Application for release of cassava varieties

Kawuki, R.S., Pariyo, A., Tumwesigye, S., Bua, A., Baguma, Y., Omongo, C.A., Alicai, T., and Orone, J.

National Crops Resources Research Institute (NaCRRI), P.O. Box 7084, Kampala Uganda

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APPLICATION FOR RELEASE OF CASSAVA VARIETIES

NAME OF APPLICANTS:	**Area of specilaisation**
Robert Kawuki	Plant Breeding and Genetics
Anthony Pariyo	Plant Breeding and Genetics
Steven Tumwesigye	Food Science and Technology
Anton Bua:	Agricultural Economics
Yona Baguma:	Molecular Biology
Chris Omongo:	Vector entomology
Titus Alicai:	Plant pathology

NAME OF INSTITUTE	National Crops Resources Research Institute (NaCRRI) P.O. Box 7084, Kampala, Uganda
SPECIES:	*Manihot esculenta* (Crantz)
ORIGIN OF PARENTS	International Institute of Tropical Agriculture (IITA-Nigeria) introductions and Ugandan land races.
MODE OF GERNERATION OF TEST MATERIALS	Natural sexual recombination
LOCATIONS OF EVALUATION AND SELECTION	Namulonge, Nakasongola, Kigumba, Bulindi, Ngetta and Kamuli
END USE	Human, livestock feed and industrial use
CHECK VARIETIES	Elite genotype from IITA (I92/0067)

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Summary

Initiatives to increase cassava production and productivity in Uganda with the dual roles of increasing food security and household income have long been a major objective of the National Cassava Programme (NCP). Attainment of this goal requires that cassava breeding be highly responsive to emerging demands. Accordingly, the NCP initiated a decentralized breeding scheme that focused on the introgression of cassava mosaic disease (CMD) resistance genes into locally adapted varieties; the local varieties are presumed to have farmer preferred culinary root qualities. The CMD resistance genes were sourced from elite genotypes from the International Institute of Tropical Agriculture (IITA). This initiative, which began in 2003, has resulted in the identification of seven outstanding cassava varieties (28-TME14, 109-TME14, 266-BAM, 349-KAK, 72-TME14, 67-TME14 and 52-TME14). Of these, we seek permission to officially release three (28-TME14, 266-BAM and 349-KAK), which have divergent background. The others that are not released will be used as elite parental lines in subsequent hybridization and/or inbreeding schemes. .

The selected varieties were generated from a polycross mating scheme that comprised of five elite (TME 5, TME 14, NASE 12, NASE 10, SE95/00036) and four local (Kakwale, Bao, Nyaraboke, Bamunanika) varieties. Generated F_1 progeny from the nine half-sib families were evaluated in a single-row trial at Namulonge. Thereafter, selections were made and clones were subjected to a decentralized evaluation scheme at six sites including Namulonge (central region), Nakasongola (central and drought prone region), Bulindi (western region), Kigumba (North western region), Ngetta (northern region) and Kamuli (eastern region). Selections and evaluations at these respective sites were jointly done by both farmers and scientists for a period of three years. Thus, the selected varieties have effectively been evaluated for five consecutive years.

Specifically, these varieties have been evaluated for desirable agronomic (plant health, plant type, yield potential) and root quality (cyanogens, taste, mealyness, texture and aroma) traits. Root quality traits were examined because they are increasingly becoming apparent that desired quality characteristics vary widely from one region to another and thus distinct quality characteristics may be required for a specific region. By the time of initiation (2003/2004) of the polycross that resulted into the identification of the selected varieties, cassava brown streak disease (CBSD) wasn't a breeding objective. However, as the selected progeny were being advanced to subsequent evaluation stages, the prevalence of CBSD was on the increase, and this required that screening for CBSD resistance be immediately started at the respective sites.

At Kigumba, the selected variety (266-BAM) is a half-sib of local variety Bamunanika. This variety is mealy, soft and has aroma. This variety had dry matter content (DMC) ranging between 30-35.4%; harvest index (HI) ranging between (0.50-0.51) and a CBSD root score of 2. At Nakasongola, the selected varieties (72-TME14 and 349-KAK) were respective half sibs of TME 14 and a local variety Kakwale. These varieties had DMC ranging between 34-44%; HI ranging between 0.53-0.62 and a CBSD root score of 2. At Kamuli, the selected varieties (28-TME14 and 109-TME14), were both halfsibs of TME 14. Both had DMC above 35%; HI above 0.50 and a CBSD root score of 2.

At Namulonge, where a complete set of genotypes were evaluated, five varieties (some of which had earlier been selected at other sites), were selected and these included: (72-TME14, 67-TME14, 52-TME14, 28-TME14, 109-TME14). The selected varieties had DMC (28 - 38%); HI (0.26 - 0.45); yield (14 - 25.5 t/ha) and a CBSD root score of 2. Moreover, these genotypes were characterized as sweet, mealy, soft and with aroma.

Average CNp for the selected varieties varied between the selection sites: 228.0-265.1 mg HCN/kg on dry weight (Kigumba); 170.9-298.7 mg HCN/kg on dry weight /kg (Kamuli); 137.9-391.6 mg HCN/kg on dry weight /kg (Namulonge); and 226.3 - 250.8 mg HCN/kg on dry weight /kg for the selections at Nakasongola. With the exception of the variety at Namulonge (52-TME14), which had CNp levels of 391.6 mg HCN/kg on dry weight /kg, all other selected varieties had CNp levels that are less than 300 mg HCN/kg on dry weight /kg, and hence regarded as safe for fresh human consumption. Cassava varieties with CNp > 300 mg/kg necessitate processing prior to their utilization.

The above mentioned selected varieties have been evaluated at four critical trial stages: seedling, clonal trial, decentralized preliminary yield trial and then the decentralized uniform yield trial. Participatory evaluations with farmers for key agronomic and culinary traits have been done twice, at the preliminary and uniform yield trials. We are therefore confident that the selected varieties will be rapidly adopted at the respective selection sites. However, one major challenge experienced during the variety development process was the increasing incidence of CBSD, which may potentially limit the usefulness of the selected varieties. Because these varieties are considered to be tolerant to CBSD (score of 2 under intensive disease pressure), when combined with phytosanitation, they can then qualify to be deployed in regions of low CBSD pressure, as frequently done in Tanzania, where CBSD has persisted for over six decades.

It is proposed that the candidate varieties for release (28-TME14, 266-BAM, 349-KAK, 109-TME14, and 72-TME14), be officially released as NASE 15, NASE 16, NASE 17, NASE 18 and NASE 19, respectively. It does suffice to note that two cassava varieties (MH97/2961 and MM964271), have since their introduction from IITA, been widely grown by farmers owing to their superior agronomic and root qualities. Accordingly, we recommend that they also be officially released as NASE 13 and NASE 14. The other selected, but not officially released varieties (67-TME14 and 52-TME14), will be used as elite parental lines in subsequent breeding activities.

Dr. James. A. Ogwang
DIRECTOR OF RESEARCH, NaCRRI

Acknowledgment

The concept to develop locally adapted cassava varieties that combine both desirable agronomic and culinary qualities began in 2003. Financial support to achieve this goal was attained through implementation of two succeeding Rockefeller Foundation supported projects (2003 FS 022 and 2003 FS 029). Professional advice and keen interest of Dr. Joe DeVries throughout the implementation of the two projects is highly appreciated.

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Staff of the National Cassava Programme, the extension agents and farmers in the evaluation and selection sites (Namulonge, Nakasongola, Bulindi, Kigumba, Ngetta and Kamuli), are highly appreciated. They displayed teamwork and commitment during the project implementation.

We also thank the National Agricultural Research Organisation (NARO), which provided us with conducive research environment and other logistical support during the project implementation.

1.0 Background

Initiatives to increase cassava production and productivity in Uganda with the dual roles of increasing food security and household income have long been and continue to be a major objective of the National Cassava Programme (NCP). In fact, within a period of ten years (1990 - 2000), upto 12 high yielding and CMD resistant varieties were released by the NCP (NASE 1, NASE 2, NASE 3, NASE 4, NASE 5, NASE 6, NASE 7, NASE 8, NASE 9, NASE 10, NASE 11 and NASE 12). Some of these varieties i.e., NASE 3 and NASE 12 were adopted extensively, while the rest were adopted to limited extent, as reflected by the acreage planted to each variety. Shortly after this variety release, farmers resorted back to their local CMD susceptible varieties owing to the inferior root qualities of most of the elite released varieties. Examined keenly, this unfortunate scenario was inevitable. Why? Firstly, because during then, cassava evaluation and selection (between 1990 - 2000) focused primarily on CMD resistance and yield potential, and was largely implemented by scientists, with farmers only participating in the final evaluation stages. Secondly, root quality traits (aroma, mealyness and taste), which are paramount for variety adoption, weren't given utmost attention then. Taken together, these factors resulted into limited adoption of these NASE series and hence their replacement with local CMD susceptible varieties. This situation inevitably resulted into increased incidence of CMD in the major cassava growing regions of Uganda, and hence reducing cassava productivity and production.

In response to this challenge, the NCP refocused its breeding objectives, and initiated a decentralized breeding scheme that focused on the introgression of CMD resistance genes into locally adapted varieties. The forte for this approach was based on the fact that local varieties had inherently farmer preferred root quality traits, but deficient in CMD resistance, which could on the other hand, be easily sourced from IITA. Hence, hybridizing the two (local and the IITA elite varieties) could result into identification of cassava hybrids that combine both CMD resistance and desirable root qualities. It does suffice to note that previously, release of a new variety could take up to eight to ten years. This period involved a series of annual stages, beginning with generation of F_1 seeds, seedling establishment and evaluation, clonal evaluation trial (CET), preliminary yield trial (PYT), advanced yield trial (AYT), uniform yield trial (UYT), on-farm trial (OFT), and then multiplication, with farmers largely being involved in the final stages i.e., during OFT implementation.

One major limitation of this approach is that it only incorporates farmer's selections latter in the breeding process. To address this limitation, we proposed a decentralized selection scheme. The modified scheme can take up to six years comprising of F_1 seed generation, seedling evaluation, CET, modified-PYT, UYT and then on-farm, with farmers participating in the selection process at the modified PYT and UYT, an aspect that could increase adoption of selected varieties. This initiative began in 2003 with the establishment of a polycross from which F_1 seeds were generated. Promising hybrids were evaluated at five stages including: F_1 seedling stage, CET, modified PYT and UYT. This evaluation has resulted into the identification of seven outstanding cassava varieties, from which, we seek permission to release initially three varieties.

2.0 Methodology

Breeding methods developed for cross-pollinated crops can practically be applied to cassava. The breeding methodology in cassava involves selection of parents (based on complimentary traits), crossing (via controlled or open pollinations) and simple phenotypic selection of individual clones based on performance across years and locations. The vegetative nature allows fixation of genotypes throughout the selection process. However, a common feature of most cassava breeding programmes is that the initial stages of evaluation and selection are usually unreplicated and during then, emphasis should be on traits of high heritability (Kawano, 2003; Ceballos et al., 2004). Lack of adequate good quality planting material and the considerable logistical complications are the justification for this tradeoff of having more genotypes being evaluated in unreplicated trials as opposed to having fewer genotypes evaluated in replicated trials. Once selections have been made at single-row trials, selected clones can then be evaluated in replicated trials with bigger plot sizes and hence emphasis placed on traits of low heritability. Hereafter, the multi-stage cassava variety development, evaluation and selection process of the selected varieties is described.

2.1 Parental selection, genetic crosses and seedling evaluation

Five CMD resistant parental lines from IITA (SE/95-00036, NASE10, NASE 12, TME14 and TME5) and four local varieties with desirable culinary qualities (Kakwale, Bamunanika, Nyaraboke and Bao) were selected and established in an open pollination crossing block in 2003/2004. The parental lines are genetically diverse, an aspect which increases the prospects of exploiting heterosis. 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 seed nursery for germination at Namulonge. At the height of 20 - 25 cm, seedlings were transplanted to the field at spacing of 1 m x 1 m. Only seedlings with CMD severity indices in the range of 1-2 were advanced for clonal evaluation. A total of 1077 clones were selected and advanced for the clonal evaluation.

2.2 Clonal evaluation trial (CET)

The unreplicated CET was established at Namulonge. During CET, emphasis was placed on traits of moderate to high heritability which included: plant type, plant health and harvest index (HI). Progeny from each family were evaluated in three separate blocks, with each clone being represented with 8 plants. At harvest, only the six inner plants per clone were used for measurements. Data were collected on root weight (kg/plant), shoot weight (kg/plant) and HI computed as a ratio of the fresh root weight to the total biomass on a fresh weight basis. Further, three data sets at three, six and nine months after planting (MAP), were collected on plant health, reaction to prevalent diseases and insect pests [CMD, cassava bacterial blight (CBB), cassava green mite and whitefly infestation]. At harvest (August 2006), an additional assessment for general plant health (to prevalent pests and diseases) was done using a scale of 1-5; where 1 = highly resistant and 5 = highly susceptible. Additionally, plant type was also scored using a scale of 1-3, 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.

All the generated data was used for selection. The selection index was computed using the formula: (V_{PT} x 2 + V_{HI} x 4 – V_{PH} x 4), where V_{PT} is the plant type; V_{HI} is the harvest index and V_{PH} is the plant health. Because of the differences in units for the variables used, data were standardized per block prior to its utilisation in the selection index. It does suffice to note that plant health and harvest index have been reported to have moderate to high heritabilities (Kawano, 2003) and, hence clones selected for good plant health and high harvest index at clonal will to a large extent express the same characteristics at other stages of selection irrespective of plot size and environment. Because the trial was established in three blocks, with each family being represented in a block, selection was done per block to limit environmental influences. Using this selection index, selections were made per block. Cuttings for each selected clone were made to generate at least 36 stakes to enable establishment of two replicate plots at the decentralized evaluation and/or selection sites in the modified preliminary yield trial (MPYT).

2.3 Modified preliminary yield trial (MPYT)

Previously, replicated two-row plots in PYT (100-300 genotypes), were established at a single site, and were exclusively under the control of the scientists. Since at PYT we are dealing with reduced number of clones we have modified this approach to establish the replicated two-row plots of PYT in different sites with farmers participating in the selection process. This modified PYT offers the advantage of making location-specific selections with farmers participating in the selection process. The clones for evaluation in the MPYT were selected from the CET. Six sites were selected for the MPYT decentralized evaluation scheme [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. Namulonge and Ngetta received complete sets of all the selected genotypes, while for the other sites (Nakasongola, Bulindi, Kigumba and Kamuli) they received a sub-set of clones derived from the different families.

At each site, 2-replicate plots were established per clone, and the number of genotypes varied: Namulonge (143 clones); Ngetta (144 clones); Nakasongola (31 clones); Kigumba (28 clones); Kamuli (23 clones); and Bulindi (24 clones). At all sites, evaluations were made for plant health during crop growth. At harvest, data were collected on HI, DMC and CBSD root necrosis. Estimation of DMC was by the specific gravity method. Because of the differences in units for the variables used, HI, DMC and CBSD mean values were standardized prior to their utilisation in the selection index. The selection index was computed using the formula: (V_{DM} x 3 + V_{HI} x 3 – V_{CBSD} x 4), where V_{DM} is the dry matter content; V_{HI} is the harvest index and V_{CBSD} is CBSD root necrosis score. The constants are weights given for the traits bearing in mind trait heritability and accuracy of measurement. In addition, at each site, farmers comprising five men and five women were identified to help in culinary tests. We adopted a participatory variety selection. Expert cassava farmers that have grown the crop for several years were selected for this purpose. The attributes examined included: taste (sweet, fairly sweet, flat, slightly bitter and bitter); mealyness (mealy, average, watery); texture (fairly hard, fibrous, hard, soft); and flavour (aroma and no aroma). These evaluations were done on cooked cassava. Basing on these root quality attributes together with the phenotypic appearance of the plant, a clone was selected or rejected.

It suffices to note that by the time of initiation (2003/2004) of the polycross, CBSD wasn't a breeding objective then. However, as the selected progeny were being advanced to subsequent evaluation stages, the prevalence of CBSD was on the increase. This inevitable situation required that screening for CBSD immediately commences at the respective sites. The evaluation sites had varying CBSD pressure: Bulindi (Hoima District; low CBSD incidence, 1-10%); Kigumba (Masindi District; low CBSD incidence, 1-10%); Nakasongola (moderate CBSD incidence, 11-35%); Kamuli (moderate CBSD incidence, 11-35%); Ngetta (Lira District; moderate CBSD incidence, 11-35%) and Namulonge (Wakiso District, high CBSD incidence, 36-100%) (Figure 1). This finding further justified location-specific selection and partly explains why CBSD was included in the selection index at MPYT.

2.4 Uniform yield trial (UYT)

Only with the initiation of bigger plot sizes and replicated trials does the emphasis shift from high heritability traits to those of low heritability, such as fresh root yield. This was the case for the UYT. The clones for advancement at the respective sites to (UYT) were selected from the clones that were evaluated during 2007/2008 growing season at the MPYT. At each site, 4-replicate plots were established per clone, and the number of clones evaluated varied among the sites: Namulonge (44 clones); Ngetta (30 clones); Nakasongola (14 clones); Kigumba (10 clones); Kamuli (8 clones); and Bulindi (8 clones). At all sites, evaluations were made as already described for the MPYT with emphasis on: 1) traits of low heritability i.e., fresh root yield and root cyanogenic potential, and 2) CBSD reaction, as the inoculum pressure was building up at all selection sites. With this in mind, the selection index was computed using the formula: (V_{HI} x 2 + V_{DM} x 2 – V_{CNp} x 0.01 – V_{CBSD} x 25 + V_{YIELD} x 4), where V_{DM} is the DMC; V_{HI} is the HI; V_{CBSD} is CBSD root necrosis score; V_{CNp} is cyanogenic potential and V_{YIELD} is fresh root yield. As described for MPYT, farmers were again involved in the selection process. The selected varieties were thereafter established on five farmer's field per selection site for multiplication. A summary of the evaluation scheme at the different stages is presented in Figure 2.

3.0 Results and Discussion

Results presented in this report were obtained from a modified cassava breeding scheme that was designed such that it takes a decentralized fashion that favours location-specific selections as opposed to broad adaptability. We proposed this modification for two major reasons. Firstly, to increase farmer participation in the selection process by way of engaging them earlier both at MPYT and UYT. Secondly, to cater for diversified cassava utilization patterns that are tailored to specific localities. With the modified scheme, evaluations and selection were done at four critical stages including: seedling stage, CET, MPYT and UYT.

Selections made at seedling stage largely focused on two highly heritable traits, plant type and reaction to CMD. These traits were further examined at the CET. Under inter-cropping systems, varieties with the umbrella and/or cylindrical shapes are desirable as compared to varieties with open and/or compact shapes. 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 and/or compact plant types are required to control weed infestation. Since plant type is highly heritable, selections for the two plant types (umbrella and compact) were considered at the seedling and CET so that farmers could make appropriate selections amongst reduced and manageable numbers of clones at the modified PYT and UYT.

Pedigree of the selected varieties together with their agronomic performance at the CET is presented in Table 2. Five of the selected varieties (52-TME14, 67-TME14, 72-TME14, 28-TME14 and 109-TME14) were all half-sibs of an elite introduction TME 14 that was sourced from IITA. Certainly, all progeny from TME 14 can't be officially released at once. The other selected varieties 266-BAM and 349-KAK are half-sibs that were respectively derived from locally adapted varieties Bamunanika and Kakwale (Table 2). At CET, assessments were made for HI and plant health (reaction to prevalent pests and diseases). HI for selected varieties ranged from 0.3 (109-TME14) to 0.76 (72-TME14), which is comparable to previous evaluations done in Latin America 0.0 to 0.75 (Kawano et al., 2003) and west Africa 0.06 to 0.92 (Egesi et al., 2007). HI is one of the agronomic traits that can substantially increase cassava productivity. The doubling of fresh root yield in cassava within a short period since the inception of cassava breeding in Latin America, was largely due to improvement in HI (Kawano et al., 2003). This should be a motivation to start utilising HI in the selection process. Indeed, previous breeding experiments have established that in single row trials (like the CET), indirect selection for yield through HI was more effective than direct selection for yield.

Mean squares depicting phenotypic variation in agronomic traits (DMC, HI and reaction to CBSD) evaluated under MPYT at the six sites are presented in the Appendix 1. Significant differences in DMC among cassava genotype were only observed at Namulonge perhaps because more genotypes (of varying genetic potential) were included in the evaluation as compared to the evaluations done at other sites. However, no significant differences among genotypes were observed for HI and reaction to CBSD at all sites, indicating relatively similar genetic yield potential and/or response to the disease.

Nonetheless, data generated from the MPYT for the selected varieties at Kamuli (28-TME14 and 109-TME14), Kigumba (266-BAM), Nakasongola (72-TME14 and 349-KAK) and Namulonge (72-TME14, 67-TME14, 52-TME14 and 109-TME14), indicated that their DMC was just equivalent and/or slightly higher than the elite check cassava variety I92/00067 (Table 3). Relatively similar trends were observed for HI (Table 3). Because these selected varieties were developed under the backdrop of inferior root qualities in the earlier released varieties, farmers were invited to participate in the assessment of root culinary qualities (taste, mealyness, texture and aroma). All the selected varieties were sweet in taste, mealy for pounding, soft in texture and had a good aroma (Table 3). These characteristics coupled with desirable agronomic traits qualify, some of the selected varieties, for official release in the respective locations where they where selected.

Mean squares for the data generated from the UYT for the agronomic traits (DMC, HI, fresh root yield and cynogenic potential) at the five sites are presented in the Appendix 1. For DMC, significant differences among genotypes were only observed at Kigumba and Ngetta. For HI, significant differences where only observed at Ngetta. No significant differences were observed among cassava genotypes at all sites for cynogenic potential.

On the other hand, significant differences in yield were observed among cassava genotypes evaluated at Kigumba, Nakasongola, Ngetta and Namulonge, depicting their varied genetic potential.

It does suffice to note that during the multi-stage cassava selection scheme, reduction in number of genotypes evaluated at a specific stage provides an opportunity for increased precisions i.e. bigger plot sizes and higher number of replications. For example, at CET, single-row plots of 1077 genotypes were evaluated; for MPYT, 24 - 144 genotypes were evaluated in two-replicated plots, while at UYT, 8 - 44 genotypes were evaluated in four-replicated plots. This increase in plot size that is associated with reduced genotypes is particularly important when evaluating traits of low heritability i.e., fresh root yield and CNp. It's this theory that we had in mind when constituting the selection indices that were used during the selection at CET, MPYT and UYT. Data generated from the UYT for the selected varieties at Kamuli (28-TME14 and 109-TME14), Kigumba (266-BAM), Nakasongola (72-TME14 and 349-KAK) and Namulonge (72-TME14, 67-TME14, 52-TME14 and 109-TME14) indicated that they had DMC that was just about and/or slightly higher than the elite check variety I92/00067 (Table 4). Relatively similar trends were observed for HI except perhaps variety 109-TME 14 at Namulonge (Table 4). Fresh root yield varied across locations, but was above the national average of 13t/ha. This finding is most likely a result of environmental influences, which in part justify location-specific selections as opposed to broad adaptability.

Cassava root form and quality has, and continues to play a decisive role in acceptability of a variety. In fact, it's increasingly becoming clear that desired root quality characteristics vary widely from one region to another and thus distinct quality characteristics may be required for different regions and/or markets. This situation could therefore require careful study and planning. Indeed, it's for this reason that we established a decentralised evaluation and selection scheme. All selected varieties were mealy, and had good aroma; one genotype 109-TME14 selected at Kamuli was rated as hard just like the check variety I92/00067 at Nakasongola (Table 4). Although two of the selected varieties were considered as slightly bitter and/or bitter (109-TME14 and 72-TME14), they were selected. These varieties had CNp levels that were less than 300 mg/kg, which makes them safe for utilization. Further, with the exception of candidate variety 52-TME14, which had CNp levels (391.6 mg/kg), all other candidate varieties had CNp levels that were less than 300 mg/kg.

The evaluation and selection sites had varying CBSD pressure. Certainly, this varying CBSD pressure has practical implications on the release of the selected varieties. For example, cassava varieties could appear tolerant to CBSD because the selection pressure wasn't optimum to express susceptibility. A maximum score of 2 was registered on some of the selected varieties. On the other hand, field observations at different sites in the country on the check variety (I92/0067) indicated it's highly susceptible to CBSD with a root score of 3. Clearly, in the absence of CBSD resistant and/or tolerant varieties, some of these selected varieties can in the meantime be grown, as the search for more resistant and/or tolerant genotypes continues at a national, regional and international level.

Compared to Tanzania where CBSD has been a problem for over 60 years, no immune variety has been identified. So far, all released varieties are classified as tolerant to CBSD because they either: 1) have foliar symptoms with no root symptoms or 2) have no foliar symptoms, but with a root CBSD score of 2 (Edward Kanju; personal communication). This classification is consistent with the data obtained in this report.

It is commonplace for elite cassava varieties to be multiplied and disseminated (after satisfactory evaluation) within specific localities without official release. The case in point are the cassava introductions from IITA notably TME 14, TME 204, I92/0067 (Akena), MH97/2961, MM96/0686 and MM96/4271 that have been widely disseminated in most cassava growing regions of Uganda owing to their popularity with farmers. Unfortunately, most of these varieties are susceptible to CBSD. Because MH97/2961 and MM96/4271 have moderate levels of CBSD susceptibility (lower incidence) and acceptable agronomic performance (Appendix 1), we propose that these two varieties be officially released respectively as NASE 13 and NASE 14. On the other hand, of the selected varieties (28-TME14, 109-TME14, 266-BAM, 349-KAK, 72-TME14, 67-TME14 and 52-TME14), we propose that three varieties notably, 28-TME14, 266-BAM and 349-KAK be officially released, as they are phenotypically distinct (Appendix 2). The others can be retained in maintenance breeding as elite parental lines and used for hybridization and/or inbreeding schemes. A summary of the agro-morphological descriptors of the selected varieties is presented in Table 5.

4.0 Conclusion and recommendations

The selected varieties (28-TME14, 109-TME14, 266-BAM, 349-KAK, 72-TME14, 67-TME14 and 52-TME14) combine: 1) high levels of CMD resistance, 2) with farmer preferred culinary root qualities and 3) CBSD tolerance. Hence, host plant resistance and/or tolerance combined with phytosanitation will make these varieties appropriate for cultivation in regions that are experiencing low CBSD pressure.

We recommend that the five phenotypically distinct varieties (28-TME14, 266-BAM and 349-KAK, 109-TME14 and 72-TME14) be officially released as NASE 15, NASE 16, NASE 17, NASE 18 and NASE 19, respectively. To fast-track the distribution of these varieties five farmers involved in the selection process were identified to participate in the multiplication of these candidate varieties. We are optimistic that this will constitute the breeders stock that will be used for further distribution and multiplication.

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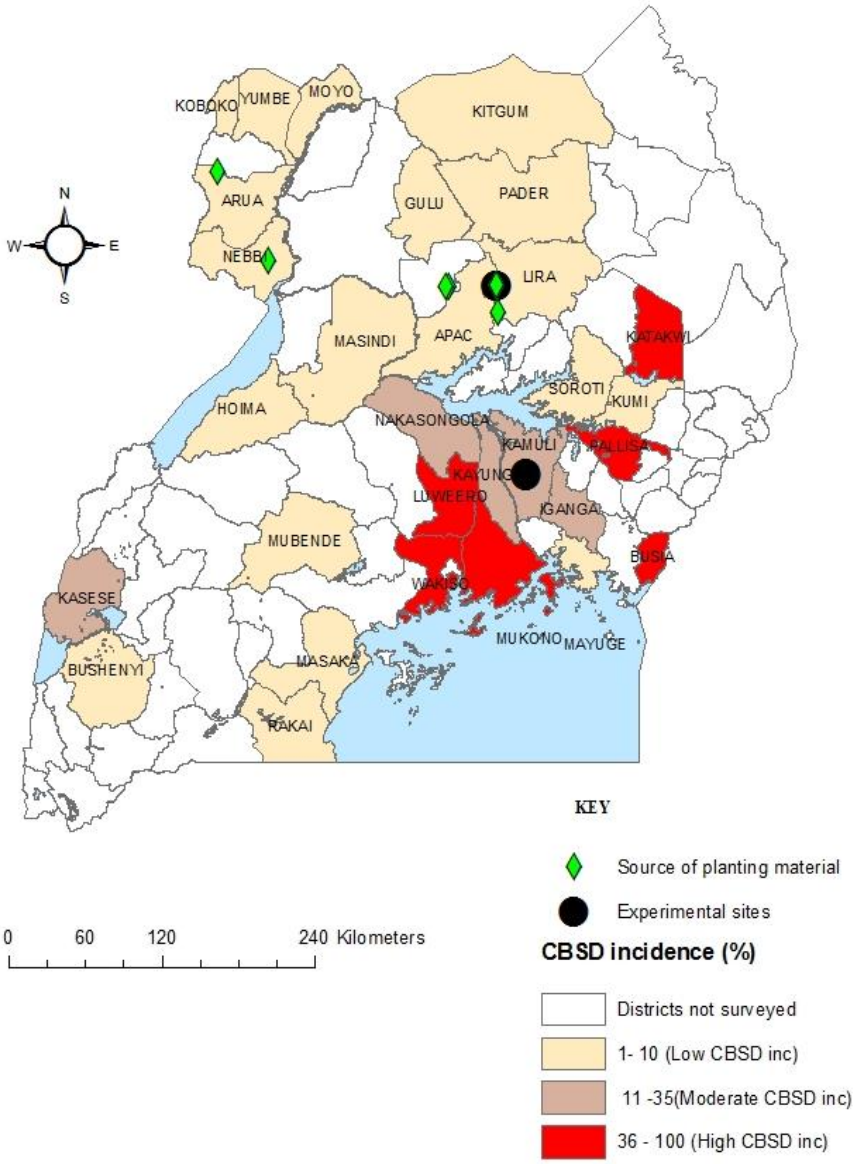

Figure 1: Map of Uganda showing the incidence and distribution of CBSD

Summary of the cassava multi-stage evaluation and selection scheme

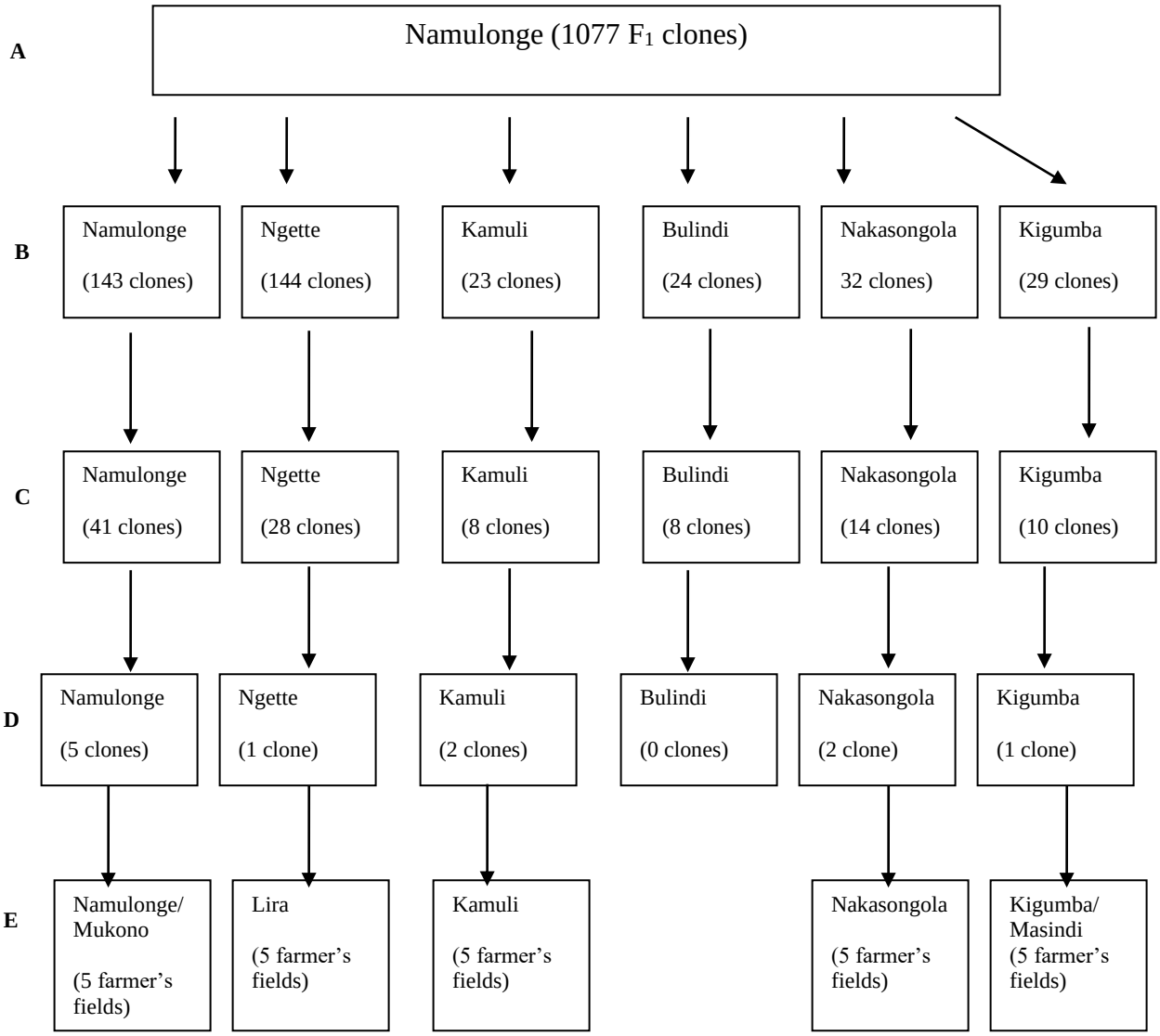

Figure 2: The decentralized participatory cassava evaluation and selection scheme. A = clonal evaluation at Namulonge (2006/07); B = Modified preliminary yield trial at six locations (2007/08); C = uniform yield trial at six sites (2008/09); D = Varieties selected (109-TME14, 28-TME14, 266-BAM, 349-KAK; 72-TME14, 67-TME14, 52-TME14) and E = on-farm multiplication (2009/10).

Table 1: Parental lines used in the polycross

Accession name	Clone name	Source/ locality	CMD reaction	Nature of resistance
Bamunanika	Landrace	Central Uganda	Susceptible	Susceptible
Kakwale	Landrace	Central Uganda	Susceptible	Susceptible
Bao	Landrace	Northern Uganda	Susceptible	Susceptible
Nyaraboke	Landrace	North-western Uganda	Susceptible	Susceptible
TME 5	Landrace	IITA	Resistant	Dominant/ monogenic
TME 14	Landrace	IITA	Resistant	Dominant/ monogenic
95/SE-00036	95/SE-00036	IITA	Resistant	Reccessive/ polygenic
NASE 12	MH95/0414	IITA	Resistant	Reccessive/ polygenic
NASE 10	95/NA-00063	IITA	Resistant	Reccessive/ polygenic

Table 2: Performance of selected varieties at the clonal evaluation trial established at Namulonge[1]

Half sib Family	Genotype	Block	Plant health	Harvest index
TME 14	52-TME14	1	1	0.40
TME 14	67-TME14	1	2	0.70
TME 14	72-TME14	1	1	0.76
TME 14	28-TME14	3	1	0.41
TME 14	109-TME14	3	1	0.30
Bamunanika	266-BAM	2	1	0.40
Kakwale	349-KAK	1	2	0.69

[1]Evaluations of 1077 clones based on single-row plots. Plant health evaluated on a scale of 1-5; where 1= highly resistant and 5 = highly susceptible.

Table 3: Performance of selected genotypes under the modified preliminary yield trial at the respective selection sites[1]

Site	Genotype	DMC	HI	CBSD	Taste	Mealyness	Texture	Aroma
Kamuli	28-TME14	38.3	0.46	1	Sweet	Mealy	Soft	Aroma
	109-TME14	41.2	0.50	1	Sweet	Mealy	Soft	Aroma
	MH97/2961	32.0	0.33	1	Sweet	Mealy	Soft	Aroma
	I92/0067	30.9	0.47	1	Sweet	Mealy	Soft	Aroma
Kigumba	266-BAM	35.4	0.51	1	Sweet	Mealy	Hard	Aroma
	MH97/2961	35.3	0.40	1	Sweet	Mealy	Soft	Aroma
	I92/0067	36.1	0.42	1	Sweet	Mealy	Hard	Aroma
Nakasongola	72-TME14	37.5	0.62	1	Bitter	Mealy	Soft	Aroma
	349-KAK	44.1	0.59	1	Sweet	Mealy	Soft	Aroma
	MH97/2961	36.7	0.50	1	Sweet	Mealy	Soft	Aroma
	I92/0067	39.9	0.67	1	Sweet	Mealy	Hard	Aroma
Ngetta	109-TME14	37.5	0.55	1	Sweet	Mealy	Soft	Aroma
	MH97/2961	38.1	0.42	1	Sweet	Mealy	Soft	Aroma
	I92/0067	38.7	0.49	1	Sweet	Mealy	Soft	Aroma
Namulonge	28-TME14	35.3	0.45	1	Sweet	Mealy	Soft	Aroma
	72-TME14	38.6	0.45	1	Sweet	Mealy	Soft	Aroma
	67-TME14	37.8	0.45	1	Sweet	Mealy	Soft	Aroma
	52-TME14	37.3	0.39	1	Sweet	Mealy	Soft	Aroma
	109-TME14	38.3	0.26	1	Sweet	Mealy	Soft	Aroma
	MH97/2961	35.4	0.35	2	Sweet	Mealy	Soft	Aroma
	I92/0067	35.2	0.27	2	Sweet	Mealy	Soft	Aroma

[1] Namulonge had a complete set of genotypes and hence some clones selected there (28-TME14, 72-TME14, 109-TME14) had also been selected at other sites. Results of culinary qualities based on assessment by 10 farmers at each selection site. The check varieties included: MH97/2961 and I92/00067. CBSD pressure varied among the six evaluation sites and hence the varied reaction of the check varieties to CBSD.

Table 4: Performance of selected varieties under the uniform yield trial at the respective selection sites[1]

Site	Genotype	DMC	HI	CBSD	CNp	Yield (t/ha)	Taste	Mealyness	Texture	Aroma
Kamuli	28-TME14	38.0	0.50	2	170.9	59.7	Sweet	Mealy	Soft	Aroma
	109-TME14	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	266-BAM	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	72-TME14	35.0	0.62	2	250.8	23.8	Bitter	Mealy	Soft	Aroma
	349-KAK	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	109-TME14	-	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	28-TME14	35.0	0.45	2	218.4	25.5	Sweet	Mealy	Soft	Aroma
	72-TME14	28.0	0.45	1	168.4	19.7	Sweet	Mealy	Soft	Aroma
	67-TME14	30.0	0.45	1	265.1	18.3	Sweet	Mealy	Soft	Aroma
	52-TME14	38.0	0.39	2	391.6	21.3	Sweet	Mealy	Soft	Aroma
	109-TME14	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

Table 5: Summary of characteristics of candidate varieties for release

Characteristics	Selected varieties								
	72-TME14	**52-TME14**	**109 -TME14**	**28-TME14**	**67-TME14**	**226 BAM**	**349-KAK**	**MH97/2961**	**MM96/4271**
Colour of young shoot	Purplish green	Purplish green	Purplish green	Purplish green	Purplish green	Purplish green	Purplish green	Purplish green	Purplish green
Pubescence	Present	Present	Present	Absent	Present	Absent	Absent	Absent	Absent
leaf shape	Elliptic-lanceolate	Elliptic-lanceolate	Elliptic-lanceolate	Elliptic-lanceolate	Elliptic-lanceolate	Lanceolate	Elliptic	lanceolate	Elliptic
Petiole colour	Purple	Purple	Purple	Red	Purple	Purple	Red	Purple	Purple
Mature stem colour	Gray	Gray	Gray	Gray	Gray	Gray	Golden	Silver	Gray
Colour of leaf	Dark green	Dark green	Dark green	Light Green	Dark green	Dark green	Dark green	Dark green	Dark green
Branching height	Low	Low	Low	Low	Low	Medium	Low	High	Low
Outer skin colour of root	Cream	Brown	Brown	Brown	Brown	White	Brown	Brown	Brown
Colour of root cortex	Cream	Cream	Cream	Cream	Cream	Pink	Pink	Pink	Cream
Colour of root pulp	White	White	White	White	White	White	White	White	White
Taste	Sweet	Sweet	Sweet	Sweet	Sweet	Sweet	Sweet	Sweet	Sweet
Cyanogenic potential	Low	Low	Low	Low	Low	Low	Low	Low	Low
Resistance to CMD	High	High	High	High	High	High	High	High	High
Resistance to CBB	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate
Resistance to CGM	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate	Moderate
Recommended harvesting time	12	12	12	12	12	14	12	12	12

Appendix 1

Mean squares for agronomic traits examined under the modified preliminary yield trial at six sites

Evaluation site	No. of clones	Mean squares		
		DMC (%)	HI	CBSD
Kamuli	24	17.9	0.010	-
Kigumba	29	9.74	0.016	0.466
Nakasongola	32	5.71	0.006	0.326
Ngetta	144	23.95	0.024	0.220
Namulonge	144	14.15*	0.016	0.414
Bulindi	25	16.1	0.010	0.305

*** Mean square significant at 5%. DMC = dry matter content; HI = harvest index and CBSD = cassava brown streak disease. No evaluation done for CBSD at Kamuli.**

Mean squares for agronomic traits examined under the uniform yield trial at six sites

Evaluation site	No. of clones	Mean squares			
		DMC	HI	Yield (t/ha)	CNp
Kamuli	8	14.9	0.012	97.5	5818
Kigumba	10	36.1*	0.015	925.8*	11325
Nakasongola	14	35.2	0.022	594.9*	11043
Ngetta	30	102.5*	0.023*	217.1*	2504
Namulonge	44	32.0	-	187.4*	998
Bulindi	8	13.7	0.027	1350.2*	1054.1

* Mean square significant at 5%

On-farm evaluation of cassava variety MM96/4271during 2004/2005 growing season in Lira

Evaluation site	CMD reaction	Yield (t/ha)	Remark
Farmer 1	High	14.9	Excellent root qualities
Farmer 2	High	21.8	Excellent root qualities
Farmer 3	High	12.4	Excellent root qualities

Appendix 2

349-KAK (NASE 17)

266-BAM (NASE 16)

28-TME14 (NASE 15)