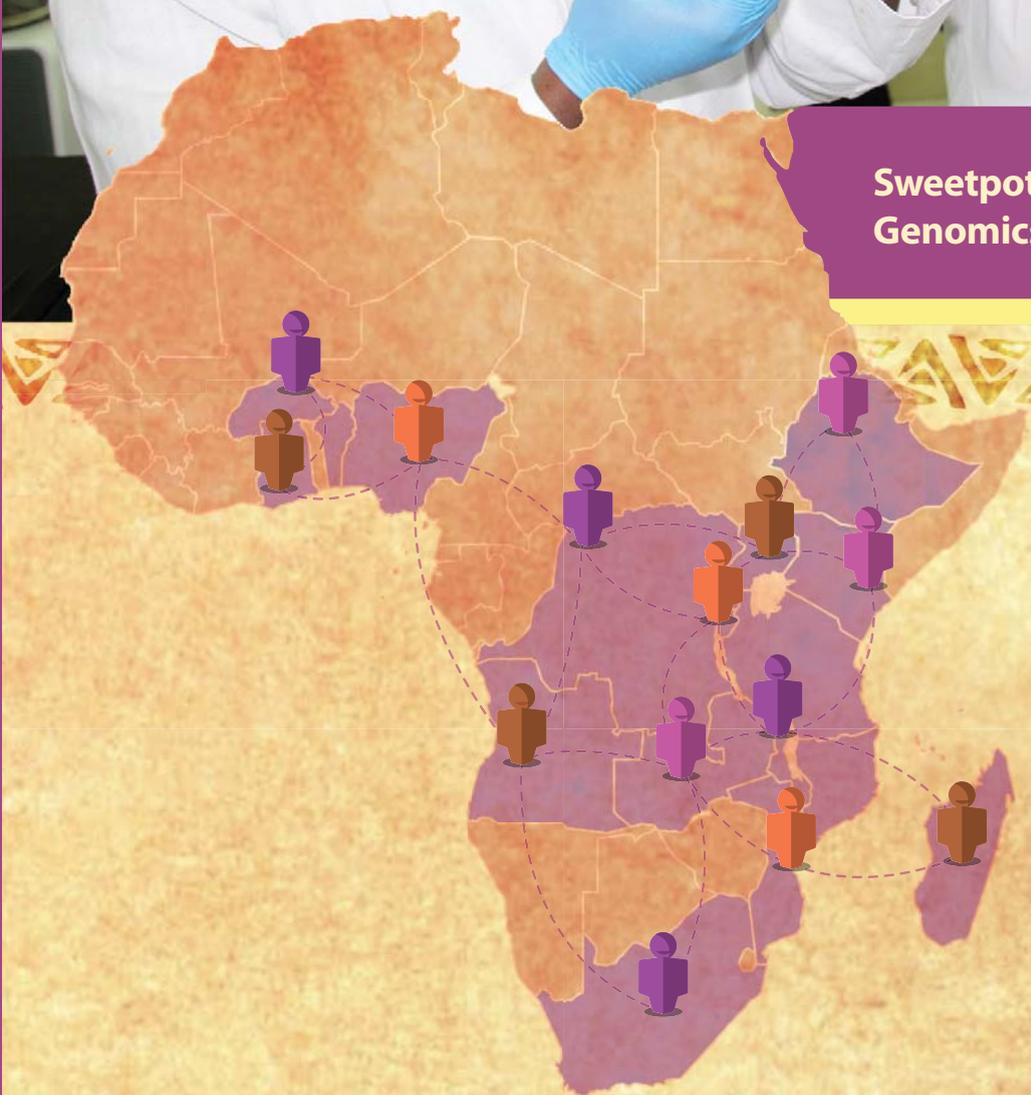




## Sweetpotato SpeedBreeders and Genomics Community of Practice



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Report of the 15<sup>th</sup> Sweetpotato SpeedBreeders' Meeting and Training Workshop on the Integration of Molecular Markers

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Held at ILRI Campus – Nairobi, Kenya

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**June 6 -10, 2016**

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Compiled by Charles Wasonga, Mercy Kitavi and Robert Mwangi

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Edited by Christine Bukania

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**International Livestock Research Institute (ILRI), Nairobi-Kenya, June 6-10,  
2016**

**Compiled by Charles Wasonga, Mercy Kitavi and Robert Mwanga; edited by Christine  
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**Photos:** C. Bukania

**Cover photo:** *Breeders participate in a practical session at the BecA-ILRI Hub in Nairobi, during the training on integration of molecular markers in sweetpotato breeding programs (Credit: C. Bukania)*

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## LIST OF ACRONYMS

ABS	Accelerated breeding scheme
AEZ	Agro-ecological zone
AGRA	Alliance for a Green Revolution in Africa
AFLP	Amplified fragment length polymorphism
AMMI	Additive main effect and multiplicative interaction
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
AOCI	African Crop Initiative Sequencing
AT	Advanced trials
BeCA	Biosciences eastern and central Africa
BMGF	Bill and Melinda Gates Foundation
BrAPI	Breeding application programming interface
BTI-CU	Boyce Thompson Institute- Cornell University
CGIAR	Consultative Group on International Agricultural Research
CIP	International Potato Center
CoP	Community of practice
CSIR-CRI	Council for Scientific and Industrial Research of Ghana – Crops Research Institute
ECA	East and Central Africa
DArT	Diversity arrays technology
DNA	Deoxyribonucleic acid
GBS	Genotyping-by-sequencing
GCA	General combining ability
GEBV	Genomic estimated breeding -Values
GGE	Genotype and genotype x environment interaction
GS	Genomic selection
GT4SP	Genomic tools for sweetpotato improvement
GxE	Genotype by environment
GWAS	Genome wide association studies
HEBS	Heterosis exploiting breeding schemes
HIDAP	Highly interactive data analysis and productivity
HKI	Helen Keller International
HQ	Headquarters
ILRI	International Livestock Research Institute
IPM	Integrated Pest Management
KEPHIS	Kenya Plant Health Inspectorate Service
KSU	Kansas State University
LAMP	Loop-mediated isothermal amplification
MAB	Marker-assisted breeding
MAS	Marker-assisted selection
METs	Multi-environmental trials
MSU	Michigan State University
NaCRRRI	National Crops Resources Research Institute
NARS	National Agricultural Research Systems
NC	North Carolina

NCM-ELISA	Nitrocellulose membrane enzyme-linked immunosorbent assay
NCSU	North Carolina State University
NIRS	Nearinfrared spectroscopy
OFSP	Orange-fleshed sweetpotato
OFT	On-farm trial
OP	Open Pollinated Seed
PCR	Polymerase chain reaction
PI	Principal Investigator
PVS	Participatory variety selection
QTL	Quantitative trait loci
RAPD	Randomly amplified polymorphic DNA
RCBD	Randomised complete block design
RDMC	Root dry matter content
RNA	Ribonucleic acid
RTB	Roots Tubers and Bananas
SASHA	Sweetpotato Action Security and Health in Africa
SCA	Specific combining ability
SNP	Single nucleotide polymorphism
SPCSV	Sweet potato chlorotic stunt virus
SPFMV	Sweet potato feathery mottle virus
SPHI	Sweetpotato for Profit and Health Initiative
SPVD	Sweetpotato virus disease
SPW	Sweetpotato weevil
SSA	Sub-Saharan Africa
SSP	Sweetpotato support platform
SSR	Simple sequence repeat
UQ	University of Queensland, Australia
US	United States

## Executive Summary



*Participants pose for a group photograph*

The 15<sup>th</sup> Sweetpotato for Profit and Health Initiative (SPHI) Sweetpotato *Speed*Breeders Annual Meeting was held between 6<sup>th</sup> and 10<sup>th</sup> June, 2016 at the International Livestock Research Institute (ILRI) Campus in Nairobi, Kenya. For the second time, the meeting brought together scientists from the Sweetpotato for Security and Health in Africa (SASHA) project and the Genomic Tools for Sweetpotato Improvement project (GT4SP), both of which target genetic improvement of sweetpotato for better adaptation, increased productivity and nutritional quality.

The first two days were dedicated to a training workshop to expose participants to molecular / genomic tools. The last three days of the meeting focused on sharing progress, improving breeding methods, and considering next steps.

### **Session A: Training workshop: An eye opener in planning the integration of molecular markers in sweetpotato breeding programs**

The tone of the workshop was set by Craig Yencho in his keynote address titled genomics-assisted sweetpotato improvement: Beginning the discussion - Hope or hype? He underscored the economic, nutritional and health benefits of sweetpotato and described the conception of, and achievements of SASHA and the GT4SP.

Over the course of the two days, presentations were made on topics such as: genetic diversity studies of the sweetpotato using DNA markers; marker-assisted selection/breeding and its potential use for sweetpotato improvement; accurate sweetpotato phenotyping of agronomic traits; and sweetpotato genotyping procedures

Through practical exercises, participants went through the steps involved in plant tissue sampling; DNA extraction and purification; DNA quantification and quality assessment; DNA amplification (marker assays); data generation, analysis and interpretation. They also practised the steps involved in DNA fingerprinting and clone identification. In another practical exercise, participants learnt about genome wide maps; single nucleotide polymorphism (SNP) marker development in hexaploid sweetpotato using genotyping-by-sequencing (GBS).

What do we know about the *Ipomoea* genome and how can this be used in breeding improved sweetpotato varieties? Was the title of a key presentation whose focus was on the status of knowledge on sweetpotato genome and the progress made in the development of a sweetpotato genome browser.

### **Session B: Sweetpotato SpeedBreeders Annual Meeting (Theme: Sharing Progress, Improving our Methods, and Considering Next Steps)**

A number of presenters focused on new tools that are aimed at improving breeding methods. These tools include the sweetpotatobase, whose features will improve collection, sharing and storage of breeding data, and which incorporates features that breeders need to have in a sweetpotato ontology/descriptors status. New tools are being developed to improve efficiency of data analysis. The work in this area has been motivated by the need for tools to enable faster routine analysis of breeding trials. The development seeks to integrate tools such as CloneSelector, sweetpotatobase, Kansas State University (KSU) FieldBook App, and AccuDataLog, breeding application programming interface (BrAPI) and HIDAP.

A presentation on crop ontology explained how it has developed since being launched within the CGIAR crop lead centres in 2008. Participants were informed that the current sweetpotato ontology has 206 variables and these continue to be improved.

The breeders got an opportunity to acquire practical skills. There was a demonstration on analysing on-farm data using CloneSelector and evaluation and interpretation of outputs of an analysis of trial data.

Presentations on progress in breeding work across the region covered genetic improvement of important traits for selection in sweetpotato (*Ipomoea batatas*) controlled cross populations in Uganda; virus resistance breeding in Uganda; marker-assisted selection (MAS) for SPVD resistance; and mother-baby trial procedure as an on-farm trial methodology in Northern Ghana. The progress made through support from AGRA in Rwanda, Burkina Faso, Nigeria and Zambia was also discussed. Preliminary results from a study demonstrating the importance and heritability of vine survival in drought-prone areas of Mozambique were presented. A planned PhD targeting genetic improvement of important traits for selection in sweetpotato in Uganda was also presented.

SPVD was cited as one of the greatest challenges to sweetpotato production in sub-Saharan Africa (SSA). In the presentation on diagnostic tools for virus detection, participants were

informed of the ongoing work to develop field level diagnostic tools that could have potential usefulness for breeders.

Climate change has an overall impact on food security. The presentation of climate change therefore reviewed observed suitable climate for sweetpotato growth based on previously published data and projected climate changes in the sweetpotato growing areas and their effect on sweetpotato production adaptation options. Participants discussed design action points for climate resilient sweetpotato production, which they felt would position sweetpotato to make a more significant contribution to food and nutrition security in a changing climate.

During a panel discussion, breeders identified the varieties that had been adopted most successfully in their countries, and the factors that contributed to the adoption. These are summarised in the table below. From the discussion it was observed that traits such as yield and root quality cut across the different countries. The main concerns for processors are related to dry matter content, susceptibility to damage during transport, sugar content, and taste/sweetness.

There is need to have a list of elite genotypes to serve as ready pathogen-tested source of best-bet genotypes for international and local distribution. The breeders were informed of an ongoing initiative to select one hundred best-bet sweetpotato varieties for SSA, which will then be cleaned up and maintained under tissue culture and screen house for use by breeders at a small charge. They also discussed and made suggestions to improve the OFSP catalogue that is periodically produced and used to promote different varieties.

Participants were provided with a snapshot of the global reporting on sweetpotato breeding progress under the Root and Tuber Crops program. They were informed that the reports on the five milestones were available upon request.

Participants received an online orientation of the Sweetpotato Knowledge Portal that had been relaunched in February 2016. Apart from introducing the new features on the portal, participants were shown how to upload files and add the metadata, add external links, projects, news items and events, join discussion fora and conduct searches. Session A: Training workshop: An eye opener in planning the integration of molecular markers in sweetpotato breeding programs

At the meeting, breeders from 14 national programs made a commitment to mainstream beta-carotene into their breeding programs and to having at least 50% of the new sweetpotato varieties that they would release being orange-fleshed. The SSA sweetpotato community of practice later issued a joint statement.

## 1. Introduction



*Appolinaire Djikeng opens the meeting*

The 15<sup>th</sup> SPHI Sweetpotato *Speed*Breeders Annual Meeting was held between 6<sup>th</sup> and 10<sup>th</sup> June, 2016 at the ILRI Campus in Nairobi, Kenya. For the second time, the meeting brought together scientists from the SASHA project and the Genomic Tools for Sweetpotato Improvement (GT4SP) project, both of which target genetic improvement of sweetpotato for better adaptation, increased productivity and nutritional quality. It was opened by Dr Appolinaire Djikeng, the director of the Biosciences eastern and central Africa—ILRI (BecA-ILRI) Hub and Dr Jan

Low, the SASHA project manager and SPHI leader.

The first two days were dedicated to a training workshop to expose participants to molecular / genomic tools. The theme of the workshop was “an eye opener in planning the integration of molecular markers in sweetpotato breeding programs”. The last three days of the meeting focused on *sharing progress, improving breeding methods, and considering next steps*.

## 2. Session A: Training workshop: An eye opener in planning the integration of molecular markers in sweetpotato breeding programs

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### 2.1. Keynote Address: Genomics-assisted sweetpotato improvement: Beginning the discussion - Hope or hype?

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*Craig Yencho*

In this presentation, Dr Yencho underscored the economic, nutritional and health benefits of sweetpotato and pointed out the fact that the importance and potential of sweetpotato was becoming widely recognised in developed and developing countries across the globe. On a global scale, the world’s leading sweetpotato production areas are SSA and Asia, especially China. However, productivity per unit land area in SSA had remained lower than that in China.



*Craig Yencho gives his keynote address*

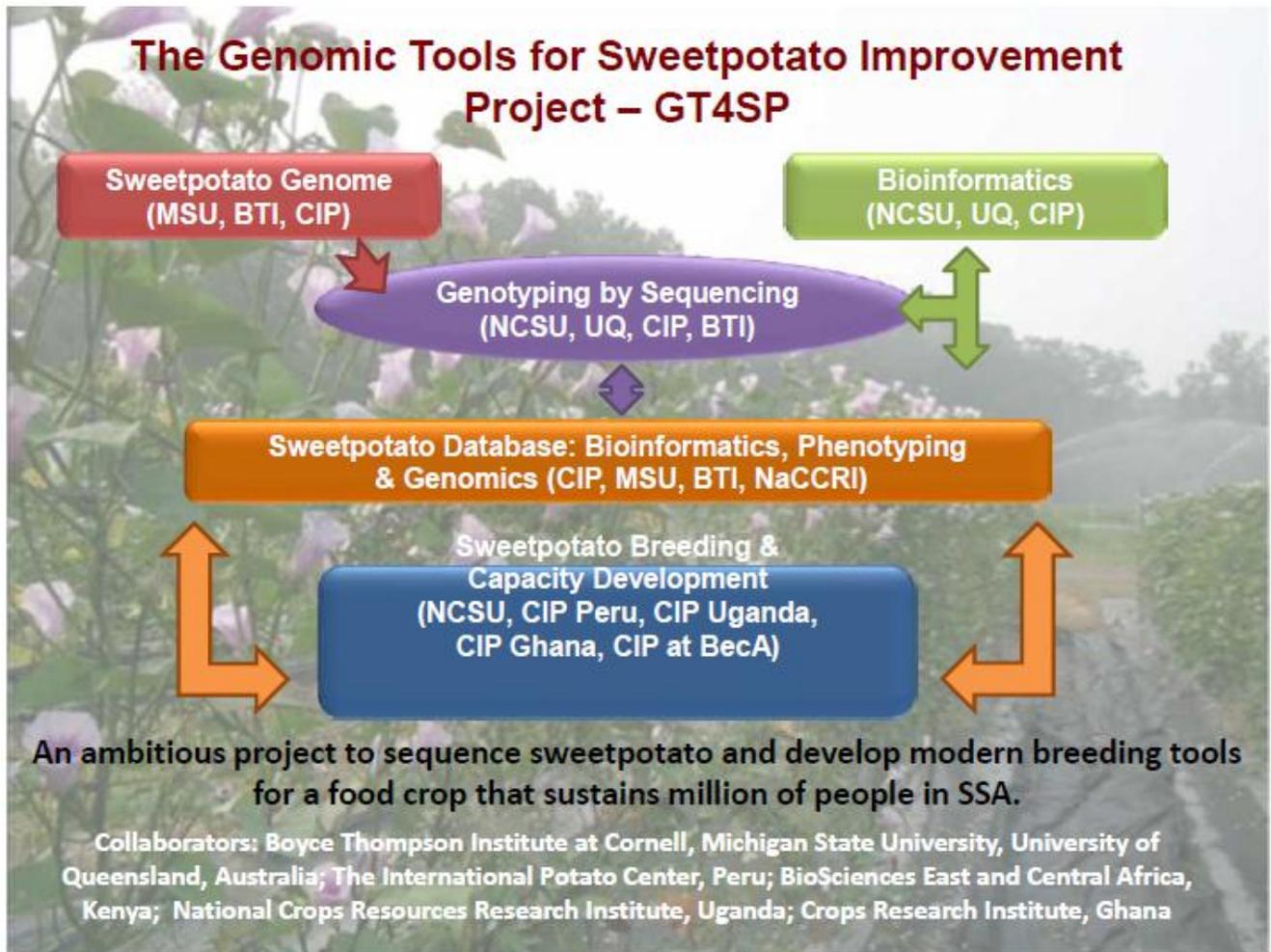
Many public and private organisations that recognised the superior nutritional value of sweetpotato as compared to other staple crops had increased investments to develop the crop further. An illustration of this was the Bill & Melinda Gates Foundation (BMGF), which funded the SASHA I project. The project produced positive results in several areas. For example, it had established ten new sweetpotato breeding programs in SSA; developed and released more than 18 new varieties; established three regional sweetpotato support platforms (SSPs) in SSA; introduced NIRS technology for use in root quality assessment by breeding programs; improved seed systems; intensified virus studies; and implemented value-added proof of concept projects.

SASHA II and SPHI partners have continued to invest in projects that are expected to further develop sweetpotato and spur new opportunities, genomic resources that could be harnessed in sweetpotato improvement have remained noticeably lacking. It is from this background that a sweetpotato convening was held in June 2013 in Seattle, Washington. The objective of the convening was to develop a vision for sweetpotato improvement in SSA with emphasis on the development and utilisation of modern breeding tools to improve genetic gain and increase the potential of sweetpotato to reduce hunger and poverty. The convening led to the development of the GT4SP. The project was established in September 2014 with USD 12.4 million funding from the BMGF. It is steered by 20 principal investigators (PIs) from seven institutions, in six countries across four continents. The lead PI, Craig Yencho, is the leader of sweetpotato and potato programs from North Carolina State University (NCSU).

In Uganda, the NCSU sweetpotato program in collaboration with the National Crops Resources Research Institute (NaCRRI) in Uganda, and with funding from the McKnight Foundation had made significant progress in constructing a sweetpotato genetic map; and in developing and releasing better adapted, high yielding and high quality sweetpotato varieties for growers in Uganda. The work the program undertook also led to the discovery that storage root quality traits such as high beta-carotene content and dry matter content were negatively linked. This explained the difficulty experienced to concurrently select for the two root quality traits. Moreover, SPVD, sweetpotato weevils, and *Alternaria* stem blight are still challenges to sweetpotato producing countries like Uganda. Further work undertaken on sweetpotato weevils by the NCSU and NaCRRI sweetpotato programs identified some form of resistance to sweetpotato weevil in a landrace called New Kawogo. They have attempted to decipher the nature of the resistance through chemical profiling of its storage root. A study of inheritance of the trait and identification of molecular markers associated with the trait using mapping populations developed with New Kawogo as one of the parents was undertaken. The NCSU sweetpotato program also attempted to use experience and learning from work with potato genetic map, Quantitative trait loci (QTLs) and molecular markers to develop methods to tackle the identified sweetpotato challenges.

The GT4SP project envisions to use a marker-assisted breeding (MAB) approach to promote sweetpotato improvement in SSA. This would be achieved through breeding pipelines investment in:

- a) Development of genomic resources with a focus on: the development of a reference genome; molecular markers; having a robust set of SNP markers and a low-cost genotyping platform; advanced laboratory sequencing linked with developing country phenotyping and breeding activities; developing diploid and hexaploid mapping, training, and test populations.
- b) Phenotyping, analytics and database resources that would include: improved phenotyping options; web-based bioinformatics resources; and a new database, data collection and analysis resources.
- c) Human resources and capacity development through continued development of a dynamic team of breeders and allied disciplines, training in the use of traditional and genomic breeding methods, effective communication and collaboration; and multi-institutional training.
- d) A common vision and continuity of effort.
- e) A stellar team to implement the different components of the project as outlined in Figure 1.



*Figure 1: The collaborators of the GT4SP and their roles*

At the time of reporting, the GT4SP had made significant progress towards achieving its milestones. Notable progress has been in areas such as: assembly and annotation of genomes of the diploids *Ipomoea trifida* and *I. triloba*; optimisation of enzyme and fragment size selection for sweetpotato to enhance the utility of genotyping-by-sequencing approach; and development and deployment of SweetPotatoBase and FieldBook App for managing phenotypic data.

The lessons learnt since the inception of the project show that the following is needed:

1. Reference genome(s);
2. A sequence-based genotyping platform;
3. A breeder friendly bioinformatics and analytical environment that is especially designed for clonally propagated, polyploid crops, and which assures technical support to breeders;
4. Populations - QTL mapping and Genome wide association studies (GWAS);
5. Improved phenotyping and data collection capabilities that include mechanisation equipment;

6. Sustained funding from multiple sources such as NGOs, government, and private sector;
7. Sustained capacity development of people, institutions, programs, farmers, and industries,

The following are highlights of the discussion that followed Dr. Yencho's presentation:

- The GT4SP will focus on specific traits first and then genomic selection later. For Africa, the important traits are yield, resistance to diseases such as SPVD, sweetpotato weevils and storability.
- The genomic tools being developed through the project are expected to be useful for sweetpotato improvement, given the diverse disciplines/expertise that has been brought together through the project. However, breeders are urged to be patient until the tools are completed.
- Molecular tools that are already available could be utilised right away in sweetpotato improvement even as more tools continue to be developed.
- One of the objectives of the workshop was to broaden knowledge on opportunities for genomics-assisted breeding.

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## **2.2. Genetic diversity studies of the sweetpotato using DNA markers: What have we learnt?**

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*Marc Ghislain*

The presentation discussed the origin, crossability and distribution of sweetpotato then went on to highlight some of the lessons that had been learnt from DNA fingerprinting studies and their significance.

*Ipomoea trifida* is considered the most likely ancestor of sweetpotato. However, a more recent hypothesis based on molecular studies has suggested that sweetpotato originated from an ancestor that is related to *I. trifida*. The crop is believed to have originated from Yucatan Peninsula in Mexico and the Orinoco Basin in Venezuela / North-western South America.

DNA fingerprinting work has confirmed Central America to be the primary centre of diversity. Through DNA fingerprinting, it has been established that *I. trifida* and the tetraploid forms of *I. batatas* are closely related to cultivated hexaploid *I. batatas*. In several publications, analysis of molecular variance (AMOVA) indicated that >90% of the total variance was within regions. DNA fingerprinting studies on sweetpotato have also revealed that there is more diversity within regions than between regions. DNA studies have also established that the secondary centre of diversity is associated with wide-spread cultivation.

DNA based approaches therefore reduce genotype errors and eliminate duplicates, hence enabling breeders to (a) distinguish different gene pools to exploit in sweetpotato breeding, (b) combine different sources of resistance corresponding to different genes; (c) exploit historic recombination and selection; and (d) identify genetic variation and trait value from wild germplasm as has been demonstrated for drought tolerance in *I. triloba*, virus resistance in *I. cairica*, resistance to stem nematode and sweetpotato viruses in *I. purpurea*.

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### **2.3. Marker-assisted selection/breeding and its potential use for sweetpotato improvement**

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*Awais Khan*

Dr. Khan reviewed the concept of MAS and its application in plant breeding. He also reviewed QTL methods and the importance of QTL mapping in crop improvement.

In MAS, the association between molecular markers and causative gene is of critical importance. Therefore, significant effort is put on marker-trait association identification. In this session, participants were shown the steps involved in developing linkage maps, in which segregating populations are phenotyped for traits and quantitative datasets. The segregating populations are also genotyped by scoring a large number of polymorphic markers in the populations to obtain marker data from which linkage maps are generated. QTLs are then located with the integration of genotype and phenotype data. The types of DNA markers, include randomly amplified polymorphic DNA (RAPDs), amplified fragment length polymorphism (AFLPs), microsatellites/simple sequence repeats (SSRs), and SNPs. A good marker is one that is polymorphic, reproducible, easy to use, economic, and has high throughput. Currently, there are more prospects for targeted and precise sweetpotato selection and breeding, especially with the ongoing developments in genome sequence, genome browser, next generation molecular markers, dense genetic maps, phenotypic data, and database and analytical tools.

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### **2.4. High-throughput and precise phenotyping**

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*Awais Khan*

Dr. Khan discussed the need for developing high-throughput and precise phenotyping techniques. He pointed out that phenotyping techniques would be crucial for effective analysis and utilisation of marker and genomics data from next generation sequencing tools. Some of the tools that could be adapted include use of cameras to enable image based phenotyping, leaf chlorophyll metre to measure leaf chlorophyll content; and adaptation of NIRS in the metabolite profiling for nutritional quality and stress tolerance. Such tools could be used to achieve high throughput phenotyping in controlled environments and field by enabling a consistent, fast and accurate capture of phenotypes of the traits of interest.

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## **2.5. Accurate sweetpotato phenotyping of agronomic traits, why it is important for MAS**

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*Awais Khan and Bramwel Wanjala*

The presentation highlighted the need for use standardised protocols for data collection and common descriptors. Characterisation of morphological diversity is useful for variety/clonal identification and is especially important for gene banks charged with the task of curating germplasm collections. Given the high numbers of germplasm involved, similarities between germplasms and the need for accuracy, information management can be improved through standardised data formats, tools for accurate field based phenotyping, data repositories, and data analysis and visualisation tools. New techniques are under development to facilitate work in this area.

The following points emerged from the discussion that took place after this presentation:

- In response to a question on how to deal with variations among individuals when scoring for qualitative traits it was suggested that it is important to look at descriptors and rehearse scoring.
- Phenotyping has not received a lot of attention, yet it can increase the usefulness of information obtained out of the genotyping work. There is therefore need for breeders to consider adoption of some of the upstream techniques for fast and accurate phenotyping.
- There is need for investment to support work aimed at improvement of high-throughput phenotyping.
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## **2.6. Sweetpotato genotyping procedures for SSA**

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*Mercy Kitavi*

Dr. Mercy Kitavi reviewed procedures for DNA fingerprinting and clone identification of sweetpotato in SSA. Participants were taken through the steps involved in plant tissue sampling; DNA extraction and purification; DNA quantification and quality assessment; DNA amplification (marker assays); data generation, analysis and interpretation.

After the presentation, participants were taken on a tour of the research laboratories at BecA-ILRI Hub. DNA is the blueprint of inheritance and extraction of high quality, quantity. Pure DNA is key for all genetic work. Therefore, the breeders were taken through a practical laboratory session on extraction of DNA from sweetpotato tubers and leaves and how to check on quality and quantity.

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## 2.7. Practical exercise: DNA fingerprinting, clone identification and sweetpotato QTL mapping

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*Mercy Kitavi and Dorcus Gemenet*



*Participants during a practical session at the BeCA-ILRI hub*

In the practical exercise participants were taken through the steps involved in DNA fingerprinting and clone identification. The facilitators explained the concept of molecular markers and how it is applied in plant breeding to identify genotypes with traits of interest. Distinctions were made among the different types of molecular markers - SSRs, AFLP, RAPDs, SNPs, and Restriction fragment length polymorphism

(RFLP). The presentation also reviewed fragment analysis systems: agarose gel; polyacrylamide gels; and capillary based fragment analysis. Since sweetpotato is a polyploid crop, most of the data analysis software are designed to analyse molecular data in a diploid format. However, there is an option to convert molecular data into binary format.

The discussion then moved to the conversion of SSR base pairs data file into binary format using ALS Binary software, and then steps in phylogeny and clone identification with DARwin software which was developed for diversity and phylogenetic analysis on the basis of evolutionary dissimilarities. Steps on the construction of phylogenetic trees using the dissimilarity file were discussed. Participants were guided through the interpretation of the constructed phylogenetic trees. And a practical exercise on QTL analysis and construction of sweetpotato linkage maps using AFLP data. Participants generated a linkage map in JoinMap for Tanzania x Beaugard F1 mapping population data set.

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## 2.8. Practical exercise – Genome wide maps; SNP marker development in hexaploid sweetpotato using GBS

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*Bode Olukolu*

Dr. Bode Olukolu's presentation covered GBS and its applications in sweetpotato. He noted the importance of interdisciplinary research in the development of genomic resources; and the central role of molecular markers in the development and utilisation of genomic resources and genetic analyses. The focus of the presentation was on GBS pipeline and covered:

- Pre-library preparation (DNA quality check, selection of enzyme combination, and barcode/adapter design);
- Library preparation (double digest, adapter/barcode ligation, size selection, PCR amplification, and Illumina sequencing);
- SNP-calling using GATK-based pipeline (pre-processing reads, alignment to reference genome, calling SNP genotypes, filtering for high confidence/quality SNPs); and
- Processing and filtering of the output Variant Call Format (VCF) file.

Participants were shown the data sets for a diploid *Ipomoea* and hexaploid sweetpotato. They were also taught how to use SNPs for a high-density linkage map in the diploid *I. trifida* F1 biparental mapping population.

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## 2.9. What do we know about the *Ipomoea* genome and how can this be used in breeding improved sweetpotato varieties?

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*Robin Buell*

This presentation first revisited the concepts of genome and genomics and then focused on the status of knowledge on sweetpotato genome and the progress made in the development of a sweetpotato genome browser. Dr. Buell described basic concepts underlying genome assembly and genome annotations (structural, functional, repetitive sequences, genome landscape).

Steps involved in genome annotation were reviewed and references made on the progress that had been achieved in relation to sweetpotato. Genomes of *I. trifida* and *I. triloba* were assembled under the GT4SP as reference genomes for sweetpotato. For *I. trifida* NSP306 (diploid) 72.6% and 90.3% of *I. batatas* genomic DNA and RNA-seq align to this genome, while for *I. triloba* NSP323 (diploid) 65.5% and 87.0% of *I. batatas* genomic DNA and RNA-seq reads aligned. A demonstration was given on accessing and exploring the genome browser. Key features of the browser were highlighted. The participants were also shown how to search sequences in the genome browser.



*Robin Buell makes her presentation*

Participants reflected on and discussed the progress made in the development of genomic tools for sweetpotato improvement. The following are some highlights from the discussion:

- There is need for diversity assessment in the populations used by different programs was pointed out.
- Work on phenotyping techniques is lagging behind genomics work and there is need to give it more focus.

- Genomics-assisted breeding in sweetpotato is expected to hasten the conventional breeding work and facilitate release of better adapted and high quality varieties e.g. through better approaches to selection of parents.
- The new tools developed through the GT4SP will need to be made available at the support platforms – to support population improvement work.
- There is need to compare application of the tools being developed for sweetpotato with the tools available for other crops.
- Continued interaction among members of the sweetpotato breeding community is needed to further promote learning about the tools under development.
- It was evident that the participants of the workshop enjoyed and learnt more from practical hands on sessions, therefore, a webinar will be organised to follow up on some of the sessions.

### **3. Session B: Sweetpotato SpeedBreeders annual meeting (theme: Sharing progress, improving our methods, and considering next steps)**

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#### **3.1. Introduction to the sweetpotato database infrastructure**

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*Lukas Mueller*

The purpose and goals of having a sweetpotato database is to (a) enable efficient storage of all sweetpotato breeding data; store trial data, phenotypic and genotypic information and metadata; (b) incorporate analysis tools; (c) enable easy querying of stored data by slice data by year, location and program; and (d) to enable utilisation of new, genome-based breeding methods.

Previously available methods for data storage such as books and hard copy files, personal computers and software such as Excel had various challenges and limitations. Hard copy files were bulky and tedious to search through. While Excel based data management had the advantage of being easy to use and giving users more control; it also had challenges, such as difficulty of sharing data, combining data across worksheets, ensuring the integrity of data, management of large datasets, and management of genotyping information.

Presently, most data is managed using the web / 'cloud'. For instance, YouTube for videos, Google for documents, Flickr and iCloud for photos, and twitter for status updates. To manage sweetpotato breeding data, sweetpotatobase was created. It has the following components of data infrastructure:

1. Main Data store (<https://sweetpotatobase.org/>)
2. Analysis (integrated with sweetpotatobase) -<http://hidap.sgn.cornell.edu/>
3. Data collection which is done using Android FieldBook App or AccuDataLogger

With sweetpotatobase one can input or get information on locations, field layout, accessions, crosses in a breeding program, phenotyping, genotyping, and import or export data or conduct analyses in R or HIDAP. The BrAPI of sweetpotatobase has a standardised way of exchanging breeding data between applications (such as HIDAP) over the internet.

As part of the database requirements, trait dictionary and measurement procedures (ontologies) as well as naming of plant accessions have been standardised. The sweetpotatobase enables integration of genotyping data with phenotyping data.

To ensure data security on the web, the data is protected by logins. There are also different levels of user access privileges, and regular on-site and off-site backups. To ensure compliance with Open Access Policy, the data in sweetpotatobase is open. However, one needs a user account to be able to download. Downloads are tracked by account.

The 'cloud' approach on which sweetpotatobase is built has the following advantages:

- Easy to use through a web browser
- No software installation necessary as software is continuously updated
- All data automatically integrated and it is possible to query over several years and locations
- Integrates phenotypic with genotypic data
- Currently the only challenge with the tool is that it requires internet connectivity.

Discussion on this presentation centred on the following issues:

Sustainability of sweetpotatobase after the project ends: The database has been developed for seven crops. When the project ends, the cassava one will be taken up by IITA.

Participants were informed that the program at Cornell would continue to maintain the database, even after the GT4SP came to an end. All the databases use the same code so they are easy to maintain as long as the institution still exists.

Integration of the databases available at different levels: There are different databases at lab, gene bank and breeding levels. These are separate tools, but they could be linked through web links.

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## **3.2. Sweetpotatobase and the need of a breeder in a database**

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*Alex Ogonna and Bryan Ellerbrock*

The design of sweetpotatobase took into consideration the features that breeders need to have in a database. Such a database would:

- Have a simple interface for data curation;
- Have a platform with the appropriate tools that ensures data quality and integrity;
- Ensure data storage and security;

- Support effortless data sharing and archiving;
- Support various forms of data retrieval for analysis and decision making;
- Provide a platform for phenotypic data analysis;
- Provide valuable metadata information on accessions, trials and weather information for trial sites;
- Have a very intuitive and user friendly web interface or framework.

Sweetpotatobase integrates these features in its design and functionality. The design has also taken into consideration the needs on data security, sharing and archiving features.

These are:

- Data protection from unauthorised access, use, change and destruction
- Open access to any registered user
- Secure network
- Backups and storage
- Data sets are easily archived
- Support file formats such as xls, csv, and txt
- Acknowledges ownership

Sweetpotatobase can facilitate phenotypic data analysis through SPBase raw data statistics, SPBase correlation analysis, SPBase population structure analysis, and through HIDAP. SPBase also provides metadata information for accessions, field trials and site weather.

A demonstration on SPBase was done with the participants. The demonstration covered aspects such as a) managing breeding programs and locations, b) managing accessions and the list manager and c) managing trials and phenotyping using FieldBook App.

The following points were discussed:

- Participants were given the context – that this initiative was a smaller project within SASHA, with key programs being the breeding programs in Lima, Ghana, Uganda and NCSU. The tools were still being developed and beta tested, after which they would be rolled out in other breeding programs.
- CloneSelector works well in many of the programs. Therefore, the aim is not to replace it, but to improve the package in an iterative process.

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### 3.3. Sweetpotato ontology/descriptors status

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*Simon Reinhard*

Ontology refers to a formal system of knowledge organisation. There are two possible ways to use ontology for big data: 1) use ontology to bridge datasets across domains and 2) use ontology to combine deep domain knowledge and raw data. An ontology is built to share common understanding of the structure of information among people or software agents; to enable reuse of domain knowledge; to make domain assumptions explicit; and to analyse domain knowledge. The ontology building process is iterative. It initially starts with nouns and verbs where a noun would be a class, attribute or instance while a verb would be a relation.

Within the CGIAR crop lead centres, an initiative was launched in 2008 to crop ontology as a resource for enabling access to breeders' data. The initiative aimed at harmonising and improving access to data. The themes for crop ontology have revolved around: general germplasm information; phenotype and traits; plant anatomy and development; location and environment; trial management and experimental design; and structural and functional genomics



*A cross-section of participants*

Sweetpotato ontology is based on FAO/ International Board for Plant Genetic Resources (IBPGRI)/CIP descriptors and other variables developed by CIP/SASHA, and NCSU. The current sweetpotato ontology has 206 variables and these continue to be improved. sweetpotato crop ontology builds on existing work. It is not static; it can change but there is a process to be followed to effect any change. Recent activities on sweetpotato ontology include:

- Continued consultation with the crop ontology community on best practices (PAG 2016, PhenoHarmonis conference, May);
- GT4SP meeting at NCSU adding/harmonising NCSU traits and reviewing existing traits;
- Adding traits from drought research on sweetpotato;
- Update on crop ontology website ongoing (to enable review at this meeting).

Ongoing work and issues on sweetpotato ontology include:

- Review of utility of traits and measurement methods
- Documentation of measurement methods
- Harmonisation of variable names

- Avoidance of trait duplication
- Maintaining backward compatibility with existing data

More research is still needed on how best to include photographic information and how to take care of time-series variables of the same type or several biological samples from a field. The next steps in sweetpotato ontology data will focus on:

- Reviewing traits and variables for adequateness and measurement procedures (breeders)
- Updating references to protocols
- Updating protocols to co-identifiers
- Establishing a process of review

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### **3.4. New tools to improve efficiency of data analysis**

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*Reinhard Simon, Raul Eyzaguirre, Luka Wanjohi, Omar Benites, Luis Duque, and Awais Khan*

The work in this area has been motivated by the need for tools to enable faster routine analysis of breeding trials. The tools under development are building upon current tools such as CloneSelector. The design of the new tools is such that they are compatible and work with current community tools such as sweetpotatobase, KSU FieldBook App, and AccuDataLog. Some of the technical updates aim to take advantage of better interactivity (through linked data and linked views), R reproducible reports for automating analyses, and ontologies to facilitate (statistical) handling of variables. In the current developments AccuDataLog and FieldBook App target the component on data capture while sweetpotatobase serves database needs and BrAPI and HIDAP on data analysis.

AccuDataLog is a mobile field data collection app that runs on Windows mobile and Android for robust data collection in the field. Developed by CIP (SASHA), the app, which operates on English, Swahili and Chinese language modes, can automatically import field books into mobile devices and allow for field based data entry. The app has the following features:

1. An integrated barcode label technology (1D and 2D)
2. Real time data entry validation: e.g. numeric, date, string length, lower limits, and upper limits
3. User defined lower and upper limits in Excel
4. Print on demand of barcode labels via mobile printing

So far the AccuDataLog has been adopted by the sweetpotato breeding programs in Ghana, Mozambique and Uganda.

FieldBook App was initially developed at KSU. It uses smartphones running on Android and can be downloaded from Google Play. It has nine trait formats: numeric, percent, categorical, date, text, Boolean, counter, photo and audio. The software has a resource folder where users can upload cheat sheets, pictures, shapes, images among others to aid phenotyping.

HIDAP is an analytical tool that is a hybridisation of CloneSelector with additional features. Unlike CloneSelector, HIDAP does not use Excel. HIDAP and CloneSelector use the same R script. The program has an interactive feature that can give automatic reports generated using actual data and metadata analysis. At the time of reporting, version 1.0 windows installer, a MET view, and genotype data were in the pipeline for HIDAP.

Improved genome sequencing and phenotyping have resulted in the generation of enormous amounts of data. To address this, an integrated analysis approach is being developed. This will provide new tools for processing data and integrating it for actual biological insights.

The next steps for HIDAP will be the development of additional functionalities and tools by GT4SP colleagues at NCSU, University of Queensland (UQ), MSU and BTI. These will enable an integrated analysis of next generation multi-dimensional data sets (QTL mapping, association mapping, selection schemes and GS).

During discussions, the following issues were raised:

- There was concern about the accessibility of the web-based applications given the challenge experienced in some countries due to poor internet connectivity. A suggestion was made that users purchase modems to improve internet connectivity in places where challenges are experienced. Programs were also encouraged to budget for improving internet connectivity, for example through purchase of modems and routers.
- For the analytical tools being developed, a Tukeys test component should be included for use in dealing with outliers.
- A suggestion was made to incorporate indices that could enable concurrent selection for many traits was made. In response, it was pointed out the fact that Pesek Baker and additive main effect and multiplicative interaction (AMMI) components had already been incorporated into the tools.
- There was a concern that AccuDataLog may be expensive. However, the advantage is that the gadgets are durable.

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### **3.5. Sweetpotato Knowledge Portal**

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*Christine Bukania and Luka Wanjohi*

Participants were given an online tour of the Sweetpotato Knowledge Portal that had been relaunched in February 2016. To prepare for the presentation, participants had been requested to register as members to the portal.

Apart from introducing the new features on the portal, participants were shown how to upload files and add the metadata, add external links, projects, news items and events, join

discussion fora and conduct searches. Those who had not managed to register were encouraged to do so.

One of the key features in the redesigned portal was the inclusion of a project pages section which gives information about key projects undertaken. Additional interactive features include discussion fora, to which any registered member can join. This means that breeders can now join discussions being held by other communities of practice and keep up-to-date with themes that cut across to their breeding work.

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### **3.6. Re-analysis of heterotic gain in Mozambique with clones derived from Ugandan inter- and intra- gene pool crosses**

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*Makunde G., M. Andrade, W. Grüneberg and R. Eyzaguirre*

The objective of the reported study was to estimate and compare family means of inter and intra-genepool crosses under water stress conditions. The genepools used were Population Uganda A and Population Uganda B which were made of parents previously separated using SSRs as distinct. For the inter-gene pool crosses, there were 64 families developed from crosses between eight Population Uganda A parents with eight Population Uganda B parents. In the intra-genepool crosses, there were 24 families each for the crosses within Population A parents and Population B parents. The clones were planted in a factorial design with 500, 700 and 1,124 clones respectively for the AxA, BxB and BxA crosses. The clones were planted under irrigated and non-irrigated conditions with two replications per treatment combination. All clones were randomised and planted together.

Storage root yield for the BxA population was higher in the irrigated (7.2 t/ha) and non-irrigated (5.5 t/ha) treatments compared to the AxA population that had 6.70 t/ha under irrigated and 4.2 t/ha for the non-irrigated treatment. The BxA population had better performance compared to the BxB population that had mean root yield 6.4 t/ha and 4.7 t/ha for the irrigated and non-irrigated treatments, respectively.

In the next steps under this work, clones will be selected from the families that had good performance under the drought stress treatment (non-irrigated) and from those families that had good performance under the irrigated treatments. The selected clones will then be evaluated in preliminary trials whose results will also be used to determine the variance components for efficiency studies of the accelerated breeding scheme. There is also a plan to undertake another heterosis exploiting breeding scheme experiment in Mozambique that will entail crossing Umbeluzi parents and Gurue parents on a large scale followed by evaluation of the offspring to enable discarding of parents that could be considered “bad family makers” at the Umbeluzi and Gurue crossing blocks. This will enable the development of populations with higher frequencies of drought tolerant clones and clones with adequate response to rains.

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### 3.7. Re-analysis of heterotic gain in Uganda

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Wasonga C., R. Mwanga, R. Eyzaguirre, and W. Grüneberg

The objective of this trial was to establish the yield gains in early generation sweetpotato clones derived from inter and intra-population crosses of two East African genepools (Population Uganda A and Population Uganda B) hypothesised to be mutually heterotic. To generate the clones used in the study, eight parents were selected from each pool and controlled crosses between gene pools were made following A8xB8 factorial cross design (64 families). Within gene pools A8xA8 and B8xB8, a diallel cross design was followed producing 28 families each. The parents were selected not on the basis of good combining ability to produce higher yields, but on the basis of having other traits of interest such as resistance to SPVD, orange-fleshed colour and good taste. Twenty clones were randomly selected for each of the families. Clones from each of the 120 families were tested in four environments, Namulonge (2014A, 2014B and 2015A) and Serere (2015A).

The data collected from the trial included, SPVD scores, Alternaria stem blight scores, sweetpotato weevil damage and storage root and vine weight. Mean storage root, vine and above ground biomass yield data were calculated for the test clones and the checks (parents) and the values used to calculate mid-parent mid-offspring heterosis. The mid-parent mid-offspring heterosis was calculated using the formula:

$$\text{Heterosis increment, \%} = \frac{[\text{Clone value} - \frac{1}{2}(P1+P2)] * 100}{(\frac{1}{2}(P1+P2))}$$

where P1 and P2 are means of parents one and two, respectively.

NASPOT 5, Huarmeyano and associated families were dropped from the final analysis. A recent genepool separation study had shown that NASPOT 5 did not belong to population Uganda B. Huarmeyano was known to belong to neither of the two Ugandan sweetpotato populations.

Results showed that vine production was higher than storage root yield. For the 48 BxA sweetpotato families evaluated, heterosis increment associated with storage root was higher than that of vine and biomass production. The combination of 6x8 B and A parents through controlled crosses that had 48 families gave an overall heterosis increment of 16% for storage root yield over the mid-parent. A total of 63% of cross combination and families (30 out of 48 families) had heterosis increments of >0% for storage root while 23% of cross combination and families (11 families), exhibited heterosis increments of >100%. Four families had storage root yield heterosis increment of above 400%. Heterosis increments for specific parents and parent combinations was high and more variable for Resisto, Wagabolige, Mugande, and New Kawogo families from genepool B, while for genepool A (which were the males) large heterosis increments were obtained from Dimbuka-Bukulula, NASPOT 1, NASPOT5/58 and NK257L.

It was concluded that in addition to improving for other important quality and adaptation traits such as SPVD resistance, exploitable heterotic yield increment for storage root is achievable through the combination of parents from the two East African sweetpotato gene pools. The large variations in heterosis yield increments observed between the BxA families suggests that there are differences among the parents due to combining ability.

Identification of testers for each population and crossing all genotypes in the two populations with the testers might be useful in the separation of heterotic groups for population improvement. Work has commenced to make crosses between parents in the two crossing blocks to identify parent combinations that produce families with high heterosis increments.

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### **3.8. Refining maturity period and quality traits per maturity period for released varieties in Mozambique**

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*Abilio Alvaro, M. Andrade, G. Makunde, J. Ricardo, O. Idowou and W. Grüneberg*

In Mozambique, OFSP plays an important role in human nutrition. It is an important source of carbohydrates, beta-carotene and other micronutrients. OFSP is also a component crop for diversification/rotation in the country. The traits that farmers and consumers in Mozambique prefer include high storage root yield, early maturity, pest and disease resistance, tender leaves (for vegetables), ability to grow during all seasons, good in-ground storability, sweetness, marketability, and good root shape.

Early maturity, which can be defined as the ability to give high yield of mature storage roots at 3 to 4 months after planting, is an important trait for sweetpotato in the country as it bridges the hunger gap before harvest of main crops like maize or cassava. Early maturity allows for piecemeal harvesting especially for those varieties with good in-ground storability. The trait is also preferred where sweetpotato is a commercial crop and yet the growing seasons are characterised by a terminal dry spell.

The objectives of the reported study were: a) to refine maturity periods of released cultivars in Mozambique; b) determine changes in key macro- and micronutrients associated with early or late harvesting of released cultivars in Mozambique; and c) to recommend to farmers on the right time to harvest. To address the outlined objectives, 25 sweetpotato varieties previously released in the country were evaluated alongside three checks in a randomised complete block design. Four trials were established under rain-fed and irrigated conditions. The varieties were evaluated at four harvest dates, at 3, 4, 5 and 6 months after planting. The traits measured included, storage root and vine yield, micronutrients (iron and zinc), beta-carotene content, dry matter content, starch and protein.

Among the early storage root yielders, nine cultivars (Irene, Bela, Melinda, Namanga, Erica, Tio Joe, Sumaia, Cecilia, and Lourdes) had yields above the national average (7 t/ha) at three

months. However, there were notable nutritional changes in the early maturity group during the growing period with a linear increase in nutrients occurring between the third and the fourth months after planting.

The study concluded that the early maturing cultivars fit well in short growing seasons and could especially be useful in situations where threats of climate change are experienced. The high storage root yields at three months could contribute to the breaking of the hunger period and also ensure income generation where sweetpotato is a commercial crop.

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### **3.9. Breeding of sweetpotato for improvement of root dry matter and beta-carotene content in Ethiopia**

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*Fekadu Gurmu Balcha*

Sweetpotato is among the most important root crops in Ethiopia. It is second in area coverage and first in production among root and tuber crops. The key traits of interest to sweetpotato breeding in the country are: storage root yield, high beta-carotene content, dry matter content, resistance to diseases (especially viruses) and resistance to sweetpotato weevils. Vitamin A deficiency is prevalent among vulnerable children, pregnant women and lactating mothers in Ethiopia. With its high beta-carotene content, OFSP could be a cheap and accessible solution to this problem. Therefore, OFSP cultivars that are adapted to Ethiopian production environments are needed. The OFSP varieties should also have increased dry matter content in order to be acceptable among the targeted consumers.

The objectives of the reported study were to:

1. Determine the combining ability, type of gene action and heritability of root dry matter content (RDMC) and beta-carotene content, and yield related traits of selected sweetpotato clones for further evaluation and breeding.
2. Estimate the magnitude of Genotype by environment (GxE) interactions and to select stable and high yielding candidate sweetpotato clones for RDMC, beta-carotene content and fresh root yield, and identify the most discriminating and representative test environments in Ethiopia.
3. Assess associations between yield and yield related traits and identify the most efficient yield-predicting traits in sweetpotato for effective selection.
4. Determine the nutritional value of newly developed OFSP clones and establish the associations between beta-carotene content and other micronutrients for targeted large scale production to alleviate nutrient deficiencies.

The first experiment focused on genetic analysis of root dry matter and beta-carotene content, and yield related traits in sweetpotato. Crosses were made between ten orange-fleshed and ten white-fleshed sweetpotato parents. The resultant F1 clones were then evaluated. Results from the study indicated that the general combining ability (GCA) to specific combining ability (SCA) variance ratios were 0.96, 0.94, 0.74, 0.96 and 0.97 for

RDMC, beta-carotene content, SPVD, fresh root yield and harvest index, respectively, indicating that the inheritance of these traits was controlled mainly by additive genes. Progenies of some of the crosses showed positive heterosis for RDMC and fresh root yield, indicating the possibility of selecting progenies that outperform both of their parents. Crosses such as Ukerewe x Resisto, Resisto x Ogan Sagan, Ejumula x PIPI and NASPOT-1 x Temesgen had high beta-carotene content, high RDMC that exceeded the mean of the best parent, and medium to high mean fresh root yield. Continuous progeny selection among these families is important to develop OFSP varieties with high RDMC.

A second experiment was done to determine GxE interaction and stability of sweetpotato clones for root dry matter and beta-carotene content, and fresh root yield. The experiment was conducted in six environments. A total of 24 F1 progenies and one check variety used for the GxE study. The GxE and stability analysis were conducted using genotype and genotype x environment interaction (GGE) bi-plot and AMMI analysis. Environment, genotype and GxE interaction variances were significant ( $p < 0.01$ ) for RDMC, beta-carotene content, and fresh root yield. Four clones, Ukerewe x Ejumula-10 (G1), Resisto x Ejumula-7 (G6), Resisto x Ogan Sagan-23 (G19) and Ejumula x PIPI-10 (G20) were selected based on their performance and stability. The study demonstrated the possibility of breeding sweetpotato varieties with a balance of high RDMC, medium beta-carotene content and high fresh root yield, with wide or specific adaptation.

An additional study was conducted to establish correlation and path-coefficient analyses of root yield and related traits among selected sweetpotato clones. Results from this study indicated that root yield was positively and significantly correlated with most traits studied, indicating that component characters should be simultaneously selected for improvement of sweetpotato. From the path-coefficient analysis it was shown that individual root weight, number of roots per plant, RDMC and above ground fresh weight had high positive direct effects of 0.821, 0.776, 0.276 and 0.410, respectively, on fresh root yield. The study established that the mentioned traits were the most important characters determining fresh root yield in sweetpotato and were recommended as indirect selection criteria.

The newly developed OFSP clones were also evaluated for nutritional quality. The candidate OFSP clones, G8 (Resisto x PIPI-2), G15 (Resisto x Temesgen-23) and G19 (Resisto x Ogansagen-23) were good sources of nutritional traits such as vitamin A, iron zinc, protein, sucrose, glucose and fructose. The study recommended the selected genotypes for large scale production, food processing and for use in sweetpotato improvement work aimed at alleviating nutritional deficiencies in Ethiopia.

### 3.10. Panel discussion on the characteristics driving adoption and the varieties that have done best

*Panellists: M. Andrade, M. Chiona, J. Ndirigwe, O. Mwenye, G. Ssemakula, S. Laurie*  
*Moderator: R. Mwangi*

During the panel discussion, breeders identified the varieties that had been adopted most successfully in their countries, and the factors that contributed to the adoption. These are summarised in the table below.

Country	Preferred varieties and factors driving adoption
<b>Benin</b>	Falanga is preferred because it is high yielding, drought tolerant, has big roots, is marketable, and it is not affected by viruses, while Jewel is preferred due to its good quality and high yield.
<b>Burundi</b>	Mugamba is the most adopted variety because of its high yield and high dry matter content. Its weakness is that it produces few vines. Nabusenganya, which is a landrace is also preferred because of its high sweetness, even though it is poor yielding.
<b>Ethiopia</b>	Hawasa 83 which was released in 1987 is widely distributed across the country because it has high dry matter, and is drought tolerant.
<b>Ghana</b>	Apomuden is preferred because of the many ways it can be utilised and because of the strong promotional activities that have been undertaken.
<b>Ivory Coast</b>	Irene has been selected because it has performed well in three of the four test regions. People also prefer it because of its purple vine/leaf colour which is believed to cure anaemia. Belabela is preferred because it pounds well.
<b>Kenya</b>	Kenspot 1 is high yielding and has good vine production. Kenspot 4 is preferred because it is orange-fleshed, high yielding, and has good processing quality.
<b>Madagascar</b>	Navito is the preferred variety in Madagascar because of its high yield, high dry matter content, and high vine production.
<b>Malawi</b>	Kenya, is the dominant sweetpotato variety because it is high yielding, has high dry matter and high vine retention that enables its propagation in the next season. The orange-fleshed Kadyabwerere is a popular variety and has been widely promoted. It is a high yielding sweetpotato with high vine retention, very sweet taste, a long shelf life and good qualities for processing.
<b>Nigeria</b>	The yellow-fleshed varieties Ex Ibarium and Buttermilk are widely grown and are marketable because they produce high quality fries. They are also drought tolerant, high yielding, have high dry matter and have good root shape. The OFSP variety Mothers' Delight has been promoted extensively, but there are concerns about its low dry matter.
<b>Peru</b>	Sweetpotato is traditionally grown in three agroecological zones in the lowlands/coast. Kwambachero and Yunatan, which are farmer field selections are grown. The deep OFSP variety Benjamin which is high yielding and is widely preferred.
<b>Rwanda</b>	Adoption is linked to participatory breeding. Farmers compare root yield of new varieties with what they have. A new variety has to be higher yielding, have high dry matter content and red root skin colour, be resistant to SPVD, and have long

<b>South Africa</b>	<p>field storability to allow for piece meal harvesting. The preferred OFSP varieties are Kabode, Vita and Gihungamukungu. Gihungamukungu is particularly liked by processors because it is ideal for puree production. For OFSP, promotional activities and associated value addition also influence adoption.</p> <p>The drivers for sweetpotato variety adoption include farmer participation in the selection of varieties, high dry matter content (28%), higher yield, good flavour and good root shape, availability of planting material, tolerance to Alternaria blight and moderate drought tolerance for the white-fleshed variety, Bophelo. The OFSP variety, Opelu, which was released in 2011 has also been adopted following promotion and awareness campaigns of its nutritional quality, starchy taste, and good root storability. Opelu has high quality processed products such as crisps and juice. The variety, Ndou, is liked for its moderate drought tolerance and tolerance to Fusarium wilt.</p>
<b>Uganda</b>	<p>High yield, high dry matter content, and pest and disease resistance contribute to the adoption of released varieties. NASPOT 8 which was released in 2008 is resistant to SPVD, has high yield (16 t/ha), high dry matter content (&gt;30%), has longer storage quality, good root shape, and is early maturing. New Dimbuka is preferred because it is high yielding (&gt;35 t/ha), has high vine production, is moderately resistant to SPVD and has high dry matter content (&gt;32%). The challenge with New Dimbuka is that sometimes its roots become too big but this can be manipulated through plant density.</p>
<b>United States</b>	<p>Covington and Beauregard dominate and North Carolina (NC) produces 45-50% of the country's total sweetpotato production. Covington, which was released in 2005 covers 85-90% of planted area in NC. The US farmers' sweetpotato commodity organisation in NC have contributed to the development of the crop. The farmers pay a levy that is reinvested into research and marketing. The major traits that drive adoption are yield, quality and root shape. Overall the development of processing industry has driven growth of the sweetpotato industry in US.</p>
<b>Zambia</b>	<p>Chingova (Tanzania) and Olympia are preferred because they are high yielding and early maturing, and also have good taste, high dry matter, and good vine survival. The successful uptake of Tanzania is attributed to the fact that it was introduced at a time when the country had experienced drought and good distribution/marketing of vines. Rising wheat prices was also a driver for adoption, since sweetpotato was a cheaper alternative source of calories. Other factors that have increased adoption of these varieties are promotional campaigns and linkage of multipliers and producers with the markets.</p>



*Some members of the panel on factors that drive adoption*

From the discussion it was observed that traits such as yield and root quality cut across the different countries. The main concerns for processors are related to dry matter content, susceptibility to damage during transport, sugar content, and taste/sweetness. The preference is to have high sugar content to eliminate addition of sugar in processed products. Processors prefer medium sized roots with regular shape to ease processing.

From a nutritional quality standpoint, the preferred traits are increased micronutrient content especially of iron and zinc, as well as higher vitamin C content which enhances iron absorption. However, it was cautioned that breeding for iron and zinc should aim at developing separate varieties because when the two minerals are in the same product, zinc outcompetes iron at the absorption sites. It was also pointed out that maltose adds flavour/taste, so there was need to look at alpha and beta amylase as these influence quality. Low asparagine content was also preferred as it ensures less acrylamides in chipping types. It was recommended that rural women be engaged in processing and utilisation of OFSP to identify preferred quality traits.

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### **3.11. An agronomist's thoughts on addressing sweetpotato resilience under changing climate conditions**

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*Mihiretu Cherinet*

The objectives of this presentation were to highlight overall impact of climate change on food security; review observed suitable climate for sweetpotato growth based on previously published data; review projected climate changes in the sweetpotato growing areas and their effect on sweetpotato production; discuss adaptation options; and facilitate discussion to design action points for climate resilient sweetpotato production.

Food and nutrition insecurity in SSA is expected to intensify with changing climatic conditions if no appropriate adaptation strategies are implemented. Today, root and tuber crops are the main source of food in SSA. These crops - including sweetpotato - are affected by temporal and spatial changes in climatic conditions, which are expected to result in a reduction of the areas currently considered as suitable for optimum sweetpotato production. Increases in temperature beyond optimal ranges for sweetpotato production are expected to reduce productivity through changes in the physiology of the crop coupled with negative effect on storage root growth. It is expected that there will be increased

severity of insect vector transmitted diseases such as SPVD, especially when the conditions favour the growth and survival of the vectors. Damage by insects such as sweetpotato weevils is also expected to increase with rising temperatures, while new pests may emerge. Water stress as a result of reduction in the amounts and duration of seasonal rains and more frequent incidences of erratic rains are expected to negatively affect sweetpotato production through reduced storage root production and loss of planting vines under drought conditions.

There is a need to identify and adopt suitable adaptation strategies that would position sweetpotato to contribute to food security under the changing climatic conditions. Genetic improvement of sweetpotato for increased resilience to the changing climatic conditions is one pathway that could be followed. Towards this goal, it would be important to consider: the current germplasm collection for sweetpotato; genetic potential of sweetpotato to adapt to climate change; the role of sweetpotato wild relatives; the traits future sweetpotato varieties would need to have; and the tools that breeders would require in order to develop resilient varieties.

Information regarding impact of climate change on sweetpotato is still inadequate. Therefore, there is need to understand the impact of changing climate and develop knowledge, models and tools that would support sweetpotato adaptation in the changing environment. Design of appropriate adaptation strategies would position sweetpotato to make a more significant contribution to food and nutrition security in a changing climate.

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### **3.12. Group discussions and feedback on sweetpotato resilience under changing climate conditions**

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*Mihiretu Cherinet and Koussao Some*

To further discuss the presentation on sweetpotato resilience under changing climatic conditions, participants were divided into five groups and tasked with discussing specific questions relating to the topic.

**Group one - Effects of current and predicted main climate change on agricultural productivity in the different countries:** This group had representation from Uganda, Nigeria, Burundi, USA, Madagascar and Ghana. The group members made the following observations:

- Uganda - increase in pest damage, sweetpotato weevil (SPW) and caterpillar, shorter growing seasons (lower yield for long season crops);
- Nigeria - unpredictable rainfall onset (planting material and yield), high temperatures influence pest dynamics; Burundi, unpredictable rains and shorter season;
- Madagascar - changing crop importance;
- Ghana - high temperatures and catastrophic rains;
- USA - unpredictable planting times.

The group discussed how these phenomena affected sweetpotato production to which they made the following contributions:

- Increased pest problems would lead to a higher use of pesticides. New pests were likely to emerge.
- Genetic erosion of sweetpotato would increase as a result of loss of propagation vines during long dry seasons.
- There would be decreased seed availability due to shortage of water.
- The cost of planting material would increase.
- The role of sweetpotato for food security would increase as a result of its higher resilience and growers challenged by climatic conditions would be more willing to buy planting vines.
- Other crops such as bananas, rice, wheat yams would be affected by the changing climatic conditions and sweetpotato could be expected to fill the gap that would arise as a result.

The group agreed that there were observed effects of climate change on sweetpotato production such as: changing distribution of rainfall in which too much rain led to flooding and too little rain led to increased pest infestation and higher levels of environmental pollution due to increased use of pesticides.

**Group two - Adaptation and mitigation strategies for climate resilient agriculture:** In the first part of the group's discussion, the focus was on the rating of sweetpotato against other crops in climate smart agriculture. The crop rated second to sorghum and cassava with regard to drought and high temperature tolerance and ahead of potato, banana, wheat, rice and maize. The group cited the following strengths of sweetpotato under changing climatic conditions: tolerance to heat and drought; genetic plasticity; short maturity period and low input requirements. However, exploitation of the crop under the changing climatic conditions was limited by its complex genetics, pests and diseases, vegetative/clonal propagation and poor/short storage/postharvest life. The group pointed out that the existing high genetic variability in sweetpotato increased the potential for improvement to adapt to climate change.

**Group three - Main traits that would position sweetpotato as suitable for climate smart agriculture:** These were: persistent vines; better storability; high yield; resistance to pests and diseases; earliness, and deep rooting to increase tolerance to drought.

**Group four - Is it timely to start breeding with a focus on climate change?** There was agreement that it was time to focus on climate change because erratic rains and drought were increasingly being experienced in different countries. The group, however, pointed out the need for a better understanding of the physiological basis and mechanisms of drought tolerance. The traits that should be focused on are root depth/architecture in relation to drought tolerance. The group emphasised that protocols would have to be developed and appropriate phenotyping tools assembled to carefully select for the traits of interest. This

work would need multidisciplinary teams made up of agronomists, physiologists, irrigation specialists, and breeders among others.



*Group discussions on climate change and sweetpotato breeding*

**Group five - Capacity of the sweetpotato breeding community to handle the problem:** The group observed that there was need for knowledge and information and more effort to profile/characterise drought tolerant varieties. To facilitate research in this area, functioning weather stations, proper greenhouse/field facilities and tools for studying roots would have to be established. Lessons could be learnt from the work done on other programs/crops and on genomic tools and methods developed for other

crops. The group highlighted the importance of creating partnerships with government advocates, university labs and students, and for sharing germplasm among breeding programs.

After the group presentations, a plenary discussion took place. The main points from this discussion are:

- The capacity of CoP members on climate change should be improved, and then suitable protocols developed. It is also important to state exactly what each program can do at their level
- The context in which drought tolerance is discussed should be clear. Drought scenarios in different agro-ecological zones (diagnostics) should be understood. Evidence research must be carried out. It will not yield quick results, but it will provide the information required to determine the type of traits that are suitable for drought tolerance.
- A multidisciplinary approach should be used to develop climate smart production systems for nutritious sweetpotato. This approach will help in identifying danger points that need to be addressed so that better adapted varieties are properly targeted and managed.
- Genetic variation is extremely important because clonally propagated crops are more vulnerable than seed propagated crops. Therefore, more investment should be directed towards germplasm conservation.
- Sweetpotato presents an opportunity to deal with drought. However, any work to improve the crop's resilience should be targeted. Diagnostics should be done properly and cost-effective approaches should be used to tackle the challenges.
- While breeders acknowledge the importance of climate change adaptation, their programs operate under limited resources. However, they were informed

- that work has already started to discuss and secure resources for research in this area.
- The participants were invited to collaborate in preparing a paper that will be presented at the African Potato Association triennial conference in October 2016.

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### **3.13. The importance and heritability of vine survival in drought-prone areas: preliminary results from Mozambique**

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*Maria Andrade, G. Makunde, A. Alvaro, J. Ricardo, J. Menomussanga, R. Eyzaguirre and W. Grüneberg*

A significant proportion of the land in Southern African countries is highly prone to dry weather. One of the greatest constraints to sweetpotato production is access to sweetpotato planting material. Lack of planting material is particularly acute for farmers in areas with prolonged dry seasons where conservation of the material is difficult. Scarcity occurs at the onset of rains. Farmers re-establish vines from re-sprouting roots or secondary growth from harvested fields, leading to loss of valuable time at the start of the rainy season. This challenge needs to be addressed since adoption of sweetpotato cultivars by farmers is related to availability of planting material and survival of vines. The objectives of the reported study were to:

1. Estimate survival of vines under drought stress in a collection of sweetpotato cultivars;
2. Measure sprouting ability of sweetpotato cultivars;
3. Measure nutrient changes of storage roots stored for three months under Triple S;
4. Determine heritability estimates of traits.

In order to address these objectives, 36 sweetpotato clones (19 released varieties, ten landraces and seven foreign introductions) were evaluated in a randomised complete block design with two replications at three sites and harvested at 5, 9 and 11 months after planting. At harvesting, stem length, petiole length, leaf size, storage root yield and foliage biomass data was collected.

The study established that clone performance varied significantly within treatments. There was a significant drop in vine yield as the harvesting period increased from five months at all sites. Introduced variety Resisto had the highest average stem length but no vines remaining after nine months at all sites. The length and thickness of vines in a clone could be responsible for drought tolerance in sweetpotato. Spatial soil differences affected survival of vines. Most clones could not survive after seven months at Gurue where the soils are lighter in texture with low water holding capacity. At Gurue, the inability to survive for long periods was exacerbated by virus infection. The ability of the vines of some clones to reach nine months and 11 months at Umbeluzi and Nwallate offers a source of planting material for the subsequent season. The rates of sprouting were also significantly different among

clones. Total biomass is key to vine survival under long dry spells in sweetpotato. Drought tolerance could be more related to survival rather than yield.

### Summary of discussion

- The following points emerged from the question and answer session that followed this presentation:
- Vine diameter is important and is usually measured. Stem length also makes a difference, it was not measured in these trials, but it will be included in the redesigned trials.
- In the North Carolina, sprouting from storage roots is done because of the weather conditions. One root produces 60 or more plants. In Mozambique, five roots could provide enough planting material for a household. For Triple S in Mozambique, the prevailing challenge is how to ensure that clean roots are used in farmer managed systems, and that people do not eat their planting material during hunger periods.
- Weevil damage in Uganda is so high that at 11 months, one would get nothing. In Mozambique, there were weevils in the plots but the level of damage was different in each.
- Remobilisation of resources was found to be very important in cassava. In sweetpotato, it has not been done, but the hypothesis is that it would be important.
- There are different types of drought in Mozambique. The study is testing drought in one agro-ecological zone. The weather pattern was checked for four years.

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### **3.14. Genetic improvement of important traits for selection in sweetpotato (*Ipomoea batatas*) controlled cross populations in Uganda**

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*Astere Bararyenya*

This presentation focused on a planned PhD study whose overall goal is to contribute to sweetpotato population development from which superior sweetpotato varieties could efficiently be selected to help producers and farmers in Uganda meet their food and nutritional security. The specific objectives of the study were to: (1) determine the relationship between phenotypic and genotypic characteristics among selected sweetpotato cultivars in Ugandan germplasm; (2) investigate the inheritance of beta-carotene content in sweetpotato; and (3) identify the yield performance of selected new developed sweetpotato clones across different environments.

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### **3.15. RTB Project reporting – a global reporting on sweetpotato progress [Theme 2.5 (2 = breeding; 5 = sweetpotato), 2015]**

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*Wolfgang Grüneberg*

The presentation focused on the reporting of progress made in sweetpotato breeding under five product lines in the RTB project: (1) Breeding tools, strategies, and approaches: sweetpotato (has 12 products with product or milestone reports); (2) Trait capture and gene discovery (has four milestone reports); (3) Population development and pre-breeding sweetpotato (with seven milestone reports); (4) Variety development sweetpotato (has four milestone reports); (5) Aligning research with farmers' and end users' priorities (with five milestone reports). Participants were informed that the reports on these milestones are available upon request.

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### **3.16. Progress in virus resistance breeding in Uganda**

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*R. Mwanga, C. Wasonga, G. Ssemakula, B. Yada, J. Kreuze, S. Fuentes, J. Low, W. Grüneberg, and C. Yencho*

SPVD which results from combined infection of sweetpotato by *Sweet potato chlorotic stunt virus* (SPCSV) and *Sweet potato feathery mottle virus* (SPFMV) is more devastating and cause significant yield losses that range from 50% to 90%. Experience from trials undertaken in Uganda showed that when very few clones were put into observation trials, all of them would be lost to virus damage. To increase chances of getting clones that could be advanced to the next level of trials, the number of initial clones under testing were increased. A total of 22 sweetpotato varieties were released in Uganda from 1995 to 2016. Among the 24 parents in the 2001/2002 polycross nursery that led to the 2007 release of NASPOT 7, NASPOT 8, NASPOT 9 O and NASPOT 10 O, four of the parents were considered resistant to SPVD, three were moderately resistant and the rest were susceptible.

Earlier studies on inheritance of SPCSV and SPFMV ruled out dominance effects for SPCSV and SPFMV resistance genes. At least 50% of all progenies derived from the resistant parent were resistant regardless of the model of inheritance (disomic, tetrasomic, tetradisomic, hexasomic). Exact allelic frequencies or dosage effects could not be estimated in this study. The data obtained suggested that while the frequency of resistant SPFMV and SPCSV alleles is high, the resistant phenotypes are not as common due to the polysomic nature of sweetpotato and the traits being recessive.

Recent efforts have focused on the development of populations for SPVD resistance and quality traits. Two distinct genepools (Population Uganda A and Population Uganda B) were assembled using molecular markers (18 SSR markers). Controlled crossing (inter- and intra-genepool) for population improvement and polycross crossing are in progress. Large numbers of the progenies resulting from the crosses with the target parents are then

screened in the field at sites in which SPVD pressure is high. One of the lessons learnt is that having the capability for distinguishing resistant and tolerant clones, for example by using real time PCR, helps to achieve progress with breeding for SPVD resistance.

A participant asked how SPVD resistance is scored to explain genetic basis for resistance. The presenter responded that clones that are disease symptom free in the field are considered resistant. Graft inoculations are also done to identify resistant ones. Real time PCR is used to distinguish resistant and tolerant clones.

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### **3.17. Progress MAS for SPVD resistance**

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*Wolfgang Grüneberg, Awais Kahn, Dorcus Gemenet, Federico Diaz, Maria David, and Raul Eyzaguirre*

The target for breeding for SPVD resistance is divided into four components:

- (i) Identification of marker associations and marker validation;
- (ii) Pre-breeding with germplasm resources exhibiting confirmed SPVD resistance, but exhibiting poor agronomic performance;
- (iii) Search for less SPVD susceptibility in advanced breeding lines and varieties with good agronomic performance;
- (iv) Heterosis exploiting breeding schemes (HEBS) – more inbreeding in two pools and offspring testing [not at headquarters (HQ) – Namulonge].

The general outlook of breeding for SPVD resistance is that more progress has been made in the area of marker associations and development, than on the side of breeding population development. At present AFLP, SSR and DArT markers have been developed but await validation. In breeding for SPVD resistance, it is of prime importance to have the right test population(s) after completing the validation of old and larger number of new next-gen markers with the VZ08. After validation, the markers will be tested on sweetpotato populations in Africa (Uganda). The target for this next step will be the large hybrid population that is being developed in Uganda and which will be put into field evaluations without pre-selection for SPVD during multiplication. This new hybrid population from genepool A and B in Uganda will allow for selection of the best parents for yield and SPVD resistance and validation of MAS for virus resistance in sweetpotato in an applied breeding program. With this, it would be possible to enter into MAS for SPVD in sweetpotato breeding testing >10,000 clones in early breeding stages with considerations duly made on the markers to be used.

The next steps in the work on MAS and SPVD resistance will entail validation of markers with about 500 clones of population VZ08, which is related to population VJ08 (same male parent). This will be done in mid-2017, followed by testing of the markers in applied breeding material at Namulonge. The best would be about 10,000 clones from the current AxB crosses on large scale. The intention is to select among parents in A and B genepools on

the basis of offspring performance AxB (yield and SPVD), and to compare predicted and observed response to SPVD resistance by using markers in applied breeding material.

The following points emerged from the question and answer session that followed the presentation:

- There is still need for work on phenotyping methods for SPVD resistance. Real time PCR would be useful for this. A challenge is that at present only a few clones (30 clones) are selected per family.
- A question was asked on whether genome editing technology could be deployed in future work to improve SPVD resistance.
- As follow up to the point made during the presentation that 12 resistant genotypes had been identified, it was suggested that the bulk of the 12 of resistant genotypes have the available markers tested on them using random permutations.
- On the role of clean seed is in controlling SPVD, it was observed that while clean seed is important, more investment should go into improving sweetpotato populations for the frequency of SPVD resistance.
- As to whether it would be better to put resources closer to where the SPVD challenge was more profound (Africa/Uganda), it was proposed that an ELISA reader be made available in Namulonge.
- Wolfgang was keen to understand the mechanism of resistance in one of the current clones whose offspring always seem to be resistant.

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### **3.18. Progress in diagnostic tools for virus detection and potential usefulness for breeders in SSA**

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*Jan Kreuze, Bramwel Wanjala, and Segundo Fuentes*

The objective in developing diagnostic tools for virus detection is to improve and validate diagnostic methods to improve seed quality, germplasm management and exchange. The target is to have a more efficient (less time, less costly) virus diagnostic and removal process in place at the support platform level and ultimately at the field level. This will be achieved by:

1. Conducting validation experiments of the ClonDiag tube-array to see if it can replace the use of NCM-ELISA and grafting in virus diagnosis;
2. Continuing to improve the design of the LAMP tool for detecting SPFMV and SPCSV in the field and validating its accuracy;
3. Evaluating the effect of Begomoviruses on sweetpotato varietal yields, either singly or in combination with other major viruses.

The ClonDiag arrays are on target for removal of unspecific probes and re-design of probes for false negative reactions for the fourth iteration array and addition of SPC6V. Validation of the fourth iteration array in parallel with standard indexing delayed due to delays in delivery of reagents. These have since been delivered. The LAMP design is being improved.

A field kit is being developed and its accuracy is being validated. Work is also ongoing to test cheaper kit components and new (cheaper and more active) enzymes.

Work had also started on evaluating the effect of Begomoviruses on sweetpotato yield. Genotypes with Begomovirus symptoms (identified by roll up/down of leaves) were indexed using *Ipomoea setosa*. Work was also undertaken to optimise PCR detection for Begomovirus. Sequencing of positive samples at the BeCA labs was planned and a survey was conducted to assess incidence and distribution of Begomoviruses in Kenya. All field material collected displaying Begomovirus symptoms were targeted for screening using PCR and the establishment of the threshold for Begomovirus detection. The target was to optimise conventional real time and quantitative PCR detection methods for other viruses using the field collected samples.

Studies were undertaken to establish the distribution of sweetpotato viruses (RNA and DNA) in East, West and Southern Africa countries. Variations in sweetpotato potyviruses, SPMV and sweet potato chlorotic mottle virus (SPCMV) were established. It was established through the study that there were different strains of SPCSV in different places. The findings from this study are important since knowing the variation of viruses in the various target regions would inform decisions on what to use for resistance screening, and why resistance may fail between regions.

In response to the presentation, participants had the following comments:

- SPVD pressure is high in parts of Ghana and Nigeria yet this was not observed in the data presented under the African Virome: distribution of viruses.
- There is a need to study the impact of Begomoviruses on sweetpotato production and to be able to make a decision on whether this is something to worry about.
- The survey on sweetpotato viruses under the African Virome work was done in 2011.
- The tool is under development and not yet available for use by breeders.

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### **3.19. Sweetpotato breeding activities at the National Root Crops Research Institute (NRCRI), Umudike in 2015**

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*Afuape S.O., Ogbonna, C.L., Uzuegbu, D.C., Nwaigwe, G., Igbokwe, C., Njoku, J.C., Tongoona, P., Offei, S.K. Asante, I.K. and Egesi, C.N.*

During the year 2015 four sweetpotato breeding activities were undertaken at the NRCRI, Umudike-Nigeria:

- 1) *Analysis of similarities and differences in farmer trait preferences to enhance effectiveness of sweetpotato varietal development*

The objectives were to identify key traits that drive farmers' preferences for variety adoption and to study similar and divergent trait preferences among sweetpotato farmers in Abia (rainforest belt) and Benue (guinea savanna) states. The questionnaires covered: farming experience in sweetpotato production; size of land planted with sweetpotato, use of fertilisers in production; number of sweetpotato cultivars planted; maturity period of planted cultivars; preferred cultivar maturity period; preferred root shape, size, colour taste, and texture of boiled roots; farming system; diversity of crops grown; and perception about SPVD.

*2) Clonal evaluation of new sweetpotato population developed in 2014*

The objective of this activity was to evaluate the clones developed in 2014 for fresh root production, SPVD resistance and root flesh colour. A total of 323 clones (including three checks) tracing back to ten families were evaluated. Beta-carotene content among the clones evaluated ranged from 0.15 to 12.39 mg/kg.

*3) Preliminary yield evaluation of new genotypes for fresh root yield and root flesh colour*

The objectives were to evaluate the 2013 cycle breeding lines for their root yield and flesh colour attributes and to select the promising lines that will be advanced to advance yield trial stage in 2016. Fifty-two clones were evaluated in a randomised complete block design with three replications. About 32% of the 52 clones evaluated were orange-fleshed. The top 13 of the genotypes evaluated had storage root yields of 10 to 14 t/ha and had low SPVD score of 1.0. Promising genotypes from the ongoing trial will be selected in 2016.

*4) Development of populations for increased yield, beta-carotene, high dry matter and resistance to SPVD*

Crosses were made among parents in a crossing block made up of 15 parents (5 OFSP - female; ten other root flesh types – male). However, flowering was a challenge for some of the crosses that targeted specific parent combinations. A total of 859 seeds were collected from the crosses made.

In response to the presentation, participants discussed the following:

- There was need to pay more attention to the minimum/thresholds of beta-carotene content in situations where OFSP are targeted for selection. The minimum to make a nutritional difference should be 3.0 mg/100g.
- Previous discussions stated that more user groups should be included, e.g. both women and men, processors and marketers, to get a diversified look at who the end-user of breeding work is. In response, the presenter explained that King J and Mother's Delight varieties had been taken to a French fries processor in Ibadan and after three days of testing, he discovered that there was willingness to buy.
- King J is very orange, but the beta carotene content is low.

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### 3.20. Sweetpotato breeding in Rwanda/ AGRA support

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Shumbusha D., J. Ndirigwe, L. Kankundiye, and P. Rukundo

The presentation focused on sweetpotato breeding activities undertaken in Rwanda using funding received from Alliance for a Green Revolution in Africa (AGRA). In Rwanda sweetpotato is a source of food, animal feed and income for farmers. The challenges for sweetpotato breeding in the country are lack of updates about varying farmer preferred traits over time, and yet preferences may vary over time depending on the actual utilisation and lack of information about the available germplasm.



*One of the participants asks a question during the discussion session*

The overall objective of sweetpotato breeding in the country is to develop farmer preferred and high yielding sweetpotato varieties (both storage roots and vines), high in quality (mainly dry matter content and beta-carotene), resistant to pests and diseases, and with wide adaptation. The breeding work targets low, mid and high altitude areas of the country. The sweetpotato activities undertaken in the country include:

#### 1) *Dissemination of new varieties released in 2013*

This activity has been targeted for the period 2014-2016 and is aimed at increasing availability of new varieties; increasing awareness of the newly released varieties; and creating a sustainable sweetpotato vine production and commercialization system (growing calendars, training of vine multipliers). So far, 17 vine multipliers have been identified in Muhanga, Gakenke, Huye, Kamonyi, Rulindo and Bugesera; 374,000 clean cuttings produced and distributed; 8.9 hectares of land area is covered by distributed cuttings; and farmers have been linked to vine multipliers through awareness creation. A growing calendar is also established at the beginning of each season ensures sustainable production and commercialisation.

#### 2) *Participatory rural appraisal (PRA) conducted to assess farmer- preferred traits and their implications to breeding new sweetpotato varieties in Rwanda*

Through the PRA study it was established that most farmers (>76%) preferred marketable root size and red skin colour. In Bugesera and Nyagatare, white-fleshed varieties which were higher in dry matter content were more preferred compared to OFSP.

#### 3) *Characterisation of available sweetpotato germplasm*

Morphological and molecular characterisation was done for 171 available accessions. Based on the level of genotypic variability, accessions were selected to constitute parents in a crossing block for population development. A crossing block was established at Rubona.

#### 4) *Sweetpotato breeding*

Eight parents selected from the characterisation study were selected and crossed in diallel and half diallel arrangements. The generated seeds were germinated to establish a seedling nursery. The F1 progenies will be evaluated in replicated trials at three locations to study among other things GCA, SCA and variance component estimates. To secure financial resources for planned breeding activities, a proposal on sweetpotato breeding was submitted to AGRA for funding.

In response to the presentation, a participant sought to know what was meant by gender equity. It was explained that the involvement of more women in roots and vines commercialisation had increased their economic empowerment.

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### **3.21. Participatory breeding of orange-fleshed sweetpotato adapted to Savanna and Sahelian environment of Burkina Faso**

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#### *Some Koussao*

Burkina Faso is divided into three climatic zones: South Sudanian, North Sudanian, and Sahelian. These zones differ in mean annual rainfall, duration of rainy season, number of days with rain and average annual temperature – all of which are higher in South Sudanian followed by North Sudanian. The Sahelian climatic zone has the highest evapotranspiration rate. Soils in the country are poor and farmers have devised ways of capturing moisture where rainfall is low. In the western region of the country where there is better rainfall sweetpotato is grown on mounds while in the central and eastern region, it is grown on ridges to improve water capture of water. The main biotic challenges to sweetpotato production are sweetpotato weevils and SPVD. Availability of planting vines remains a challenge and only an informal system is used in which farmers obtain planting vines from fellow farmers.

The global objective of the sweetpotato breeding program in Burkina Faso is to contribute towards enhancing household food security and alleviating malnutrition and poverty in the country. More specifically the program aims to: (1) develop and release new adapted high yielding sweetpotato varieties with high beta-carotene and dry matter content for targeted regions; (2) enhance farmers' access to high yielding and clean planting material of newly developed OFSP varieties; and 3) create farmer awareness on the benefits of released OFSP varieties.

In the breeding program, the traits of interest are: yield, quality (dry matter and beta-carotene content), earliness, and drought tolerance, resistance to weevils and SPVD, and upper biomass (for vines and animal feed). To address these objectives the planned activities include:

- Development of populations with the traits of interest;
- Farmer participatory evaluations and selection of advanced lines for target agro-ecologies;

- On-station production of basic planting materials on-station for distribution to multipliers;
- Large scale demonstrations to increase farmer adoption of new improved OFSP;
- Field days;
- Training of farmers and farmer organisations in root production;
- Training of seed companies in quality planting material multiplication;
- Development and distribution of manuals and posters;
- Radio programs and TV shows in local dialects.

In population development and evaluation, effort has been made to continue hybridising parents with different attributes (drought tolerance, dry matter, beta-carotene content, SPVD resistance, and other traits). So far, three OFSP clones from the developed populations are at an advanced stage towards release. Sixty-four genotypes from a new set of populations including drought tolerant progenies from Mozambique are under evaluation in preliminary trials. Nine of the genotypes evaluated in the preliminary trials produced storage root yield in the range of 17 to 28 t/ha.

Participatory variety selection (PVS) was also undertaken. There were 12 clones in advanced trials in three agro-ecological zones: Eastern, Central East, and western region (one check variety used per zone). The 256 farmers who participated in the PVS trial were from eight communities. On-farm demonstrations were held in 60 communities in partnership with Helen Keller International (HKI) (1460 farmers, ten primary schools) and nine communities with Catholic Relief Services (CRS/BF). An additional four communities (with 93 farmers) in the 'Jumpstart' project area were involved. Storage root yield in the evaluated 12 clones was in the range of 13.5 to 19.7 t/ha and had beta-carotene content in the range of 0.8 to 8.3 mg/100g.

To produce clean planting materials of foundation/pre-basic vines were first grown in pots in protected screen houses to start a seed system and later disseminated to 55 trained vine multipliers. A total of 1.18 million cuttings were distributed to farmers and participating schools through the input of the project's collaborating partners HKI and NAFASO.

Among the challenges that continued to be experienced by the program included the fact that there was some difficulty encountered in the release process (which at the time of reporting had been resolved). Also the fact that the farmers' white variety, Fardagan, was higher yielding (35 t/ha) than the newly developed OFSP varieties, a limitation to adoption of the new varieties in the western region. The informal nature of the seed system has also remained a challenge.

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### 3.22. Breeding and promotion of sweetpotato genotypes for consumer preferred traits in time and space in Zambia

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*Martin Chiona*



*Martin Chiona pays attention to discussions*

AGRA initially supported the breeding program in Zambia to develop and select high yielding sweetpotato varieties with consumer preferences (high dry matter and beta-carotene content) and resistance to pests and diseases. The initial support from AGRA ended in 2013 with a promise of renewal in 2015. The program aims to develop virus resistant, early to late maturing, high yielding, weevil resistant sweetpotato varieties that take into account farmer- and consumer-desired traits such as potential for leaves to be utilised as vegetables and also able to produce vines with better survival ability. A total of 59,233 open pollinated and 1,428 hand pollinated seed (from a diallel crossing arrangement) was obtained from the hybridisation activities undertaken. From this, the project developed 246 clones (65 from targeted crosses). These clones were tested at four primary sites: Mansa, Msekera, Copperbelt, and Mutanda. The test sites lie between 1,025 and 1,386 m above the sea level. PVS was undertaken on-farm in trials set up in an augmented design.

During the 2015/16 season 17 clones were planted and evaluated in uniformity trials, 20 clones in advanced trials, 25 clones in preliminary trials and 30 families were planted in seedling nurseries. One of the concerns noted during the recent trials was rampant cracking of roots which was believed to be the result of erratic seasonal rains. The cracking of roots was expected to negatively impact farmer adoption of newly released varieties. It was also observed that for some unclear reason(s), viruses were becoming a problem despite the country's long dry season.

The program faces challenges of limited funding both from donor and the government. With recent realignments at AGRA, Zambia is no longer one of the priority countries for continued funding by AGRA. Funding from the government is also limited and unpredictable.

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### **3.23. Commitment to mainstreaming beta-carotene into breeding programs**

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Jan Low

A major step forward in assuring sustained commitment to biofortification was made when the CGIAR centres committed to make breeding for minerals and vitamin traits in their regular food crop development programs the norm. When CIP and partners commenced work on the breeding of sweetpotato for higher beta-carotene content (a precursor for vitamin A biosynthesis), there was fear that selection for the trait could have a penalty on yield. However, the results proved that that this was not the case. From 2009 onwards significant progress has been made in breeding for higher beta-carotene content with 75% of all the newly released sweetpotato varieties since then being orange-fleshed.

This achievement was made even without a formal commitment by breeders to achieve specific targets for this trait. It was therefore proposed during the 15<sup>th</sup> Breeders' meeting that breeders discuss and agree to make breeding for higher beta-carotene the norm in their programs and to set specific targets to which they would commit their programs. During the discussion that followed, a cautious approach was urged when setting the targets, given that there were outstanding challenges such as SPVD, sweetpotato weevils and negative linkage of high beta-carotene content with dry matter content, which needed to be resolved to be able to fully unleash the potential of the crop. The participants committed to having at least 50% of the new sweetpotato varieties that they would release being orange-fleshed. The SSA sweetpotato community of practice later issued a joint statement during the 15<sup>th</sup> breeders' meeting in which they declared their commitment as follows:

*"We, the sweetpotato breeders active in SSA that are engaged in breeding and/or varietal selection, agree that prioritising the integration of significant levels of beta-carotene into sweetpotato cultivars is of high priority given the high levels of vitamin A deficiency on the continent. We commit to striving to assure that out of every ten varieties released by our national programs, 50% are orange-fleshed".*

See Annex 1 for the signed statement of commitment.

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### **3.24. Mother-baby trial procedure as an on-farm trial methodology in Northern Ghana**

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*E. Carey, K. Acheremu, E. P. Abidin, K. Asare, E. Dery, D. Akansake*

The mother-baby trial strategy is an on-farm trial approach in which a set of new breeding lines are compared with local checks using farmers' crop management practices. It has the advantage of allowing farmers to fully participate in the planting and harvesting of trials at a central location (mother trial) while evaluating some entries on their own farms (baby

trials). This ensures effective participation of both farmer based groups and breeders and takes into account the effects of actual farmer practices and conditions, which may differ substantially from on-station practice.

The mother-baby trial strategy aimed at selecting breeding clones in Northern Ghana. Five genotypes: TU-Purple, TU-Orange, Nanugungungu, Apomuden and Kuffuor were evaluated. All the genotypes evaluated were orange-fleshed with the exception of TU-Purple which was purple-fleshed. The study was conducted over two seasons (in 2014 and 2015). There were nine locations in 2014 and 11 locations in 2015. For each year, a mother trial was established at all the locations for participatory evaluation. At the same time, farmers grew on their own farms a genotype of their choice from among those evaluated in the trial. The genotypes in the mother trial were planted in a split plot arrangement in which one site of the field was fertilised using NPK fertiliser (15:15:15 applied at 300 kg/ha) to also enable determination of the effect of fertiliser on sweetpotato production.

A total of 254 (152 female and 102 male) farmers across all the locations participated in the evaluation of the trial. The evaluation involved farmers choosing their preferred genotypes from the fertilised and unfertilised plots. Group pair-wise ranking in which farmers ranked the different genotypes from most preferred to least preferred, and sensory evaluation of the storage roots were conducted.

Despite erratic weather that was experienced in 2014, Apomuden and Nanugungungu had higher yields compared to Kuffuor, TU-Purple, and TU-Orange in both years. Fertiliser application resulted in significantly higher storage root and vine yields. However, the quantity of marketable storage roots was lower for the fertilised treatment compared to the unfertilised, a situation that was attributed to increased incidence of storage root defects, weevil and millipede damage on roots produced under the fertilised treatment. Farmers ranked Apomuden and Nanugungungu as the best genotypes in overall field performance compared to the other three. More than half of the farmers agreed that all the genotypes evaluated performed better with fertiliser application. In the sensory evaluation test, the majority of farmers described the texture of TU-Orange, TU-Purple and Nanugungungu as just about right while Apomuden and Kuffuor were considered as too soft.

Some challenges experienced during the trial were:

- The prevailing short rainy season that made it difficult to cover many locations. Planting and harvesting had to be hurriedly done within a short period.
- Farmers' participation in the evaluation was low in some locations since the time coincided with the harvest of other crops.
- The exercise coincided with other on-station breeding activities. There was increased pressure on field staff and on vehicles for field visits since communities were very far apart.

On the basis of findings and challenges experienced during the trial, it was recommended that:

- Further trials be carried out to study the relationship between fertiliser application and storage root quality.
- More baby trials and fewer mother trials be conducted. The mother trials can be reduced to about two locations per region and if possible established on fields where they can be irrigated and protected from animal destruction.
- Focus group discussions and individual interviews be conducted after the harvest season to enable more farmers to freely participate in the exercise.
- More research/field staff be involved to help in breeding activities in Northern Ghana.

After the presentation, participants were given time to ask questions and make comments. These are summarised as follows:

- Farmers' perception of the purple flesh genotype: Farmers did not like it at first sight but the number of those who liked it increased upon testing.
- The response to fertiliser was poor (only very small yield increments): This issue needed to be studied further, and there may be need to check the harvest index under the two fertiliser regimes.
- Fertiliser application resulted in higher weevil damage: This is because of increased exposure of roots to weevils and as a result of higher growth in roots – both in numbers and sizes.
- There is need to also incorporate in the design for future studies economic aspects on fertiliser use.

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### **3.25. Demonstration on analysing on-farm data using CloneSelector**

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Gerald Kyalo and Luka Wanjohi

The participants were taken through a demonstration on how to analyse data from on-farm trials using CloneSelector. As an introduction, they were reminded how to use CloneSelector to design field trials and generate field books in which to record data from the trials. With pre-recorded data from, the participants were shown the steps taken to check recorded data prior to launching the analyses. The demonstration then focused on the data analysis process using CloneSelector, with data generated from an experiment designed in a randomised complete block design (RCBD).

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### 3.26. Group evaluation of analysed trial data referring to publication by Tumwegamire et al. (2016) in Crop Science

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*Group evaluation of analysed data underway*

In this session the participants were divided into six groups and tasked with interpreting outputs of an analysis of a data set of trials conducted in Uganda, which had recently been published in Crop Science Journal. The outputs that the groups interpreted had been analysed using HIDAP, statistical software that is still under development and planned for release and use by the sweetpotato breeding community for designing and analysing data from field trials. Participants looked at the data

output reports without referring to the publication, considered the meaning of the results of the analysis and how they would be presented/discussed in a paper.

The group members worked in pairs. The first pair looked at root yield, foliage yield and harvest index. The second pair looked at root yield, dry matter and sucrose while the third one looked at root yield, iron and beta-carotene content.

For each of the traits, the analysis of the outputs had three main parts: a) descriptive statistics that included means by genotypes, means by environments, and means by genotype and environments; b) ANOVA with the assumption that the error had a normal distribution with the same variance for all genotypes and environments was first assessed. When the normality assumption was satisfied, the focus shifted to the ANOVA table (in which it was assumed that the genotypes and environments had fixed effects and that the blocks were random) where the statistical significance of the sources of variation were inferred; finally the estimates for variance components were examined; c) Stability analysis was also done because of the significant interaction effect. This involved looking at the outputs from AMMI biplots, regression stability analysis and Tai plots for Tai stability analysis as alternative methods for making inference on stability. In analysing the AMMI biplots of varieties for particular traits, the participants were reminded that under biplot1 in which only PC1 is presented, the further a variety is from the zero line, the more unstable a variety is while in the second bi-plot in which PC1 and PC2 are presented (in situations where PC1 does not sufficiently account for the variation in the data), the varieties which are closer to the centre are considered more stable.

The groups made their presentations, which were followed by discussions and in conclusion, the participants were advised to always verify the output obtained by looking at the original data.

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### **3.27. Genetic gains: standard and simplified approach**

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*Wolfgang Grüneberg*

According to FAOSTAT data on sweetpotato, storage root yields increased by region between 1992 and 2011, SSA still has the lowest yields compared to other world regions, but this varies extremely among the SSA countries. However, it is notable that across the past 20 years, there was a 1% yield increase per year across all countries in SSA, and a lot of marginal soils came into use. This observation could be attributed to genetic gain.

Determination of genetic gain always entails comparing old varieties with new ones. This is often done at different levels including through analysis of historic productivity data, on-station or on-farm experimentation, by making inferences from analysis of FAO statistics on sweetpotato yield estimates. Genetic gains can be estimated at country level by looking at performance of old and new varieties over a long period of time by way of regression.

To study genetic gain in experiments such as those designed to compare breeding methods like the accelerated breeding scheme (ABS) or HEBS, it is important that baselines are established. This is done by ensuring that all the parents are conserved in the gene bank to enable later use in trials designed to compute observed response to selection or genetic gain.

A standard approach could also be adopted in the estimation of genetic gain. This could for example entail a series of multi-environmental trials (METs) conducted over a period of 2 to 3 years to enable estimation of genetic gain over shorter periods of time. In practice, 10 to 20 years of METs from variety release time using 8 to 18 METs allows for estimation of long term yield trends and changes in long term yield trends (through regression analysis or plots of year and/or genotype means against time - assess time trends) including gain components associated with better practice.

A simplified approach that could also be adopted in the estimation of genetic gain would entail modification of demonstration trials (established for new varieties) by planting together with new varieties at least one or two sets of old varieties (3 to 4 varieties which have been predominantly grown over the preceding 10 years and 3 to 4 varieties which have been predominantly grown over the past 20 years). Genetic gain data from such modified demonstration trials could be linked to impact studies by taking into consideration during calculations the adoption rates of the new varieties and making corrections, where necessary, for results comparing on-station and on-farm trials.

At the time of the breeders' meeting, genetic gain studies had started in the SASHA project with studies in Peru (18 genotypes with two common check clones) and Mozambique (25 genotypes with four common check clones). Additional studies were also planned to commence in Uganda and Ghana.

An example of a recent genetic gain estimate paper was referred to in *Crop Science* 56:1–17. The benefit of establishing estimated genetic gains is that these could indicate the contribution of released varieties to the country by looking at productivity of adopted varieties on overall productivity of sweetpotato.

In response to the presentation a question was asked on how clonal degradation per generation affects genetic gain. The response was that without good quality seed, genetic gains are compromised and there was need to minimise use of poor clones. Instead high quality clones (cleaned clones) should be used and these should be planted at the same time.

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### **3.28. One hundred best-bet sweetpotato varieties for SSA and feedback on performance of germplasm distributed by CIP since 2009**

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*T. Carey, R. Mwangi, M. Andrade, R. Gatimu, B. Wanjala, B. Kivuva and J. Low*

This presentation reviewed the feedback obtained from the sweetpotato community on best-bet sweetpotato varieties for SSA and feedback on performance of distributed germplasm distributed by CIP since 2009. The rationale for this was borne out of the need to have a list of elite genotypes to serve as ready pathogen-tested source of best-bet genotypes for international and local distribution.

The demand for these varieties varies across the countries, and there are some that are no longer being requested. In order to rationalise the use of resources, the SASHA project embarked on an initiative to identify varieties that had to be saved for use by national programs. These varieties, dubbed “100 best-bet” have special traits. They are unique in that they have important and desirable characteristics such as dry matter, beta-carotene, drought tolerance, weevil resistance etc.

The target was to assemble all the listed genotypes for clean-up, finger printing and further research. The list of 100 genotypes obtained from the respondents in 16 countries (10 genotypes per country) was assembled out of approximately 220 genotypes selected by the sweetpotato breeders in the countries. The selected varieties will be maintained in tissue culture and screen house at KEPHIS PQBS Muguga, and will be distributed to countries on request at a small charge.

In response to the presentation, participants made the following recommendations:

- The 100 best-bet clones should be sequenced by GT4SP in partnership with African Crop Initiative Sequencing (AOI).
- Once the 100 best-bet clones are genotyped, the information should be kept as fingerprints that will enable confirmation of the clones later - using DNA extracts if necessary.

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### **3.29. Catalogue Development: Traits to include and how they will be collected until June 2017**

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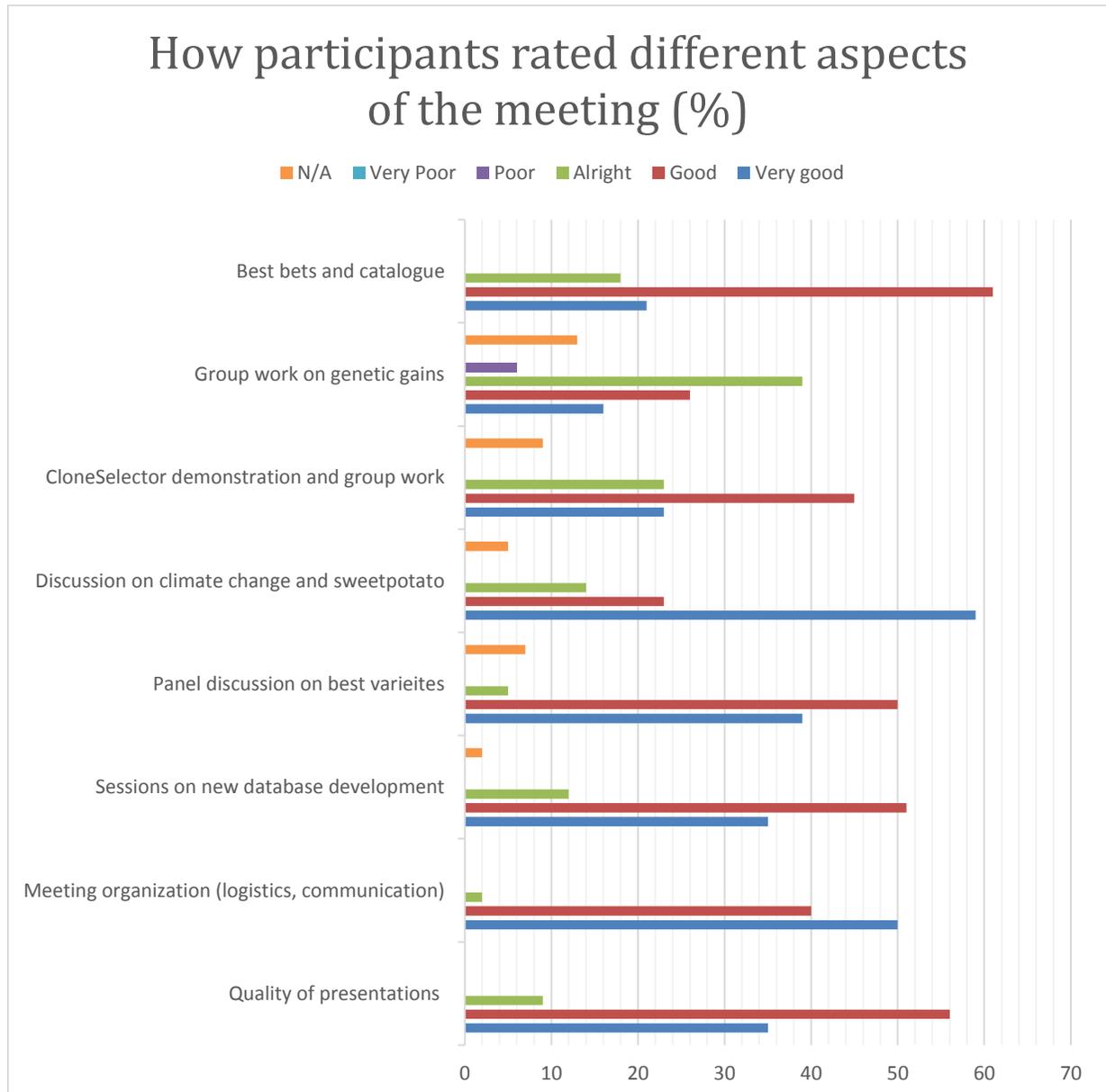
*Ted Carey*

The discussion during this session focused on improvements needed for the catalogue that under the SASHA project has been periodically produced for the orange-fleshed sweetpotato (OSFP) varieties developed and promoted by the project's partners.

- To further increase the utility of the catalogue, it should be linked to a database that holds information on all the varieties in the catalogue. Through the database, updates on individual varieties can be made based on results/feedback from users (researchers and consumers) of the varieties.
- There should be a review and update of information on the maturity period for the included varieties. Additional data could be included in the catalogue e.g. nutritional quality information using NIRS for beta-carotene content, sugars and dry matter content.
- Caution should be exercised with regard to the depth of information included in the catalogue and the information provided needed to mostly target the end users. Therefore, the document should not have too much technical information but should instead be simplified and targeted to specific audiences.

## Annex 2: Evaluation of Speed Breeders Meeting held in Mukono, Uganda June 6-10, 2016

The evaluation form was completed by 44 participants. One main reason is that by the time the form was distributed, some participants had already departed. Overall, the meeting was rated quite positively, with 25% stating that the meeting exceeded their expectations and 50% stating that it completely met their expectations. The remaining 25% were of the opinion that the most of their expectations were met.



**Parts of the meeting that participants found most useful (brackets = frequency)**

- 1) Breeding for climate change (15)
- 2) Development of databases and new packages (15)
- 3) Data analysis and interpretation (14)
- 4) CloneSelector demonstration (9)
- 5) Genetic gain (9)
- 6) Characteristics driving adoption (6)
- 7) Presentations on sweetpotato breeding in different countries (3)
- 8) Discussion on 100 best-bet clones from the regions (3)
- 9) Heterotic gains reports (3)
- 10) Catalogue development (2)
- 11) Genomic tools (2)
- 12) Social hour/cocktail was good for mingling (2)
- 13) Development and progress of virus phenotyping tools (1)
- 14) Discussion on commitment to mainstreaming beta-carotene content in breeding programs (1)
- 15) National program presentations and updates (1)
- 16) Panel discussions (1)
- 17) Presentations (1)
- 18) Sufficient time for presentations and questions (1)

**Parts of meeting considered least useful (brackets = frequency)**

- 1) Best bets and catalogue development (3)
- 2) Work on genetic gains (3)
- 3) DNA extraction/Fingerprint/Lab work (3)
- 4) CloneSelector (2)
- 5) Mother and baby trial was hurriedly done
- 6) Interpretation of stability analysis/ MET analysis (2)
- 7) Analysis of genotyping data
- 8) DNA extraction/Fingerprint/Lab work (3)
- 9) HIDAP
- 10) SPbase discussion not clear
- 11) Presentation and use of software on website
- 12) Unavailability for ease of use of new programs
- 13) Climate change section
- 14) Varieties that best perform
- 15) RTB

## Suggestions for improvement or topics for next meeting

- Sweetpotato/hexaploid mapping
- Breeding method and integration of genomics into sweetpotato breeding
- In next meeting provide a free afternoon for shopping relaxation and site seeing/  
End future meeting early, say by lunch time to give participants free time for own activities such as shopping/ Make the program less tight and provide for some free time, at least shopping
- Include some activity to break monotony of sitting for too long
- More coverage of modelling of yield estimates
- More hands on training on data analysis and results interpretation/ Detailed results and interpretation of data
- Organise a field visit
- Half a day training on use of R for statistical analysis
- More practical on genotyping/ More practical training/ Hands on training on phenotyping tools
- More training on methods and statistical techniques/ Have more time for data analysis
- Make feedback on germplasm performance and refinement of catalogue a regular feature
- Combine genomics project and breeders
- More discussion sessions
- Increase time for exercises on new software/ More training/information on HIDAP/  
More time on use of CloneSelector/ Develop tutorial for CloneSelector
- Have a session for data clinic with biometrician/database managers
- Breeding for climate change: draft methodologies for discussion
- Need more in depth discussion on genetic gains
- Give more room for more than one country representative to attend the breeders meeting – South Africa being an example
- Fertiliser trials on sweetpotato
- Marketing and commercialisation

## Annexes

### Annex 2: Commitment by sweetpotato breeders to mainstream beta-carotene



#### 15<sup>th</sup> Annual Sweetpotato SpeedBreeders Meeting 6-10 June 2016 Nairobi, Kenya

We, the sweetpotato breeders active in sub-Saharan Africa that are engaged in breeding and/or varietal selection, agree that prioritizing the integration of significant levels of beta-carotene into sweetpotato varieties is of high priority given the high levels of vitamin A deficiency on the continent. We commit to striving to assure that at least 50% of the clones we submit for release are biofortified, orange-fleshed types.

First Name	Country
Kwabena Acheremu	Ghana
Solomon Olufemi Afuape	Nigeria
Daniel Akansake	Ghana
Abilio Dos Santos Alvaro	Mozambique
Maria Isabel Andrade	Mozambique
Ernest Baafi	Ghana
Astere Bararyenya	Burundi
Ted Carey	Ghana
Martin Chiona	Zambia
Konan Eurard Brice Dibi	Cote D'Ivoire
Fekadu Gurmu	Ethiopa
Laura Karanja	Kenya
Benjamin Musembi Kivuva	Kenya

Sunette Laurie	South Africa
Godwill Simbarashe Makunde	Mozambique
Robert Mwanga	Uganda
Obed John Mwenye	Malawi
Jean Ndirigwe	Rwanda
Gaspard Nihorimbere	Burundi
Grace Nwaigwe	Nigeria
Michelin Bruno Rasoloniaina	Madagascar
Jose Ricardo	Mozambique
Placide Rukundo	Rwanda
Damien Shumbusha	Rwanda
Koussao Some	Burkina Faso
Gorrettie Ssemakula	Uganda
Godfrey Sseruwu	Uganda
Obaiya Grace Utoblo	Ghana
Charles Wasonga	Uganda
Bernard Yada	Uganda



## 15<sup>th</sup> SPHI Sweetpotato Breeders Annual Meeting 6-7 June 2016 Workshop

BecA-ILRI Research Platform, Nairobi, Kenya

*Theme: An eye opener in planning the integration of molecular markers in sweetpotato breeding programs*



Time	Activity/Session	Responsible
June 5	Arrival	Tassy Kariuki
June 6	<i>Day 1, Monday</i>	
7:30 am	<b>Registration</b>	Tassy Kariuki
	<b>Chair: Dr. Edward Carey</b>	<b>Note taker: Dr. Bode Olukolu</b>
8:00 am	Welcome note from the BecA-ILRI hub Director, and SASHA Leader	Dr. Appolinaire Djikeng, Dr. Jan Low
8:30 am	<b>Keynote Address</b> Genomics-assisted sweetpotato improvement: Hope or hype?	Dr. Craig Yencho
9:30 am	Genetic diversity studies of the sweetpotato using DNA markers: what have we learnt?	Dr. Marc Ghislain
10:10 am	<b>Health Break</b>	Tassy Kariuki
10:30 am	Basics of marker-assisted selection/breeding and its potential use for sweetpotato improvement	Dr. Awais Khan
11.10 am	Accurate sweetpotato phenotyping of agronomic traits; why it is important for MAS	Dr. Awais Khan & Bramwel Wanjala
12:00 pm	Sweetpotato genotyping procedures for SSA (recorded video/ppt)	Dr. Mercy Kitavi
12.30 pm	<b>Lunch break</b>	Tassy Kariuki
2:00 pm	<b>BecA lab tour facility; An advantage in SSA</b> what is available and how the sweetpotato community can make use of it regarding the incorporation of molecular procedures in their breeding programs	Dr. Mercy Kitavi
3:00 pm	<b>Laboratory practical exercise</b> DNA extraction from sweetpotato roots and leaves Assess DNA quality & quantity PCR preparation (markers assays)	Dr. Dorcus Gemenet Dr. Mercy Kitavi Dorcah Ndege
4:00 pm	<b>Health Break</b>	Tassy Kariuki
4:30-6.00 pm	Laboratory practical exercise – continued	Dr. Dorcus Gemenet Dr. Mercy Kitavi Dorcah Ndege

June 7	<i>Day 2, Tuesday</i>	
8:00 -8.30 am	<b>Briefing session</b>	Dr. Dorcus Gemenet & Dr. Mercy Kitavi
8:30 am	<b>Practical exercise</b> – Clone identification, germplasm fingerprinting, parent selection & Genetic diversity analysis using SSR data	Dr. Mercy Kitavi
10:00 am	<b>Health Break</b>	Tassy Kariuki
10:20 am	<b>Practical exercise</b> – Sweetpotato QTL mapping	Dr. Dorcus Gemenet
12:30 pm	<b>Lunch Break</b>	Tassy Kariuki
2:00 pm	<b>Practical exercise</b> – Genome wide maps; SNP marker development in hexaploid sweetpotato using Genotyping by sequencing (GBS)	Dr. Bode Olukolu
4.00 pm	<b>Health Break</b>	Tassy Kariuki
4:20 pm	What do we know about the <i>Ipomoea</i> genome and how can this be used in breeding improved sweetpotato varieties?	Dr. Robin Buell
5:00 pm	Discussions/Consultations and AOB	Dr. Mercy Kitavi
5:30 pm	<b>End</b>	



## 15<sup>th</sup> SPHI Sweetpotato *Speed*Breeders Annual Meeting 8-10 June 2016

BecA-ILRI Research Platform, Nairobi, Kenya

*Theme: Sharing Progress, Improving our Methods, and Considering Next Steps*



Time	Activity/Session	Responsible
June 7	Arrival	Tassy Kariuki
June 8	Wednesday	
	<i>Chair: Dr. Sunette Laurie</i>	<i>Note taker: Solomon Afuape</i>
8:30	Workshop expectations	Robert Mwanga
8:45	The importance of a central database and an overview of Sweetpotatobase	Lukas Mueller

9:15	Managing Accession, Breeding Programs, Location, and Trial Data in Sweetpotatobase – What do breeders need in a database?	Alex Ogbobonna, Bryan Ellerbrock
<b>10:00</b>	<b>Health Break</b>	
	<b>Chair: Dr. Maria Andrade</b>	<b>Note taker: Bramwel Wanjala</b>
10:15	Sweetpotato descriptors/Sweetpotato ontologies	Reinhard Simon
11:00	New tools to improve efficiency of data analysis	Simon Reinhard, Raul Eyzaguirre, Luka Wanjohi
11:45	Discussion	Craig Yencho
11:45	Sweetpotato Knowledge Portal	Luka Wanjohi, Christine Bukania
12:45 pm	Lunch Break	Tassy Kariuki
	<b>Chair: Dr. Craig Yencho</b>	<b>Note taker: Sunette Laurie</b>
2:00 pm	Re-analysis of heterotic gain in Mozambique	Godwill Mukonde
2:30	Re-analysis of heterotic gain in Uganda	Charles Wasonga
3:00	Refining Maturity Period & Quality Traits per Maturity Period for Released Varieties in Mozambique	Abilio Alvaro
	Breeding of sweetpotato for improvement of root dry matter and beta-carotene content in Ethiopia	Fekadu Gurmu Balcha
<b>3:30 pm</b>	<b>Health Break</b>	
4:00 pm	What are the characteristics driving adoption? Panel discussion on which varieties have done best? <i>Maria (Mozambique), Martin (Zambia), Malawi (Kennedy or Maggie), Uganda (Gorrettie), Rwanda (Jean Ndirigue), South Africa (Sunette): Top two varieties &amp; why have they emerged. 5 minutes each.</i>	Robert Mwanga
<b>June 9</b>	<b>Thursday</b>	
	<b>Chair: Dr. Dorcus Gemenet</b>	<b>Note taker: Ted Carey</b>
8:30	An Agronomist's Thoughts on Addressing Sweetpotato Resilience under Changing Climate Conditions	Mihiretu Cherinet
9:00	Break up into five groups: discussion on presentation by Mihiretu & feedback by groups to plenary	Mihiretu & Some Koussao
10:30	<b>Health Break</b>	
11:00	The Importance and Heritability of Vine Survival in Drought-Prone Areas: Preliminary Results from Mozambique	Maria Andrade
11:30	Genetic improvement of important traits for selection in sweetpotato ( <i>Ipomoea batatas</i> ) controlled cross populations in Uganda	Astere Bararyenya
11:50	RTB Reports and Discussion	Wolfgang Grüneberg
12:30 pm	Lunch Break	
	<b>Chair: Simon Reinhard</b>	<b>Note taker: Solomon Afuape</b>
2:00	Progress in Virus Resistance Breeding in Uganda	Robert Mwanga
2:20	Use of Molecular Markers for SPVD Breeding: Progress & the Way Forward	Wolfgang Grüneberg

<b>3:00 pm</b>	<b>Health Break</b>	
	<b>Chair: Titima Tantinkanjana</b>	<b>Note taker:</b> Charles Wasonga
3:15	Progress in Diagnostic Tools for Virus Detection & Potential Usefulness for Breeders in SSA	Bramwel Wanjala
3:45	Sweetpotato breeding/AGRA support (Nigeria)	Solomon Afuape
4:05	Sweetpotato breeding/AGRA support (Rwanda)	Damien Shumbusha
4:25	Sweetpotato breeding/AGRA support (Burkina Faso)	Some Koussao
4:45	Sweetpotato breeding/AGRA support (Zambia)	Martin Chiona
5:00	Commitment to mainstreaming beta-carotene as a biofortified trait	Jan Low
5:15	Discussion	
<b>June 10</b>	<b>Friday</b>	
	<b>Chair: Jan Low</b>	<b>Note taker: Godwill Makunde</b>
8:30	Mother-Baby Trial Procedure as an On-farm Trial Methodology in Northern Ghana	Daniel Akansake
9:00	Demonstration on Analysing On-farm Data Using CloneSelector.	Luka Wanjohi Gerald Kyalo
9:30	Breakout session to evaluate analysed trial data Datasets for discussion: 2 groups (root yield, foliage yield, harvest index), 2 groups (root yield, dry matter, sucrose), 2 groups (root yield, iron, beta-carotene)	Wolfgang Grüneberg
10:30	Health Break	
	Interactive discussion of results of the breakout groups, referring to forthcoming Tumwegamire et al. (2016). <i>Crop Science</i>  <b>Bonus discussion: Genetic Gains - Is a Simplified Approach the Answer?</b>	Wolfgang Grüneberg
12:30	Lunch Break	
	<b>Chair: Gorrettie Ssemakula</b>	<b>Note taker: Benjamin Musembi</b>
2:00	One hundred best-bet sweetpotato varieties for SSA and feedback on performance of distributed germplasm distributed by CIP since 2009	Ted Carey
3:00	Health Break	Note taker: Godfrey Sseruwu
3:15	Catalogue Development Traits to include and how they will be collected until June 2017	Ted Carey
5:00-5:30	Wrap up	Robert Mwanga Craig Yencho
<b>June 11</b>	<b>Saturday 2016, Departure</b>	Tassy Kariuki

## Annex 4: List of participants

1	Kwabena	Acheremu	Root Crops Breeder	CSIR - Savanna Agricultural Research Institute: Scientific Support Group (SSG) Root and Tuber Improvement	CSIR-SARI, P.O. Box 52	Tamale	Ghana	+233 243960803	<a href="mailto:acheremuk@yahoo.com">acheremuk@yahoo.com</a>	kacheremu2
2	Solomon Olufemi	Afuape	Head of Sweetpotato Breeding Program	National Root Crops Research Institute Umudike	PMB 7006	Umuahia, Abia State	Nigeria	+234-803-777445	<a href="mailto:solomonafuape@yahoo.com">solomonafuape@yahoo.com</a>	solomonafuape
3	Sammy	Agili	Senior Research Associate	International Potato Center	P.O Box 25171, Nairobi, Kenya	Kenya	Kenya		<a href="mailto:s.agili@cgiar.org">s.agili@cgiar.org</a>	
4	Daniel	Akansake	Assistant Sweetpotato Breeder	CIP-Ghana	C/o Box 52, Tamale	Tamale	Ghana	+233 508065227	<a href="mailto:d.akansake@cgiar.org">d.akansake@cgiar.org</a>	
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The **Sweetpotato for Profit and Health Initiative (SPHI)** is a 10-year, multi-donor initiative that seeks to reduce child malnutrition and improve smallholder incomes through the effective production and expanded use of sweetpotato. It aims to build consumer awareness of sweetpotato's nutritional benefits, diversify its use, and increase market opportunities, especially in expanding urban markets of Sub-Saharan Africa. The SPHI is expected to improve the lives of 10 million households by 2020 in 17 target countries.



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