levels of branching. At harvest 12 months after planting (MAP), six plants per clone were uprooted and used for assessment of HI as described by Kawano (1990). All the generated data was used for selection. The selection index (SI) was computed using the formula:

$(V_{PT} \times 2 + V_{HI} \times 4 - V_{CMD} \times 4)$

where V_{PT} is the plant type; V_{HI} is the HI and V_{CMD} is the reaction to CMD.

The weights associated with each variable reflect the assigned level of importance attributed to it, while the negative signs are used for those traits where lower values represent the most desirable phenotypes (Ceballos et al., 2004). Because of the differences in units for the variables used, data were initially standardized per block prior to its utilisation in the SI. Further, because the trial was established in three blocks, with each family represented in a block, selection was done per block. Each selected clone was chopped into at least 36 stakes to establish two replicate plots in the modified preliminary yield trial (MPYT).

Modified preliminary yield trial (MPYT)

A typical preliminary yield trial is established at one location (IITA, 1990). However, in this study, six sites were selected for the MPYT: [Namulonge (central Uganda), Nakasongola (a drought prone area in central Uganda), Bulindi (north-western Uganda), Kigumba (north-western Uganda), Ngetta (northern Uganda) and Kamuli (eastern Uganda)]. The selected regions are major cassava growing areas characterized by different cassava utilization patterns, differing soil types and seasonal patterns. Since at MPYT there were fewer clones, we established replicated two-row plots at this locations and invited farmers to participate in evaluation and selection.

A different number of clones were evaluated per site: Namulonge (123 clones), Ngetta (129), Nakasongola (30), Kigumba (29), Kamuli (22) and Bulindi (24). Each site received a sub-set of clones derived from the different families. It is only Namulonge and Ngetta that nearly had a complete set of all advanced clones from the CET. At all sites, evaluations were made for HI, DMC and cassava brown streak disease (CBSD) root necrosis. Estimation of DMC was based on the specific gravity method (Kawano et al., 1987). Severity of CBSD was scored for all harvested roots using a scale of 1 to 5, where: 1 = no visible necrosis; 2 = < 2% necrosis; 3 = 2 to10% necrosis; 4 =10 to 30% necrosis and; 5 = > 30% necrosis (Hillocks et al., 2001).

Because of the differences in units for the variables measured (HI, DMC and CBSD), mean values were standardized prior to their utilisation in the SI. The SI was computed using the formula:

$(V_{DMC} \times 3 + V_{HI} \times 3 - V_{CBSD} \times 4)$

where V_{DMC} is the DMC; V_{HI} is the HI; and V_{CBSD} is CBSD root necrosis score.

In addition, at each site, farmers (cassava growers for a period of not less than 10 years) comprising five men and five women were identified to help in culinary tests of the selected varieties. The attributes examined included: taste (sweet, fairly sweet, flat, slightly bitter and bitter); mealiness (mealy, average, watery); texture (fairly hard, fibrous, hard, soft); and flavour (aroma or no aroma). These evaluations were done on cooked cassava roots, which is the preferred method of food preparation in Uganda. Basing on these root quality attributes together with the measured agronomic traits, a clone was selected for advancement to the next evaluation stage, the modified uniform yield trials (MUYT).

Modified uniform yield trial (MUYT)

A typical uniform yield trial is established at different sites with same genotypes (IITA, 1990). However, in this study, the MUYT trials were established at Namulonge (40 clones); Ngetta (28); Nakasongola (13); Kigumba (9); Kamuli (8); and Bulindi (8). At each site, 4-replicate plots were established per clone**.** At this stage**,** evaluations were made as described for the MPYT but with two additional traits, fresh root yield and root cyanogenic potential (CNp). Fresh root yield was measured from all the plants harvested from the 2-inner rows per plot and converted to tones/ha. Root CNp was estimated from harvested root samples using the enzymatic assay method as described by Cooke (1978). Accordingly, the SI was computed using the formula:

$(V_{HI} \times 1 + V_{DMC} \times 1 + V_{YIELD} \times 3 - V_{CNp} \times 2 - V_{CBSD} \times 3)$

where V_{DMC} is the DMC; V_{HI} is the HI; V_{YIELD} is fresh root yield; V_{CNp} is total cyanogens; and V_{CBSD} is CBSD root necrosis score.

As described for MPYT, the same farmers were again involved in the selection process. The selected clones at each site were thereafter established on farmer's fields for multiplication.

Since cassava evaluation and selection is undertaken at different stages with varying number of entries and experimental layout per stage, we examined realised heritability (H) to enable us make a comparative analysis at different stages. H is based on the effect of selection that is actually maintained in the next cycle of propagation and this was estimated using the formula:

$H = R/S$

where R is the selection response and S is the selection differential in the population in which actual selection was made (Hill, 1972). The R and S values were estimated between evaluation stages: a) CET and MPYT, and b) MPYT and MUYT. These estimates were computed only for HI data because: 1) HI was the trait measured throughout the evaluation stages and 2) HI is one of the most critical agronomic traits in cassava, as direct selection for HI is more important than direct selection for fresh root yield (Kawano, 2003).

RESULTS

The data presented herein presents a genetic improvement scheme that began with parental hybridization

Table 2. Seedling evaluation trial established at Namulonge during the growing season 2004/2005.

Family	F_1 seeds generated	F_1 seedlings evaluated	CMD severity	Selected F_1 seedlings (%)
Bamunanika	2500	1232	3.6	11.2
Kakwale	940	447	2.9	26.3
Bao	215	194	2.8	20.6
Nyaraboke	1200	534	3.3	17.4
TME5	1890	658	2.2	35.2
TME14	220	210	2.1	40.4
95/SE-00036	1200	173	1.9	68.2
NASE12	600	32	1.8	68.7
NASE10	600	600	2.5	41.8
Total	9365	4080		

followed by four annual evaluation and selection stages that comprised of SET, CET, MPYT and MUYT. The data from the SET is presented in Table 2. Pollination efficiency varied among the parental lines and hence the different numbers of F_1s generated and evaluated. The parental lines: NASE12, 95/SE-00036, TME14, TME5 and NASE10 generally produced many CMD-resistant progeny as reflected by the family CMD scores that ranged between 1.8 and 2.5 (Table 2). Progeny from the parental line Bamunanika were most susceptible to CMD with family average of 3.6 (Table 2). Selections made at SET largely focused on reaction to CMD and plant type. Basing on these two traits, >35% progeny in the CMD resistant parental lines NASE12, 95/SE-00036, TME14, TME5 and NASE10 were selected and advanced, while < 20% of progeny from CMD susceptible parental lines Bamunanika and Nyaraboke were selected and advanced (Table 2).

The data generated from the CET is presented in Table 3. Generally, most of the evaluated clones were resistant to CMD as reflected by the low family average CMD scores that ranged between 1.0 and 1.5 (Table 3). Data on HI varied both between the families and the evaluation blocks (Table 3). It was generally observed that progeny derived from parental lines Kakwale, NASE10, TME14, Nyaraboke, and TME5, had HI values >0.4. On average, progeny from Bao had the lowest HI (Table 3). The SI varied among the blocks (Table 3). For example within Block 1, SI ranged from -19.4 to +19.1; for Block 2, (-19.0 to +30.9); and for Block 3 (-18.5 to +13.7). This justifies the need to separate families into blocks especially when evaluating several clones as often done at CET.

The check clone MH96/2961 had a value of 5.89 and thus, a cut-off score of >6.0 was used in the selection of clones for advancing. With the exception of NASE12 family, over 70% of progeny from the other families were rejected at CET. Thus, of the evaluated 1014 clones, only 143 clones (representing 14%) derived from different parental lines were selected and advanced (Table 3).

The results of the MPYT are presented in Table 4. With selection to CMD having been done twice at both SET and CET, in the MPYT, emphasis shifted to CBSD, which was by then rapidly spreading in Uganda. Results indicated that progeny from TME14 consistently had lower CBSD root severity score that ranged between 1.0 - 1.4 (Table 4). Progeny from parental lines Bao, NASE12, Nyaraboke, 95/SE-00036, and NASE10 could at some locations attain an average root CBSD score of 2 (Table 4). On average DMC ranged between 34.5% for progeny evaluated at Namulonge to 38.1% for progeny evaluated at Nakasongola. At both Ngetta and Namulonge, progeny derived from Nyaraboke consistently had the highest average DMC (Table 4). However, progeny derived from Bao also had higher average DMC at Kigumba (41.7%), Bulindi (39.2%) and Nakasongola (40.0%). Just like DMC in the MPYT, average HI ranged from 0.34 for progeny evaluated at Namulonge to 0.57 for progeny evaluated at Nakasongola. It was generally observed that progeny from NASE10 consistently had relatively higher HI > 0.40 (Table 4). Compared to HI values obtained at CET, we observed an increase in HI at MPYT particularly for the progeny in the families SE/95-00036 (18.9% increase); Bao (15.8%); NASE10 (11.3%); Bamunanika (11.4%) and Nyaraboke (9.1%). When the three traits (DMC, HI and CBSD) were constituted into a SI and farmer's input considered at each site, over 50% of the clones were not selected at the various selection sites (Table 4).

The results of the MUYT are presented in Table 5. Under the MUYT we noted an increase in root severity of CBSD, with severity of >2 being recorded at all evaluation sites. In fact, this increased CBSD incidence contributed to the rejection of a significant number of clones at the MUYT. Root DMC was on average higher for clones evaluated at Ngetta (40.7%) and lowest for clones evaluated at Namulonge (30.1%). It was further observed that at each evaluation site, clones with >35% DMC were identified (Table 5). Clones evaluated at the MUYT, had generally higher HI (>0.4). CNp was highly variable with some clones having >300 mg HCN/kg on dry weight basis. On average, clones evaluated at Namulonge, Ngetta and Nakasongola had relatively higher CNp.

Table 3. Clonal evaluation trial established at Namulonge during growing season 2005/2006.

Family	Block	No. of clones	Mean CMD	Mean HI	Min. SI	Max. SI	Selected clones
Bamunanika	1	37	1.3	0.57	-12.0	13.3	4
Bamunanika	2	35	1.1	0.30	-7.6	10.9	2
Bamunanika	3	34	1.2	0.27	-10.1	6.4	2
Bao	1	8	1.2	0.41	-14.3	7.9	1
Bao	2	9	1.2	0.36	-5.5	13.3	4
Bao	3	6	1.5	0.25	-14.5	4.9	0
Kakwale	1	39	1.1	0.68	-13.2	20.2	6
Kakwale	2	31	1.1	0.38	-13.7	9.3	5
Kakwale	3	34	1.2	0.28	-14.2	13.7	4
NASE10	1	81	1.1	0.58	-12.9	15.2	8
NASE10	2	82	1.1	0.39	-13.7	14.1	18
NASE10	3	83	1.1	0.35	-10.9	12.2	18
NASE12	1	9	1.0	0.51	-2.0	10.6	1
NASE12	2	10	1.0	0.41	-5.3	30.9	6
NASE12	3	9	1.0	0.24	-9.5	11.8	3
Nyaraboke	1	27	1.5	0.57	-7.8	10.8	3
Nyaraboke	2	28	1.2	0.37	-10.8	9.5	2
Nyaraboke	3	26	1.2	0.30	-10.5	8.8	3
SE95/00036	1	23	1.0	0.56	-7.4	6.5	3
SE95/00036	2	24	1.2	0.32	-16.3	12.3	4
SE95/00036	3	15	1.0	0.22	-5.3	10.2	4
TME14	1	29	1.3	0.51	-11.6	15.2	7
TME14	2	30	1.2	0.41	-6.8	11.2	8
TME14	3	28	1.2	0.35	-8.1	11.4	9
TME5	1	96	1.5	0.57	-19.4	19.1	7
TME5	2	96	1.1	0.34	-19.0	8.4	5
TME5	3	85	1.1	0.32	-18.5	12.3	6

Min. SI = minimum selection index value; Max. SI = maximum selection index value. The check clone MH96/2961 had a SI value (V_{PT} ×2 + V_{HI} × 4 – V_{CMD}×4) of 5.89 and thus, a cut-off score of > 6.0 was used in the selection of clones for advancing.

Similarly, yield data was highly variable with some clones yielding >25 t/ha (Table 5).

When the five traits (CBSD, DMC, HI, CNp and fresh root yield) were constituted into a SI and farmer's input considered at each site, >75% of the clones were not selected for advancement; the extreme scenario was observed at Bulindi where no clone was selected (Table 5). The specific details of the selected clones at the MUYT are presented in Table 6. Depending on the selection site, the selected clones had:

(1) DMC values that ranged from 28 to 38%.
(2) HI that ranged from 0.26 to 0.62.
(3) CBSD score of either 1 or 2.
(4) CNp that was less than 300 mg HCN/kg on dry weight basis.
(5) Yield that ranged between 14 to 59 t/ha.

Further, basing on the farmer's evaluation criteria, majority of the selected clones were sweet in taste, mealy and soft in texture, and had good aroma (Table 6).

Data on response to selection, selection differential and realized heritability for HI are presented in Table 7. For the selection from CET to MPYT, it was observed that highest response to selection and hence released (> 0.55) for most locations except at Kamuli and Kigumba

Table 4. Modified preliminary yield trial established at six sites in Uganda during the growing season 2006/2007.

Site	Family	No. of clones	DMC (%)	HI	CBSD	Min. SI	Max. SI	Selected clones
Namulonge	Bamunanika	8	33.9	0.39	1.8	-9.7	3.7	0
	Bao	5	33.6	0.28	1.5	-20.3	5.6	1
	Kakwale	13	32.3	0.36	1.3	-42.1	8.8	4
	NASE10	42	34.6	0.36	1.4	-16.7	7.9	14
	NASE12	6	33.9	0.38	1.3	-9.2	5.2	1
	Nyaraboke	9	36.0	0.35	1.1	-4.4	7.9	6
	SE95/00036	12	34.5	0.34	1.7	-19.6	3.5	0
	TME14	19	35.9	0.32	1.2	-14.7	10.4	8
	TME 5	19	35.4	0.30	1.3	-10.1	11.6	6
	Check clone	3	35.4	0.39	1.5	-0.02		
Ngetta	Bamunanika	8	34.1	0.32	1.2	-14.3	1.1	0
	Bao	5	29.2	0.34	1.6	-34.8	4.3	1
	Kakwale	14	34.9	0.35	1.4	-42.3	4.4	1
	NASE10	41	37.8	0.43	1.5	-40.5	10.1	11
	NASE12	5	35.9	0.37	1.5	-12.4	2.4	0
	Nyaraboke	8	38.9	0.42	1.5	-12.6	12.2	2
	SE95/00036	12	38.5	0.38	1.4	-16.1	14.4	1
	TME14	17	38.9	0.39	1.4	-11.4	12.9	6
	TME 5	19	32.8	0.39	1.2	-39.2	11.4	6
	Check clone		38.1	0.41	1.0	4.1		
Nakasongola	Bamunanika	3	37.1	0.56	1.3	-5.9	1.5	0
	Bao	1	40.0	0.59	2.0	-0.9	-	0
	Kakwale	4	38.8	0.58	1.5	-8.9	10.9	2
	NASE10	8	38.6	0.62	1.8	-17.1	6.5	4
	NASE12	1	35.0	0.50	2.0	-11.4	-	0
	Nyaraboke	2	37.6	0.63	2.0	-6.3	1.5	0
	SE95/00036	2	40.8	0.60	2.0	-6.8	7.5	1
	TME14	4	38.9	0.59	1.2	-11.1	8.9	3
	TME 5	5	38.1	0.62	1.3	-6.9	10.1	3
	Check clone		36.7	0.49	1.0	-3.0		
Kigumba	Bamunanika	4	35.7	0.36	1.4	-4.8	1.8	1
	Bao	2	41.7	0.34	2.2	-8.7	-1.5	0
	Kakwale	2	36.9	0.50	1.0	0.3	5.7	1
	NASE10	6	36.7	0.57	2.0	-10.0	3.1	1
	NASE12	4	36.9	0.42	1.2	-8.6	4.2	1
	Nyaraboke	4	38.1	0.52	1.1	-2.0	7.2	3
	SE95/00036	2	34.3	0.53	1.0	0.54	1.6	0
	TME14	3	39.5	0.47	1.2	-2.2	6.9	2
	Check clone		35.3	0.40	1.0	-1.3		
Bulindi	Bao	1	39.2	0.42	2.0	0.43	-	0
	Kakwale	3	34.7	0.50	1.0	1.25	7.7	2
	NASE10	12	33.9	0.52	1.5	-8.6	7.9	4
	SE95/00036	2	37.1	0.49	2.0	-4.8	3.4	1
	TME14	1	31.5	0.47	1.0	-2.1	-	0
	TME 5	4	35.3	0.40	1.7	-9.5	0.9	0
	Check clone		37.5	0.43	1.0	4.3		

Table 4. Contd.

	Kakwale	1	40.0	0.32	1.0	2.0	-	1
	NASE10	9	39.8	0.44	1.7	-6.7	8.8	3
	Nyaraboke	1	37.7	0.41	1.5	-0.8	-	0
Kamuli	SE95/00036	2	35.5	0.37	1.5	-5.6	-2.9	0
	TME14	5	38.2	0.41	1.3	-10.8	9.0	3
	TME 5	4	39.3	0.42	1.6	-2.7	1.8	1
	Check clone		32.0	0.33	1.0	-4.7		

Min. SI = minimum selection index value; Max. SI = maximum selection index value. The check clone MH96/2961 SI value derived from the formula ($V_{DMC} \times 3 + V_{HI} \times 3 - V_{CBSD} \times 4$) was used as the cut-off in the selection of clones for farmer selection and advancing. – indicates that because only one clone was evaluated, SI could only be computed.

heritability was observed at Nakasongola, while the lowest was at Namulonge, where, no response was where no response was observed.

DISCUSSION

The data presented herein presents an account of a rapid improvement scheme for locally adapted cassava varieties. This genetic improvement scheme began with parental hybridization followed by four critical annual evaluation and selection stages that comprised of: SET, CET, MPYT and MUYT. Principally, the SET and CET that had ≥1000 clones for evaluation were carried out at a single site at Namulonge, while the MPYT and MUYT that had ≤143 clones for evaluation were conducted at six different sites with farmer participation in the selection process. Because of no replication in the SET and CET, emphasis for selection was placed on traits of moderate to high heritability, that is, CMD resistance, HI and plant type, while for MPYT and MUYT that were replicated, emphasis was placed on traits of low heritability, that is, fresh root yield, root CNp and CBSD reaction.

So often, the attainment of cassava breeding objectives by NARS breeding programmes is largely achieved through adoption of either the IITA or CIAT cassava improvement schemes that do not take less than six years and have limited farmer involvement in the selection process.

In our cassava breeding scheme that was tailored to local needs of subsistence farmers, the objective was to combine pest and disease resistance particularly CMD resistance, with desirable root culinary qualities, and this was to be achieved within a relatively short period with increased involvement of farmers in the selection process. This breeding scheme took five years. The first year involved generation of up to 9365 F_1 botanical seeds. Year two involved the conduction of the SET at a single site with 4080 seedlings. Year three involved the conduction of the unreplicated CET at a single site with a total of 1014 clones. Year four involved the conduction of the replicated MPYT at six sites with clones ranging from 22 to 129 per site. Uniquely, the MPYT also involved the observed. On the other hand, for the selection from MPYT to MUYT, response to selection was much higher participation of farmers in the selection process at each site. Year five involved the conduction of the replicated MUYT at six sites with participation of farmers in the selection process. This multi-stage cassava evaluation and selection process resulted into the identification of seven outstanding cassava clones, whose application for official release has been submitted.

The SET established at one location (Namulonge) largely focused on reaction to CMD. Namulonge is an optimal selection site for CMD evaluation as it has a mixture of different strains of cassava mosaic virus including the highly devastating *Ug* strain (Sserubombwe et al., 2008). At SET, family responses to CMD varied, with progeny derived from CMD resistant parental lines, that is, NASE12, 95/SE-00036, TME14, TME5 and NASE10 having relatively lower CMD severities. Nonetheless, from all the nine families, progeny with acceptable CMD resistance (score of 1 or 2) were identified indicating high heritability of CMD resistance and perhaps good combining ability of these parental lines. Evaluations at SET are based on single plant evaluations, which can be largely biased especially when evaluating traits of low heritability.

It is for this reason that selected seedlings are cloned and re-evaluated in the CET, where evaluations are made on 6 to 10 plants per genotype. However, selection at SET offers the advantage of working with a reduced number of clones in subsequent stages and thus reducing costs associated with evaluation of clearly undesirably phenotypes that will eventually be discarded in latter evaluation stages.

When the selected 1014 seedlings (25% of the population) were established in CET, they were evaluated for three traits: plant type, HI and CMD. These traits are of moderate to high heritability (Hahn et al., 1979; Ceballos et al., 2004). Under intercropping systems that characterize subsistence farming, varieties with the umbrella and/or cylindrical shapes are desirable. This is largely because they will form fewer canopies and hence limit competition with the low-growing crops in the intercrop. On the other hand, under monoculture, open

Table 5. Modified uniform yield trial established at six sites in Uganda during the growing season 2007/2008.

Site	Clones evaluated	Clones selected	CBSD			DMC			HI			CNp			Yield (t/ha)		
			Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean
Namulonge	43	5	1.0	3.8	2.5	20.0	38.0	30.1	0.26	0.55	0.41	114.9	395.1	249.1	0.7	26.3	11.6
Ngetta	30	1	1.0	5.0	2.2	36.4	45.2	40.7	0.28	0.64	0.49	67.1	463.1	246.9	7.8	50.0	21.5
Nakasogola	14	1	1.0	3.0	2.1	30.0	40.0	34.8	0.59	0.71	0.65	99.7	559.4	244.8	6.4	39.6	24.5
Kamuli	8	2	1.0	3.0	2.0	30.0	40.0	35.9	0.31	0.50	0.41	170.8	321.6	243.3	6.7	22.2	13.8
Kigumba	10	1	1.0	3.6	2.2	26.0	38.7	33.6	0.47	0.67	0.48	137.1	358.4	231.1	17.2	36.4	26.9
Bulindi	8	0	1.0	2.8	2.4	32.4	40.0	36.7	0.42	0.64	0.52	131.1	366.1	239.4	11.6	35.7	20.7

Table 6. Performance of selected varieties under the modified uniform yield trial at the respective selection sites.

Site	Family	Selected clone	DMC	HI	CBSD	CNp	Yield (t/ha)	Taste	Mealiness	Texture	Aroma
Kamuli	TME14	Clone 28	38.0	0.50	2	170.9	59.7	Sweet	Mealy	Soft	Aroma
	TME14	Clone 109	38.0	0.46	1	298.7	28.5	Slightly bitter	Mealy	Hard	Aroma
		MH97/2961	34.0	0.21	2	168.6	26.6	Sweet	Mealy	Soft	Aroma
		I92/0067	35.0	0.38	2	187.4	24.5	Sweet	Mealy	Soft	Aroma
Kigumba	Bamunanika	Clone 266	30.0	0.51	2	265.1	35.7	Sweet	Mealy	Soft	Aroma
		MH97/2961	34.0	0.41	2	228.0	24.8	Sweet	Mealy	Soft	Aroma
Nakasongola	TME14	Clone 72	35.0	0.62	2	250.8	23.8	Bitter	Mealy	Soft	Aroma
	Kakwale	Clone 349	34.0	0.53	1	226.3	45.8	Sweet	Mealy	Soft	Aroma
		I92/0067	30.0	0.67	3	103.8	24.1	Sweet	Mealy	Hard	Aroma
Ngetta	TME14	Clone 109	-	0.32	2	103.1	28.8	Sweet	Mealy	Soft	Aroma
		MH97/2961	41.0	0.37	2	270.6	23.0	Sweet	Mealy	Soft	Aroma
Namulonge	TME14	Clone 28	35.0	0.45	2	218.4	25.5	Sweet	Mealy	Soft	Aroma
	TME14	Clone 72	28.0	0.45	1	168.4	19.7	Sweet	Mealy	Soft	Aroma
	TME14	Clone 67	30.0	0.45	1	265.1	18.3	Sweet	Mealy	Soft	Aroma
	TME14	Clone 52	38.0	0.39	2	391.6	21.3	Sweet	Mealy	Soft	Aroma
	TME14	Clone 109	33.0	0.26	2	137.9	14.0	Sweet	Mealy	Soft	Aroma
		MH97/2961	33.0	0.35	3	231.2	11.9	Sweet	Mealy	Soft	Aroma

and/or compact plant types are required to control weed infestation. Since plant type is highly heritable, selection for the two plant types (umbrella and/or compact) were considered at the CET so that farmers involved in selection at latter stages (MPYT and MUYT) could make selections from reduced and manageable numbers of clones.

For the CET evaluations, CMD was being done

Table 7. Response to selection, selection differential and realized heritability for harvest index at different stages of evaluation and selection.

Location	Selection from CET to MPYT[1]			Selection from MPYT to MUYT[2]		
	Response to selection (R)	Selection differential (S) of CET	Realised heritability (H)	Response to selection (R)	Selection differential (S) of MPYT	Realised heritability (H)
Namulonge	-0.05	0.26	-0.19	0.07	0.10	0.70
Ngetta	0.01	0.26	0.03	0.09	0.12	0.75
Nakasongola	0.21	0.26	0.80	0.05	0.09	0.55
Kamuli	0.02	0.26	0.07	0.00	-0.01	0.00
Bulindi	0.10	0.26	0.38	0.03	0.05	0.60
Kigumba	0.09	0.26	0.34	0.00	0.08	0.00

[1]For CET to MPYT, R = mean for all clones evaluated at specific location under MPYT less the mean of all clones evaluated under CET; S = mean of selected clones less the mean of the unselected clones under the CET. [2] For MPYT to MUYT, R = mean for all clones evaluated at a specific location under MUYT less mean of all clones evaluated at specific locations under MPYT; S = mean of selected clones less the mean of the unselected clones under the MPYT. The negative values are ~ = 0.00.

for the second time, while HI was being evaluated for the first time. Previous studies have established that HI is one trait that can substantially increase cassava productivity and that indirect selection for yield through HI is more important and effective than direct selection for fresh root yield in early stages of evaluation (Kawano et al., 1998; Kawano, 2003). It was against this background that these traits were evaluated in the CET. Thus, clones selected for CMD resistance, high HI and desirable plant type at CET using a combined selection index ($V_{PT} \times 2 + V_{HI} \times 4 - V_{CMD} \times 4$), will most likely express the same phenotypes at latter selection stages.

Our forte for this is that all the three traits evaluated at CET are of moderate to high heritability. It was this premise that was used during the implementation of the CET and hence the selection of the outstanding clones in each block and family for advancing for the multi-locational MPYT. Of the evaluated 1014 clones at the CET, only 143 (14.1% of the breeding population) were selected, implying that approximately 86% of the breeding population at the CET was not advanced to the MPYT.

In practice, most preliminary yield trials (implemented after CET) are conducted at the same location with two replicates (Kawano et al., 1998; Ceballos et al., 2004). In our breeding scheme however, we conducted the two-replicated preliminary yield trial in six different sites, with each site having different sets of cassava clones. This MPYT is a slight modification of the traditional preliminary yield trial in that:

(1) Each site evaluated a different set of clones and thus focuses on location-specific selection and not broad adaptability.
(2) Clones evaluated at a specific site are derived from parental lines that are locally adapted and/or popularly grown in that location.
(3) Farmers are involved in the selection process.

These three endeavors make this evaluation scheme slightly different from the traditional preliminary yield trial and hence the name MPYT. A major justification of this scheme is that only outstanding clones (which are a significantly reduced and manageable number selected from the CET) based on highly heritable traits, are being evaluated under specific local conditions in partnership with the ultimate beneficiaries, the farmers. This provides for best opportunities for variety identification and adoption, as experienced farmers are involved in the selection and evaluation process.

At MPYT, three traits were measured in replicated plots: HI, DMC and root CBSD severity. Thus, HI was being evaluated the second time, while DMC and CBSD were being evaluated for the first time. High DMC has been, and continues to be a major breeding objective of most cassava programmes, while tolerance and/or resistance CBSD as a breeding objective, is largely limited to the East and Southern Africa region (Ceballos et al., 2004; Hershey, 2011). Indeed, in Uganda, the disease was reported at high incidence in 2006 and hence the need to screen the developed cassava populations at MPYT.

Because HI is highly heritable and high values are desirable (Kawano, 2003; Ceballos et al., 2004), it is not surprising that most clones evaluated at MPYT had HI > 0.4. Indeed, HI in MPYT increased by over 10% (for some families),

when CET and MPYT harvest index (average values) are compared. This finding corroborates earlier findings that indicated that selection for HI will be effective at any stage of evaluation (Kawano et al., 1998). Similar observations were made for CMD response at MPYT, where most clones had severity scores of either 1 or 2 that reflected high levels of CMD resistance. This finding suggests that with optimum CMD pressure at an evaluation site, field assessments of CMD at SET and CET can suffice to categorise cassava clones as either susceptible or resistant and hence a decision made to either advance and/or reject a clone.

Results indicated that DMC was on average higher for clones evaluated at Ngetta (40.7%) and lowest for clones evaluated at Namulonge (30.1%). Further, each selection site had some clones that had > 35% DMC. Previous studies in Uganda have indicated that DMC is highly variable ranging from 16.4 to 49.6 % with averages of 39.3 and 37.2% respectively for elite and local varieties (Kawuki et al., 2011). Compared to these studies, we note that DMC values obtained in MPYT are relatively higher.

This is most likely due to the fact that clones evaluated at MPYT had gone through two propagation cycles of evaluation and selection for two key agronomic traits, CMD resistance and HI that have a bearing on root DMC. Just like DMC, CBSD was evaluated for the first time at the MPYT. CBSD attained epidemic status in 2006 when it was observed in most cassava growing regions of Uganda (Alicai et al., 2007). This rapid spread of CBSD in the country was unusually high and coincided with the implementation of the MPYT. We therefore had to include CBSD evaluation at MPYT. This is a classical example that demonstrates typical field challenges experienced by cassava breeders and thus the need to be responsive to emerging challenges. Though the evaluation sites had varying CBSV inoculum pressure, we observed root severity score of > 2 at all the evaluation sites. To increase precision, CBSD was given the highest weight: ($V_{DMC} \times 3 + V_{HI} \times 3 - V_{CBSD} \times 4$) and it's partly for this reason that over 50% of clones at all the sites were rejected, as they had succumbed to the disease.

Only with the initiation of bigger plot sizes and more replicates being adopted was the emphasis shifted to traits of low heritability, such as fresh root yield and CNp. Thus, at the MUYT five traits were evaluated: CBSD, DMC, HI, CNp and fresh root yield. Because evaluation and selection at the SET, CET and MPYT stages was largely based on traits of moderate to high heritability, the clones evaluated at MUYT are by far outstanding and hence the need to examine their yield potential and CNp toxicity levels prior to their official release. Indeed, by the implementation of the MUYT over 90% of the starting population had been rejected. It is worthy to mention that HI was being evaluated for the third time given its significance, DMC and CBSD for the second time, while CNp and fresh root yield for the first time. These traits were assigned different weights with traits of low heritability (CNp and CBSD) assigned relatively higher weights: ($V_{HI} \times 1 + V_{DMC} \times 1 + V_{YIELD} \times 3 - V_{CNp} \lambda 2 - V_{CBSD} \times 3$).

Thus, based on the quantitative data and farmer preferences, variable number of clones was selected per site. Of interest however, was the selection of a number of progeny from TME14 family that included clones: 28, 52, 67, 72 and 109 (Table 6), which suggest that the parental line TME14 could be a good combiner for a number of agronomic traits that were examined.

Conclusion

This study presents an account of our pioneer efforts to breed for locally adapted cassava varieties in partnership with the cassava famers. This scheme, a slight modification of the IITA breeding scheme, was accomplished within five years that involved four critical stages: SET, CET, MPYT and the MUYT. Participatory evaluations with farmers for key agronomic and culinary qualities (taste, mealiness, texture and aroma) have been done twice, at the MPYT and MUYT, which were characterized with reduced number of clones and bigger plot sizes that typify subsistence farm conditions. We are therefore confident that the selected varieties will be rapidly adopted at the respective selection sites and thus, recommend this breeding scheme for breeding programmes that target subsistence farmers. Because during participatory approaches farmers select for present needs and not for tomorrow, we are currently broadening our germplasm base through undertaking continued hybridization of local varieties with both CIAT and IITA elite lines, with a goal of generating heterogeneous populations from which future selections will be made. Developed elite lines are also being hybridized among themselves to generate base populations for further selection and advancement.

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REFERENCES

Alicai T, Omongo CA, Maruthi MN, Hillocks RJ, Baguma Y, Kawuki R, Bua A, Otim-Nape GW, Colvin J (2007). Re-emergence of cassava brown streak disease in Uganda. Plant Dis., 91: 24-29.

Ceballos H, Iglesias CC, Pérez JC, Dixon AGO (2004). Cassava breeding: opportunities and challenges. Plant Mol. Biol., 56: 503-515.

Cooke RD (1978). An enzymatic assay for the total cyanide content of cassava (*Manihot esculenta* Crantz). J. Sci. Food Agric., 29: 345-352.

Frey KJ (1992). Plant breeding perspectives for the 1990s. In:

Stalker, H.T., and J.P. Murphy (eds.), Plant breeding in the 1990s, Proceedings of the symposium on plant breeding in the 1990s held at North Carolina State University Raleigh, NC. CAB International Wallingford Oxon OX10 8DE, UK, pp. 1-13.

Hill WG (1972) Estimation of realized heritabilities from selection experiments. II. Selection in one direction. Biometrics, 28: 767-780.

Hillocks RJ, Raya MD, Mtunda K, Kiozia H (2001). Effects of brown streak virus disease on yield and quality of cassava in Tanzania. J. Phytopathol., 149: 389-394.

Hershey C (2011). Cassava breeding: Theory and practice. A publication by Food and Agriculture Organisation (FAO), In press.

Hahn SK, Terry ER, Leuschner K (1980). Breeding cassava for resistance to cassava mosaic disease. Euphytica, 29: 677-683.

Hahn SK, Terry ER, Leuschner K, Akobunda IO, Okali C, Lal R (1979). Cassava improvement in Africa. Field Crops Res., 2: 193-226.

IITA (1990). Cassava in tropical Africa. A Reference Manual. International Institute of Tropical Agriculture, Ibadan, Nigeria.

Jennings DL (1957). Further studies in breeding cassava for virus resistance. East Afr. Agric. J., 22: 213-219.

Kawano K (2003). Thirty years of cassava breeding for productivity-biological and social factors for success. Crop Sci., 43: 1325-1335.

Kawano K, Narintaraporn K, Narintaraporn P, Sarakarn S, Limsila A, Limsila J, Suparhan D, Sarawat V, Watananonta W (1998). Yield improvement in a multi-stage breeding program for cassava. Crop Sci., 38: 325-332.

Kawano K, Goncalves WMF, Cenpukdee U (1987). Genetic and environmental effects on dry matter content of cassava root. Crop Sci., 27: 69-74.

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

Kawuki RS, Ferguson M, Labuschagne M, Herselman L, Orone J, Ralimanana I, Bidiaka M, Lukombo S, Kanyange MC, Gashaka G, Mkamilo G, Gethi J, Obiero H (2011). Variation in qualitative and quantitative traits of cassava germplasm from selected national breeding programmes in sub-Saharan Africa. Field Crops Res., 122: 151-156.

Nweke F, Spencer D, Lynam J (2002). The cassava transformation: Africa's best kept secret. Michigan State University Press, East Lansing, USA.

Ojulong H, Labuschagne MT, Fregene M, Herselman L (2008). A cassava clonal evaluation trial based on a new cassava breeding scheme. Euphytica, 160: 119-129.

Sserubombwe WS, Bridden RW, Baguma Y, Ssemakula, GN, Bull SE, Bua A, Alicai T, Omongo C, Otim-Nape GW, Stanley J (2008). Diversity of begomoviruses associated with mosaic disease of cultivated cassava (*Manihot esculenta* Crantz) and its wild relative (*Manihot glaziovii* Mull. Arg.). Uganda. J. Gen. Virol., pp. 1759-1769.