Sweetpotato SpeedBreeders and Genomics Community of Practice

SPHI
Sweetpotato for Profit and Health Initiative

GT4SP
GENOMIC TOOLS FOR SWEETPOTATO IMPROVEMENT

Report of the 17th Annual Meeting

Introducing Next Generation Breeders' Tools and Understanding Winning Varieties

Swiss Lenana Mount Hotel, Nairobi, Kenya

June 5-8 , 2018

Compiled by Reuben Ssali and Robert Mwanga

Report of the 17th Sweetpotato *Speed*Breeders' and Genomics Community of Practice Meeting

Theme: Introducing Next Generation Breeders' tools and Understanding Winning Varieties

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Correct citation:

Ssali, R and R. Mwanga. 2018. Introducing Next Generation Breeders' tools and Understanding Winning Varieties. F. Njung'e (Editor), Proceedings of the 17th Sweetpotato SpeedBreeders' and Genomics Community of Practice Meeting, held 5-8 June 2018, Nairobi, Kenya, p 61, International Potato Center, Nairobi.

Acknowledgements
This work is undertaken as part of the CGIAR Research Program on Roots, Tubers and Bananas (RTB). The CGIAR Research Program on Roots, Tubers and Bananas (RTB) is a partnership collaboration led by the International Potato Center implemented jointly with Bioversity International, the International Center for Tropical Agriculture (CIAT), the International Institute of Tropical Agriculture (IITA), and the Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), that includes a growing number of research and development partners. RTB brings together research on its mandate crops: bananas and plantains, cassava, potato, sweetpotato, yams, and minor roots and tubers, to improve nutrition and food security and foster greater gender equity especially among some of the world's poorest and most vulnerable populations.
www.rtb.cgiar.org

Photos: F. Njunge
Cover photo: *Participants of the breeders meeting in Nairobi, Kenya*

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List of Acronyms

ABS	Accelerated breeding scheme
AFLP	Amplified fragment length polymorphism
ANOVA	Analysis of variance
AT	Advanced trials
ABCF	Africa Biosciences Challenge Fund
BecA	Biosciences eastern and central Africa
BMGF	Bill & Melinda Gates Foundation
BTI-CU	Boyce Thompson Institute- Cornell University
BrAPI	Breeding Application Programing Interface
CIP	International Potato Center
CoP	Community of practice
CV	Coefficient of variation
DArT	Diversity arrays technology
DArTseq	Sequencing-based diversity array technology
DMC	Dry matter content
FANEL	Food and Nutritional Evaluation Laboratory
Fe	Iron
FYTHA	Foliage yield in tons per ha
GAB	Genomics-assisted breeding
GCA	General combining ability
GBS	Genotyping-by-sequencing
GG	Genetic gain
GS	Genomic selection
GT4SP	Genomic tools for sweetpotato improvement
GWAS	Genome wide association studies
HEBS	Heterosis exploiting breeding schemes
HCA	Hydroxycinnamic acid

HI	Harvest index
HIDAP	Highly interactive data analysis and productivity
HQ	Headquarters
IGSS	Integrated Genotyping Service and Support
ILRI	International Livestock Research Institute
KALRO	Kenya Agriculture and Livestock Research Organization
KASP	Kompetitive allele specific PCR
LSD	Least significance difference
MAS	Marker assisted selection
METs	Multi-environmental trials
MSE	Mean Squared Error
MSU	Michigan State University
MT	Multilocation trial
NaCRRI	National Crops Resources Research Institute
NARS	National Agricultural Research Systems
NCSU	North Carolina State University
NGO	Non-governmental Organization
NIRS	Near infrared spectroscopy
NSSP	Non-sweet sweetpotato
OFSP	Orange-fleshed sweetpotato
PCA	Principal component analysis
PCR	Polymerase chain reaction
PYT	Preliminary yield trials
PVS	Participatory variety selection
PVy	Potty virus Y
QTL	Quantitative trait loci
RAPD	Randomly amplified polymorphic DNA
RCBD	Randomized complete block design

RFLP	Restriction fragment length polymorphism
RKN	Root knot nematodes
RRS	Reciprocal recurrent selection
RTB	Roots, tubers and bananas
RYTHA	Storage root yield tons per hectare
SASHA	Sweetpotato Action Security and Health in Africa
SCA	Specific combining ability
SME	Small-to-medium scale enterprise
SNP	Single nucleotide polymorphism
SPBase	Sweetpotatobase
SPHI	Sweetpotato for Profit and Health Initiative
SPVD	Sweetpotato virus disease
SRFB	Storage root formation and bulking
SSA	Sub-Saharan Africa
SSP	Sweetpotato support Platform
SSR	Simple sequence repeat
SWCA	South West and Central Asia
SPW	Sweetpotato weevil
Zn	Zinc

Executive Summary

Welcome remarks and Introductions

Participants pose for a group photograph

The 17th Sweetpotato *Speed*Breeders and Genomics Community of Practice (CoP) annual meeting was held at Swiss Lenana Mount Hotel, Nairobi, Kenya, from 5th to 8th June 2018; with the theme of **'Introducing Next Generation Breeders' Tools and Understanding Winning Varieties'**. Fifty participants (14 of them female) from 14 countries attended the meeting. The meeting started with welcome remarks from Dr. Dorcus Gemenet from the International Potato Center (CIP) headquarters, who extended thanks to the organizers of the meeting and then led the members present in a round of self-introductions. Dr. Robert Mwanga, the regional breeder at CIP's East and Central Africa sweetpotato support platform, also welcomed breeders attending the CoP, especially those attending for the first time. Robert, briefly highlighted the need for breeders to prepare to embrace next generation tools for sweetpotato breeding that are under development but also look forward to having an interactive meeting.

Dr. Craig Yencho, co-leader of the CoP, leads the genomic tools for sweetpotato improvement (GT4SP) project, hosted at North Carolina State University (NCSU), Raleigh. Craig underlined the valuable resources for sweetpotato breeding now at the disposal of the community including the reference genome which can be used to identify genes and markers, tools for quantitative trait loci (QTL) and linkage analysis, the sweetpotato database linked to the Highly Interactive Data Analysis Platform (HIDAP) that are all supported by the capacity development component led by Dr. Mercy Kitavi. He further thanked GT4SP project partners like CIP, Michigan State University (MSU), the Boyce Thompson Institute (BTI), University of Queensland and recently, the University of Tennessee in California and the National Crops Resources Research Institute (NaCRRI). Going forward, he urged the CoP to start thinking of how to integrate these tools into applied sweetpotato breeding.

Dr. Jim Lorenzen, the program officer at the Bill and Melinda Gates Foundation (BMGF), expressed his appreciation to the leaders for developing such a great CoP integrating genomics and breeding teams to work with national programs. Such exciting work makes it easy to empower women farmers who in turn invest in their families while providing nutritious foods.

The Director of Crop systems, Kenya Agriculture and Livestock Research Organization (KALRO), Dr. Lusike Wasilwa, addressing the participants

The meeting was officially opened by Dr. Lusike Wasilwa, the Director, Crop systems, Kenya Agriculture and Livestock Research Organization (KALRO). She emphasized the importance of breeding in the cropping systems of sub-Saharan Africa (SSA). She highlighted the growing importance of the sweetpotato crop in Kenya, where it was the highest ranked commodity in the 2011 priority setting exercise. She congratulated Dr. Benjamin Kivuva for the five sweetpotato varieties recently released in Kenya. However, there is need to maximize the yields from the current 6-8 t/ha to 60 t/ha. She also assured the co-leaders of the CoP that although Dr. Kivuva has been moved to the KALRO headquarters, he will continue with the sweetpotato breeding. She then urged the *speedbreeders* to draw inspiration from the World Food Prize laureates, Robert Mwanga, Jan Low and Maria Andrade. She concluded by challenging the CoP to think of more innovative ways of informing policy formulation.

During the four-day meeting, speedbreeders shared recent advances in the development and application of tools for data management and genomics assisted breeding. An interactive practical training session on how breeders can use sweetpotatobase and HIDAP for managing, analyzing, storing and sharing data was conducted. The potential of using PhotoSynQ, a tool that measures multiple photosynthetic parameters like quantum yields of photosystems (I and II) and non-photochemical quenching was introduced, which breeders can now use to select genotypes that have inherent abilities for photoprotection. The meeting also featured a field trip to the University of Nairobi, Kabete campus, where the 100 best bet genotypes for SSA were under evaluation for morphological characterization. The breeders also shared progress in sweetpotato breeding from their breeding programs highlighting the breeding objectives, approaches, recent variety releases, ongoing trials, promising clones for release and available funding for sweetpotato breeding. Panel discussions captured the perspectives of the breeders on the role of genomic tools in sweetpotato improvement and characteristics of winning sweetpotato varieties.

Session 1: Data management, analytics, storing and sharing

1.1 Statistical update: Westcott Design

Raul Eyzaguirre

Background

Field experiments/trials are often conducted in heterogeneous fields, i.e. under spatially differentiated soil conditions, terrain characteristics, or microclimate, a fact that might affect an objective comparison of crop growth and yield of the tested plants. The effect of the variations of the field conditions is often minimized with an appropriate number of replications, randomly assigned in the field. Breeders are often faced with the challenge of having many genotypes which could make the replication of the test materials very costly. The Westcott design is a method for controlling for heterogeneity in field experiments that enables evaluating the performance of many genotypes without replicating the test genotypes. The Westcott design uses a grid of two checks to map the heterogeneity in a rectangular field. One column of two alternating check clones (e.g. 'A' and 'B') and n columns of testing materials (Fig 1). You can design an experiment with a Westcott design in either HIDAP, sweetpotatobase.org or the st4gi R package (function cd.w). Each plot will have precise row and column identification

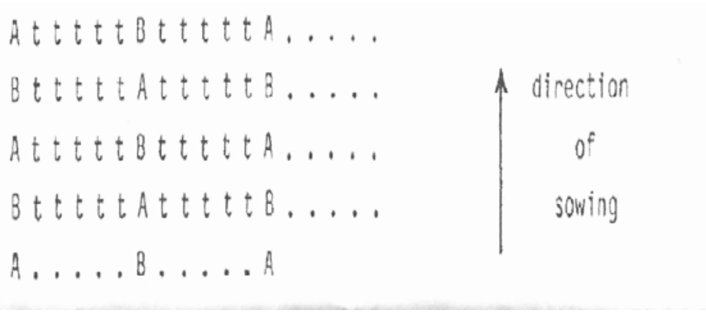

Figure 1 An example of the field layout of the Westcott design with genotypes 'A' and 'B' as the alternating check clones with 5 plots of testing genotypes 't'.

Adjusting values to account for heterogeneity

The test genotype is assessed by expressing its yield as a percentage of the nearest controls in the three rows spanning it. For instance, if the mean of all checks is 100, and the mean of the 6 checks adjacent to the plot is 110, then the observed plot value is adjusted by 10%. The Westcott design has been verified for sweetpotato using 3 field trials from Peru and 1 field experiment from Ghana:

- Phenotyping trial for high Fe and Zn population: 3292 clones, 56 progenitors
- Phenotyping trial for wide adaptation population: 9881 clones, 82 progenitors.

- Phenotyping trial for low sugar population: 3742 clones, 53 progenitors
- Heterosis experiment –Fumesua, Ghana

The reduction in mean squared error (MSE) in estimating adjusted values proves the method can control field heterogeneity. The method does not require complicated computation routines so it can be used with large experiments (thousands of clones). However, using the full differences among the checks can increase the error, it is recommended to weigh the adjustment between 20% and 60%. Default value in HIDAP is set at 40%.

Discussion

Did you consider a smoothing function?

Raul and Wolfgang clarified that the study was an improvement to the design from the way it was originally published or used by many private companies. It is very difficult to simulate homogeneity in the field that makes such statistical research with respect to field trials very important. The weights used in adjusting the observed values enable us to capture important patterns in the data, while leaving out noise.

Would it be better to eliminate the outliers before smoothing the data?

The Westcott design enables you to get an estimate of the error term and use it to adjust the observed values. It is better to eliminate the outliers after making the adjustments.

Do you get a significant difference in ranking the genotypes when adjustment is made?

The examples did not compare the ranking of genotypes before and after adjustment but depending on the magnitude of the error term or the plot effect, the ranking of genotypes could be different. Instead, the study compared the mean squared error (MSE) for the different models for adjusting the observed values.

The parents were included in the trial, but were they not used in the analysis?

The presentation focused on adjusting the observed values which you can then use for statistical analysis. The parents are treated like other genotypes when adjusting the values.

Many times, our fields are not rectangular does that mean we cannot use the Westcott design?
If your field is not rectangular you may have to split the field into small rectangular pieces that can enable you to use the Westcott design.

1.2 Introduction: HIDAP/SPBASE development, interaction and status

Omar Benites and Bryan Ellerbrock

Background

Omar Benites explains salient features of HIDAP

HIDAP is an acronym for Highly Interactive Data Analysis Platform, which is part of the Global Trial Data Management System suite of tools at CIP. These are in-house efforts to unify best practices. Breeders can now design their trials, collect data and do data quality checks and processing in HIDAP. HIDAP can generate statistical analysis reports for breeding data. The stand-alone version of HIDAP does not require access to the internet.

Sweetpotatobase is a global database for sweetpotato breeding data, which is web-based and easy to use. It is part of the family of roots tubers and bananas (RTB) databases- Cassavabase, Musabase, Sweetpotatobase and Yambase. Sweetpotatobase implements a digital ecosystem for plant breeding to ensure data quality. Since digital data never 'leaks' into 'analog' domain. The widely used barcoding system ensures data collection quality. Sweetpotatobase now has quality filtering upon upload of your data. Currently Sweetpotatobase is home for 326 trials, 33,237 accessions and 648,833 phenotypic observations. Over 100 different traits have been measured by the five breeding programs which include Ghana, Uganda, NCSU, GT4SP-CIP and Mozambique.

Some of the new features in HIDAP include:

1. The HIDAP online version, connects directly to Sweetpotatobase and users can access and analyze their data.

2. Data collected from the mobile (Android) FieldbookApp can now be moved into HIDAP for quality check and processing and soon we shall be able to upload data from HIDAP to Sweetpotatobase.

The new features in Sweetpotatobase include:

1. Crop ontology request form

The crop ontology describes the traits, measurements methods and scales which are key for data integration. However, development of an ontology is a continuous process and Sweetpotatobase users who have come up with a new trait and measuring method or scale can describe it and submit a request for inclusion in the sweetpotato ontology.

2. Workflows

Sweetpotatobase now has easy to use data entry dialogs and the workflows manage the entire process guiding you through the different dialogs.

3. Seedlot tracking and inventory

This feature enables you to track seed or planting materials with the crossing tool/trial generation interface.

4. Improved barcode management-design

This has greatly improved the barcode management with a flexible label designer, an android fieldbook barcode support which are compatible with Zebra printers.

5. Genotyping trials

Sweetpotatobase now has a provision for integrating genotyping and phenotyping data. You can now prepare the plates for genotyping on Sweetpotatobase, track the progress of genotyping on the website (depending on the service provider - Cornell and Intertek, are now supported and hopefully NCSU will soon be supported).

6. Sweetpotatobase and BrAPI

Sweetpotatabase now supports BrAPI which is the Breeding Application Programing Interface that allows data exchange across databases.

7. BrAPI R

This is an Rpackage that can be used to access data in BRAPI databases like Sweetpotatobase from R.

Discussion

What comparative advantage does the database have over traditional tools?

Sweetpotatobase has improved access to the data, can combine both phenotypic and genotypic data for a given trial which can also be shared with the wider breeding community.

1.3 HIDAP off-line training: Trial sites, create list of genotypes, Fieldbook Management – Field book creation, data quality of field data and statistical analysis in HIDAP Offline

Omar Benites and Raul Eyzaguirre.

Mercy Kitavi, helps a breeder, Goretti Ssemakula, in using HIDAP

This was a practical session that required the participants to open HIDAP on their laptops. HIDAP has several already inbuilt lists like the table of locations and CIP's institutional germplasm lists. However, there is an option to add a trial location or genotypes that are not on the list. Omar Benites demonstrated how trial sites can be added and how a list of genotypes can be created in HIDAP offline. You can also create fieldbooks for various designs in HIDAP. Raul demonstrated how you can design a trial with the offline version of HIDAP using the example of the Westcott design for 200 genotypes, with 'Dagga' and 'Cemsa' as the check clones. All the participants worked this out on their computers and could download the created fieldbook. HIDAP also has a provision for checking your data for outliers using the interquartile range method. You can also calculate computed (derived) traits and analyze data in HIDAP and generate both single trial and multi-environmental trial (MET) reports. The single trial report contains:

- Model specification and data description
- ANOVA and CV
- Plots to check assumptions
- Genotype means
- LSD and Turkey test (Only if ANOVA is significant for genotypes)
- Dot plot for genotype (only if the number of genotypes is less than 10)
- Variance component estimations

While the MET report contains

- Model specification and data description
- Means by genotype, environment and GXE interactions
- ANOVA and CV
- Plots to check assumptions
- LSD and Turkey test (Only if ANOVA turns out significant for genotypes)
- Dot plot for genotype (only if the number of genotypes is less than 10
- Variance component and broad sense heritability estimation
- Stability analysis (only if ANOVA is significant for interaction)

1.4 Sweetpotatobase and HIDAP on-line training: Import fieldbooks from Sweetpotatobase, check fieldbooks, descriptive plots and reports.

Alex Ogbonna

This was also a practical session on the use of Sweetpotatobase. Alex showed the participants how to log in sweetpotatobase.org, creating new accounts, recover password, add a new breeding program and add accessions to the database. Sweetpotatobase supports both new and existing trials and the speedbreeders had the opportunity to tryout both workflows with their new Sweetpotatobase accounts. During the process of uploading the trials the breeders had a discussion on data curation, highlighting how the database can help you avoid creating new accessions for synonyms using the options from the fuzzy search. A trial for the 100 best bet genotypes was created in preparation for the field day.

1.5 User perspectives SPBase/HIDAP: CIP Ghana representing CIP's Support Platforms

Jolien Swanckaert

Jolien demonstrated how CIP's sweetpotato breeding support platform for West Africa was using both the Sweetpotatobase and HIDAP to manage breeding data. It is always good to create your material list in Sweetpotatobase to avoid mistakes in accession names. HIDAP is mainly used to check the data set for any outliers, however, there have always been challenges of having to copy and paste every time you change from the Sweetpotatobase to HIDAP. CIP Ghana also uses Seedlots to manage planting materials.

1.6 User perspectives Sweetpotatobase/HIDAP: NaCRRI representing National Programs

Doreen Chelang'at

The National Crops Resources Research Institute (NaCRRI) in Uganda is actively using SPBase to manage breeding data which enables archiving and retrieval of all information associated with a trial. Using SPBase has also made it easy to transition from collecting data in the hard copies to electronic capture using the FieldbookApp. SPbase is continuously being updated with new features such as the label designer, workflows for various tasks which makes it easy to work with. The team at NaCRRI has managed breeding data for 38 trials using 3,475 of the accessions in Sweetpotatobase.

Discussion

How is the CIP Ghana breeding program using the datasets from other breeding programs, say Uganda?

All SPbase users have access to the data from other breeding programs but currently it is not yet possible to use it because some of the genotypes have different synonyms in other breeding programs.

Do the speedbreeders have any reservations about open datasets like SPbase?

Craig Yencho noted that sometimes it is not the breeders with reservations about open datasets but it could be an institutional limitation. This will be a good time to start a conversation on how to solve such issues.

1.7 Introduction to PhotoSynQ

Isaac Dramadri and Astère Bararyenya

Data collection using the photoSynQ tool takes only fifteen seconds per sample

MultspeQ's PhotoSynQ tool is a web-based data capture platform that can measure multiple photosynthetic measurements. One PhotoSynQ measurement can be done in only 15 seconds and will give you multiple measurements such as the geo reference position, micro-climate, photosystem 1 and photosystem 2 efficiency, non-photochemical quenching, stomatal conductance, leaf thickness, temperature differentials, chlorophyll/pigments and photorespiration. Breeders can use these parameters to select genotypes that have inherent abilities for photoprotection or minimizing photodamage. For quality control the research should ensure that measurements are taken on plants of the same age and following the order of treatments during data collection. Isaac demonstrated how to set up a project for the PhotoSynQ tool using the trial evaluating the '100 best bet genotypes' in preparation for the field day.

1.8 Field trip to the University of Nairobi, Kabete Campus

Participants collect data on tablets using the fieldbookApp during the field trip

On the morning of 6th June 2018, 37 participants went for a field trip to the University of Nairobi, Kabete campus, where the '100 best bet genotypes' collected from 14 countries in SSA had been grown for morphological characterization by the Africa Biosciences Challenge Fund (ABCF) fellow, Eunice Wainaina. Luka Wanjohi, Bryan Ellerbrock and Alex Ogbonna illustrated to the speedbreeders how data can be captured using the FieldbookApp. The participants who had been grouped in six teams had hands-on experience in data collection for six traits, namely, vine vigor, virus symptoms, Alternaria blight symptoms, leaf shape, leaf type and leaf size.

Dr. Isaac Dramadri then attempted to demonstrate how the PhotoSynQ tool could be used to take measurements in the field but unfortunately equipment could not work due to limited charge. The participants collected a set of detached vine shoots to test the PhotoSynQ tool in the meeting room.

1.9 PhotoSynQ – download data, processing

This session was led by Isaac Dramadri and Astère Bararyenya. They demonstrated how to create a project in PhotoSynQ and how to upload the data that was collected in the field. In the meeting room, the participants broke into three groups and successfully collected data from intact leaves on shoots that were collected from the field.

Isaac Dramadri demonstrates the use of a tablet to download data collected by the photoSynQ

1.10 Field book App-download data and processing

The session was led by Brian and Luka. Traits that were collected from the field were exported to the computer and uploaded onto SPBase. The uploaded data was checked for integrity, outliers and summary stats displayed. For more complex analyses, it is recommended to use HIDAP.

Discussions and field day wrap up

How can we merge data that has been collected on the same trial from two tablets?

Alex Ogbonna clarified that even when you collect data for the same trial on more than one tablet, you simply upload the data from each tablet unto Sweetpotatobase and it will automatically merge the two subsets (files) of the data.

How many people have used the FieldbookApp before, and how can breeders be helped implement use of the FieldbookApp in their breeding programs?

Some breeders do not have tablets for collecting data but android phones can serve the purpose. There is a slight learning curve involved in adopting some of these tools and many of the breeders might be busy attending to other issues in their line of duty but it will be better to identify assistants in their programs that can drive the use the FieldbookApp in their breeding programs. Mercy Kitavi informed the breeders that webinars have been routinely conducted, that specifically address issues of using Sweetpotatobase. These webinars are recorded and posted onto http://www.sweetpotatoknowledge.org and everyone is encouraged to watch them to increase their knowledge in specific areas. Robert Mwanga highlighted the importance of photosynthesis data to give insight on drought and shade tolerance.

1.11 Sweetpotato knowledge portal

Faith Njung`e and Luka Wanjohi

This was a practical session in which participants opened their accounts in the Sweetpotato Knowledge Portal. Faith guided the participants through an exercise on how to upload different documents such as published papers onto the portal. Participants uploaded their stories and published them on the Sweetpotato Knowledge Portal.

Session 2: Genomic Resources (Tools and Methods)

2.1 Setting the stage for genomics assisted breeding in sweetpotato

Craig Yencho

The key partners in the GT4SP project are NCSU, Boyce Thompson Institute (BTI) - Cornell University, University of Queensland, CIP, Michigan State University (MSU) and NaCRRI. Project activities have been implemented over the last three and a half years. Great progress has been made on all the objectives as the project winds down. For instance, reference genomes have been developed for wild relatives of sweetpotato, *Ipomoea trifida* and *I. triloba*. We need a hexaploid genome and work towards this is already underway with the leadership of Zhangjun Fei at BTI. A genome browser for sweetpotato has been developed by MSU. Genes associated with beta-carotene production have been identified from the browser by some ABCF fellows. We have also done transcriptome profiling of key traits in sweetpotato. The single nucleotide polymorphism (SNP) development pipeline has been developed by the NCSU group, which is the first of its kind in sweetpotato. The GT4SP project has developed high quality linkage maps in sweetpotato. New QTL mapping algorithms have been developed in hexaploid sweetpotato. The team has identified QTL of key traits. Great progress has been made in weevil resistance research. We hope to make even greater progress in GT4SP phase II. The breeders need to understand the key principles and application for their needs. We also plan to deepen genomic selection in sweetpotato in phase II for improving populations. The key traits we will focus on will be sweetpotato weevil resistance and sweetpotato virus disease resistance. All these genomic tools will be rolled out for implementation in the breeding programs in the SSA region.

Craig Yencho highlights the genomic tools that have been developed by the GT4SP project

2.2 Genotyping by sequencing in hexaploid sweetpotato – Status and future directions

Bode Olukolu

Molecular markers are essential in molecular breeding applications for developing genetic maps, genome-wide association studies (GWAS), genomic selection, and diversity analysis. Morphological markers are equally important in breeding, however, they have limitations due to environmental plasticity. This led to the development of molecular markers, evolving from isozymes to DNA markers, including restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs) and SNPs. SNP chips are great for breeding communities like ours, if the costs for development of the chips can be paid by the community as they are expensive to develop. Sequence based genotyping like GBS is inexpensive but leads to a lot of missing data. Sequencing-based diversity array technology

(DarTSeq) is used in sweetpotato genotyping but cannot capture dosage effect as the makers are scored as diploid. The sweetpotato GBS under the GT4SP was done using GBSpoly that accounts for dosage effect and you can determine the read depth suitable for capturing more SNPs. Filtering of the data is critical for removing noisy signals and detecting the correct SNPs. Always start with high quality DNA, followed by accurate library preparation, then select appropriate restriction enzymes *in silico* (i.e. on computer or via computer simulation), select right adaptor and run your samples in illumina sequencer. The SNP calling pipeline for sweetpotato has also been developed through the project. We need to develop GBSArray from the GBSPoly for future genotyping. The costs will go down to below USD 5 per sample through the array chip.

Discussion

Is the GBSpoly technology going to be a service?

Bode Olukulu explained that the GT4SP project was developing the technology, so programs and service providers can adopt and develop the technology for out scaling and application. Craig Yencho emphasized that in the short term NCSU will provide the service through GT4SP Phase II. Sweetpotato is unique, so the GT4SP team can provide the service up to analytics using the private sector model. Long term, a private sector can take up and out scale the service. However, there is need for a better concept on how to integrate genomic selection into breeding programs. It will be good to apply it in variety selection and not population improvement.

2.3 New Methods for construction of genetic linkage maps in hexaploid sweetpotato

Marcelo Mollinari

Genetic maps are linear arrangements of markers along the chromosomes. The maps can be used for understanding the inheritance of traits such as weevil resistance but they also serve as proxies for key traits and can be used for selecting for key traits in populations. Genetic mapping is based on recombination events among chromosomes. This is simple in diploids, however, it gets more complex in hexaploid sweetpotato. Phasing is complex in hexaploids as you can have up to six homologous chromosomes. Recombination fraction matrixes for a hexaploid can now be developed through the Polymap software developed by the GT4SP project at NCSU. High-density genetic maps for hexaploid sweetpotato have been constructed through the project. The software can now be extended to develop high-density linkage maps for sweetpotato segregating for other key traits. Polyploidy models have been developed for constructing linkage maps for sweetpotato for the first time. Now, we can develop maps for single parental maps instead of bi-parental maps that have been done earlier in sweetpotato. The linkage maps are very useful for QTL analysis.

Discussion

Was double reduction considered in the model for constructing the genetic linkage maps?

Double reduction was calculated but was not considered in this linkage mapping model because it was only accounting for 3% of the genome.

2.4 Quantitative Trait Loci Mapping in Autopolyploid Species

Guilherme Da Silva Perreira, Marcelo Molinari and Zhao-Bang Zeng

QTL analysis involves development of populations segregating for traits under consideration. The phenotypic data of these segregating populations can be used to determine whether the individual genotypes in the population are different from each other but these differences can be attributed to different sources like the environment and the genetic composition of each individual genotype. The differences due to the genetic composition of each individual genotype (genetic variance) is determined by the proportion of alleles each individual genotype inherited from the parents (identical by descent-IBD). A QTL is a region of DNA which contributes to the variation of a trait and QTL analysis attempts to identify any specific loci that are associated with the phenotype. The guiding principle is that in the region of a gene influencing a trait of interest 1) Individuals which are more correlated in their trait values have higher IBD allele they share 2) Individuals which are less correlated phenotypically have a lower genetic relationship. Unfortunately, even after genotyping segregating populations using the appropriate platform like GBSpoly in sweetpotato it is still hard to see the associations between genotypes and phenotypes because most of the individuals in the population share the same alleles. Therefore, QTLs are identified according to their statistical significance using a stepwise procedure. The GT4SP project team initially used the tetraploid potato data for developing models for QTL analysis of key traits in polyploids. The tetraploid models were then extended to map QTLs of storage root yield, harvest index in hexaploid sweetpotato. QTLs can be used for prediction of performance for traits, do marker assisted selection, candidate gene identification and genomic selection in sweetpotato. The project has developed the PolyQTL software for QTL analysis in sweetpotato. The software is still being further developed.

Discussion

Do we need to sequence the hexaploid sweetpotato genome if we can already do QTL analysis? Can we use CRISPR Cas9 technology for removing unwanted genes?

Guilherme Da Silva Perreira elucidated that the diploid reference genome is limited and cannot be used to detect all the needed genes, so there is still need for sequencing the hexaploid genome to identify more genes and help in haplotype identification. Craig Yencho stressed that a good reference genome is critical for good CRISPR Cas9 technology to be efficient. GT4SP I set the stage to develop these polyploid-based tools to address these traits. It is necessary to fine-tune these tools for application in real life breeding programs for progeny and parental performance prediction and selection.

2.5 The potential of genomics-assisted breeding of sweetpotato in SSA given the new genomic tools: Towards genomics assisted breeding in sweetpotato at CIP: Product advancement processes

Dorcus Gemenet

Genome assisted breeding involves use of molecular markers linked to traits of interest to aid early selection of progeny with the desire for advancement. It is time saving and helps shorten the breeding cycle. Product development starts with designing of breeding objectives, optimizing breeding protocols, product development and testing. CIP has identified QTLs of beta-carotene, dry matter content, storage root yield, harvest index and conducted transcriptome analysis of key traits in sweetpotato like drought tolerance studies.

Discussion

Why were the markers for beta-carotene and flesh color different?

Markers for carotene biosynthesis are mapped on the same chromosome as those for flesh color but there are many other pigments involved in flesh color.

2.6 QTL mapping of resistance to root knot nematodes (RKN), root quality traits and resistance to sweetpotato weevils in the New Kawogo x Beauregard (NKB) and Tanzania x Beauregard (TB) populations

Bonny Oloka

The NKB population was developed in 2010 and it segregates for weevil resistance, Sweetpotato virus disease (SPVD) resistance, yield, and dry matter content. The population was phenotyped in Uganda for the above traits and GBS was done at NCSU. Sequences aligned to the reference genome for selecting 11,000 SNPs and ended up with 9,000 SNPs that were then used for linkage and QTL analysis. Allele dosage was determined and used for QTL analyses. All the QTLs were mapped using PolyQTL. Four QTLs of SPVD resistance, 2 QTLs of hydroxycinnamic acid (HCA) based resistance, 4 for beta-carotene, dry matter content and starch were identified using the NKB population. QTL analyses of root knot nematode were done using the Tanzania x Beauregard population. Five QTLs of RKN were identified in the study with combined heritability of 0.5 explained. A blast search showed that the genes of these QTLs are associated with stress resistance.

2.7 Population diversity and genome wide association studies (GWAS) of sweetpotato varieties in Burundi

Gaspard Nihorimbere

Studies were conducted at Biosciences eastern and central Africa - International Livestock Research Institute (BecA-ILRI) Hub under the ABCF fellowship. The focus of the study was to contribute to the development of sweetpotato varieties with resistance to Alternaria blight and weevil resistance. This involved collecting germplasm along with farmers' knowledge on Alternaria disease from Burundi for characterization. A total of 172 accessions were phenotyped at multiple sites in Burundi and genotyped at BecA using DarTseq technology for diversity and GWAS analyses. Sequences were aligned to *Ipomoea trifida* and *I. triloba* sequences developed by the GT4SP project. The accessions clustered according to origin and nutritional content especially the beta-carotene content. SNPs linked to beta-carotene content loci were identified and explained about 13% of variation. GWAS additionally identified SNPs associated with weevil resistance. There is need to validate those SNPs for use in the breeding program.

Discussion

How did you impute genotypic and phenotypic data?

Gaspard Nihorimbere highlighted that some varieties had missing data and so he had to impute to take care of missing data using the TASSEL program.

2.8 Phenotyping and QTL analysis for storage root chemistry of sweetpotato (Tanzania x Beauregard, TB, and Beauregard x Tanzania, BT)

Victor Amankwaah

Evaluated the TB and BT populations for root chemistry for his PhD dissertation research at NCSU. Field trials were conducted in North Carolina, USA and Ghana for two seasons. Root chemistry analysis was done using freeze-dried samples by near infrared spectroscopy (NIRS) at NCSU and Ghana. Genotype distribution for dry matter content (DMC) and starch content showed normal distribution with many transgressive segregants for these traits. Sugar content was normally distributed as well. Alpha amylase activity in storage root samples was analyzed in the samples of the TB population. Many genotypes showing transgressive segregation were observed in the population. A similar trend was obtained for beta amylase activity. The team is calibrating NIRs for profiling sugars in the populations.

Victor Amankwaah explains how alpha and beta amylase affect the cooking quality of sweetpotato roots

Why did you bake instead of cooking as normally done in SSA?

For curve development, baking is the right path as it helps in producing more maltose.

Why use a food processor for dry matter analysis?

The food processor was improvised for handling many samples. Bode Olukulu noted that for all the populations under study, dry matter and beta-carotene are negatively correlated, although the QTL effect is different for many population, here marker assisted selection (MAS) can help breed for these traits at the same time in the populations.

Which amylase is more important in sweetpotato?

Victor Amankwaah explained that beta-amylase is more important than alpha-amylase as it affects the cooking quality, especially the cooked root texture and flavor.

2.9 Phenotypic and QTL analysis of the BT population in Ghana.

Obaiya Utoblo

Drought causes yield loss of 50-80% in sweetpotato depending on the timing, duration and intensity of the dry spell. In Ghana there has been an increase in temperatures with a decrease in rainfall (20%) over the past 40 years. This study aimed at evaluating the effect of drought on sweetpotato in Ghana using the Beauregard x Tanzania (BT) mapping population. The specific study objectives include

- Estimation of the effect of drought on sweetpotato grown in the field under drought conditions in Ghana
- Mapping quantitative trait loci for drought tolerance using the BT population in Ghana.
- Evaluation of the effect of drought on the early above ground parts and root system architecture (RSA) of sweetpotato in the screenhouse in Ghana
- Evaluation of the effect of drought on quality traits of sweetpotato grown under drought conditions in Ghana

Results revealed a general reduction in the mean for storage root yield in tons per ha (RYTHA), foliage yield in tons per ha (FYTHA), total biomass and harvest index (HI) under drought conditions. Of all traits studied, RYTHA had the highest relative yield reduction under drought. A drought tolerance selection index was used to select top best and bottom least performing genotypes. Five drought tolerance QTLs were identified and the effect of drought on early above ground parts and root system architecture was determined from the preliminary analysis. The fourth objective involves impact of drought on root quality/chemistry traits and the study will be conducted in collaboration with Victor Amankwaah. The timeline of the PhD program was presented, with thesis submission slated for December 2018.

Discussion

Why does Beauregard perform better for yield than Tanzania under drought?

It seems Tanzania is not well adapted for Ghana (and some other locations like the US; confirmed by Craig Yencho) but performs well in East and southern Africa (confirmed by Maria Andrade).

Why is it that none of the PhD students or ABCF fellows is using data management tools (SPbase, HIDAP, CloneSelector)?

Adoption is a work in progress but also the tools are limited for the kind of studies that were conducted.

2.10 SNP discovery and genome wide association study (GWAS) of continuous storage root formation and bulking traits in sweetpotato (*Ipomoea batatas*)

Astère Bararyenya

This study highlighted the importance of piece meal harvesting in the sweetpotato cropping system in SSA. Most popular farmer varieties can be harvested during the entire growing season. The objectives of the study were to identify genetic variability and SNP markers associated with continuous storage root formation and bulking (CSRFB). The results showed that most of the landrace sweetpotato varieties in Uganda have CSRFB and SNP markers associated with CSRFB were identified.

Discussion

Ted Carey noted that one of the accessions selected for CSRFB, Huarmeyano, is a Peruvian landrace and not a Ugandan landrace even though it was obtained from the Ugandan germplasm repository.

2.11 Building capacity to empower breeders for use of genomics/molecular assisted breeding in sweetpotato programs

Mercy Kitavi

Sweetpotato is important as a food source and a phytomedicine against vitamin A deficiency and blindness. It is also used as animal feed. The GT4SP capacity building supports breeders, agronomists, and other scientists working on sweetpotato improvement through online training webinars and face to face courses that help make full use of genomic resources. Various approaches will be adopted to reach out to a larger group of people. These include but not limited to workshops, online webinars (such as the webinar presented by Robin Buell). Short and long-term hands-on-training at BecA, such as in a study that designed primers from genes underlying beta-carotene, which were used for diversity study. Another study evaluated the taxonomic abundance of sweetpotato viruses, which can be important for the customs/immigration department for quarantine purpose. Mercy Kitavi emphasized understanding the needs of different sweetpotato users. She highlighted the importance of extracting quality DNA for genomics-assisted breeding.

Discussion

If you have three requests for your constituents as the capacity building personnel, what will they be?

(1) Know your parental materials, (2) what is the purpose/use/utility of specific clones you are breeding for, and (3) Identify your training needs. Felistus Chipungu made a fourth request for institutional infrastructure.

2.12 IGSS: Integrated Genotyping Service and Support

Catharine Ziyomo

Integrated Genotyping Service and Support (IGSS) Africa is a BMGF funded platform contributing to increasing genetic gain by lowering the cost of genotyping. The platform also handles kompetitive allele specific PCR (KASP) assays and provides bioinformatics support. Impacts of these markers are only felt if they are integrated into marker-assisted breeding pipeline. Genotyping is DArTseq based and Catharine provided some details about it except for proprietary components.

Discussion

It seems DArTseq may not be the future of genotyping, given the advances in sequencing technology?

Catherine Ziyomo informed the meeting that DArTseq recognizes the dynamic nature and changing technologies in genotyping and is trying to keep abreast with these changes. Craig Yencho noted that it might not be the right approach to turn conventional breeders into molecular breeders considering the complexity of the technology? The point is to provide the skills to enable the breeders to appreciate the new tools.

2.13 Panel Discussion: Perspectives on applications of genomics to the NARs sweetpotato breeding programs.

Craig Yencho

Panelists: Benard Yada, Obed Mwenye, Wolfgang Grüneberg, Gaspard Nihorimbere and Koussao Some

What can genomics-assisted breeding realistically offer us?

Some Koussao (holding the microphone) elaborates the potential of applying genomics-assisted breeding in SSA during the panel discussion. Panelists (left to right) Benard Yada, Wolfgang Grüneberg, Obed Mwenye, Koussao Some and Gaspard Nihorimbere

The panelists enlisted two outstanding propositions of what genomic assisted breeding can realistically offer 1) markers associated with important breeding traits which can be used to accelerate breeding and 2) hexaploid and dosage-based tools for genetic linkage maps.

However, Wolfgang Grüneberg highlighted that there is still a gap between applied and molecular breeding which needs to be changed by fast-tracking the integration of applied and molecular breeding.

Craig Yencho agreed with Wolfgang Grüneberg, that there is still a big gap between applied and molecular breeding and he wondered whether it is a reality to close that gap within the next 5 years?

The meeting suggested some strategies that could be used to address this gap including;

- Documenting and sharing workflows for each of the genomic tools and how it can be applied for the applied breeders
- Working towards developing some pilot projects for each region to apply these tools in SSA
- Step up the capacity building efforts for applied breeders taking into consideration their knowledge level (beginners, intermediate and highly skilled) of the individuals
- Identify few appropriate traits for marker assisted selection and focus on their application
- Identify what works and bring it to scale
- Identify the services (and profile service providers) that can be out-sourced like DNA extraction, genotyping and genomic prediction.

The role of genomics-assisted breeding in sub-Saharan sweetpotato breeding

The panelists highlighted their expectations from the deployment sweetpotato genomics assisted breeding in SSA which included:

- It will increase the precision and accuracy of breeding for different traits,
- An increase in the turnover of variety releases,
- Enable breeders effectively to exploit the wide sweetpotato diversity in SSA
- Increase the genetic gains especially for the recalcitrant traits

Craig Yencho, illustrated how his potato breeding program uses only 4 markers, that were developed by other colleagues, to screen his parental materials for potato virus y (pvy) and root knot nematodes (RKN). Breeders can successively be adopting the tools as they are developed. He further proposed breeders to select their top 50 clones for genotyping on condition that they are phenotyped and the data uploaded on SPbase.

Major areas of research for genomics-assisted breeding

The panelists underlined some research areas that might need to be addressed to make genomics-assisted breeding a reality in SSA and these included:

- Optimizing genomic selection models
- Markers for SPVD and weevil resistance
- Making the genomic tools breeder friendly
- Markers for various consumer acceptability traits

Conclusion

Largely, the panelists thought there is need to improve on the breeding efficiency by using genomic resources available to the community of practice. This implies that breeders must conduct business differently and consider adjustments like:

- Embracing data sharing and open access
- Working together as a team to exploit synergies
- Learn to be better advocates
- Have an entrepreneurial spirit to supplement on the little government support
- Continuously learn and apply the new skills
- Consider technologies for high-throughput phenotyping

Session 3: Progress in Sweetpotato Breeding

3.1 One hundred Best bet catalogue

Jolien Swanckaert and Edward Carey

Jolien Swanckaert explaining how the catalogue for the one hundred best bet genotypes for SSA will be used

It is important to characterize the best varieties in Africa for the benefit of farmers and breeders to be able select the best for their conditions. Africa is diverse due different rainfall patterns, biotic and abiotic constraints, edaphic and other physical properties. The best bet catalogue will be put online. Trials to characterize the 100 best bet genotypes were set up in April 2018 in Kenya. However, data on performance of individual varieties in the country of origin is required and shall be compared to performance in Kenya. Each variety will get a CIP number from the gene bank. Synonyms will be included to common varieties in different countries.

Discussion

Catalogue format

The final format of photos has not yet been decided but the best photo would include the whole plant with roots attached to the stems. Photos for leaves will include both the adaxial and abaxial surfaces. Although it might be difficult to have roots attached to stems because some of the varieties have huge biomass. Some of the desirable attributes to include in the catalogue would be postharvest traits. Jan Low highlighted the value of the catalogue, in that, all these varieties have been cleaned up of viruses and kept at KEPHIS and will be available support to any country in need of the variety (ies).

3.2 Progress Breeding at CIP HQ (including Hybrid Breeding)

Wolfgang Grüneberg

Breeding at CIP HQ is guided by a global product concept and is geared towards supporting ongoing breeding efforts for 1) early maturing varieties (<90 days) to fit in the crop rotation of the Asian cropping system, 2) non-sweet sweetpotato varieties for West Africa, 3) drought tolerant varieties for Southern Africa and 4) SPVD resistant OFSP varieties for the high virus pressure Eastern and Central Africa.

Wolfgang Grüneberg explains how hybrid breeding will revolutionize sweetpotato improvement

Hybrid breeding in sweetpotato follows principles/scheme by Schnell F.W. 1982. There are many different hybrids, including (i) population hybrids, (ii) top cross hybrids, (iii) 4-way hybrids from low to highly inbred lines, (iv) 2-way hybrids from incomplete inbred lines and (v) 2-way hybrids from complete inbred lines. For hybrid breeding, you need two populations which are mutually heterotic, therefore, genepool separation is key to hybrid development. At CIP HQ populations are improved through either polycrosses- with parental selection based on clone performance *per se* or reciprocal recurrent selection and offspring parent analysis. The reciprocal recurrent selection approach is better, as the H0 population is compared to the original parents and the H1 population is also compared to best parents and base parents. For instance, the offspring mean storage root yield for 3292 H1 hybrids in the high iron (HIFE) population (44.8 t/ha) was higher than the best parents (32.6 t/h) and the base parents (22.8 t/ha); this translates to a total genetic gain of 96.2% derived from the heterosis increment of 36.4% and 43.8% after one reciprocal recurrent selection cycle. A similar trend was observed with the 9,881 H1 hybrids of the wide adaptation and earliness (WAE) population and the 3742 H1 non-sweet population. These hybrid breeding schemes / heterosis exploiting breeding schemes have resulted in the production of elite crosses

Some of the additional lessons may include:

- Varcomp general combining ability (GCA) is considerably much larger than specific combining ability (SCA). Since GCA is due to genes which are largely additive in their effects while SCA is due to genes with dominance or epistatic effects. This implies that their higher prospects for breeding progress whenever GCA is greater than SCA.
- Potential testers have been identified from several cross combinations and high GCA
- Logistics and operations of these large populations requires special field design like the Westcott (1982);
- SSR markers separate genepools quite well as seen with the – a) PJ and PZ pools in Peru and b) population Uganda A (UG_A) and UG_B in Uganda;

In the future, breeding at CIPHQ will be able to support heterosis exploiting breeding (HEB) schemes at CIP's breeding support platforms in SSA. Most of our national breeding programs in SSA will benefit from receiving true seed from the elite crossing (on basis of "Super Parents"). Elite crossing will become our target for genome wide prediction + marker assisted selection – this is within the logistical and operational capacity (1,000 to 2,000 clones)

Discussion

For reciprocal recurrent selection, how do you select the parents to make sure they are genetically different?

It is difficult to use agronomic traits to select parents that are genetically different because epistasis influences heterosis increments. Molecular markers will do it well and achieve it through principal component analysis (PCA), cluster analysis, population structure as was applied to parental materials for Uganda. Population Uganda A and Population Uganda B were identified and are expected to be mutually heterotic. Some traits like storage root yield outbreeding will give you the heterotic increment while other traits like SPVD resistance, you might need inbreeding hybrid performance to allow selection/use of good gene pools. Craig Yencho noted that SSRs may not be trusted because for the Ugandan population the GBS data showed that some genotypes in pop A and pop B were incorrectly grouped.

3.3 Progress – Southern Africa Sweetpotato Support Platform

Maria Andrade

The breeding milestones for the Southern Africa Sweetpotato Support Platform include:

- Studies demonstrating that breeding can achieve significant genetic gain (2% per year in yield) in 2 years in early generations and 4 years for selected varieties
- At least 150 thousand seeds with drought tolerance genes disseminated to at least 10 NARS partners in SSA and South West and Central Asia (SWCA),
- Hybrid progeny exhibiting yield jump of 10 to 20% in hybrids from populations with drought tolerant and enhanced efficiency for drought tolerance breeding,
- Clones with 200%RDA for young children of pro-vitamin A, 25% RDA of iron and 35% RDA of zinc under high intakes.

Progress was presented from the genetic gain studies of 11 varieties that had been released between 2000-2016. Agronomic data for vine yield, commercial root yield and number of commercial roots per plant from five locations in three seasons 2016, 2017 and 2018 were combined for analysis. The analysis of variance revealed that genotype and location were highly significant ($P<0.05$) for the three traits. However, the interaction between genotype and location were only significant for commercial root yield and vine yield. The genotype mean was above 30.38%, an indication of improvement from population means of varieties released in 2011 and 2016. The number of commercial roots per plant was increasing by 0.18 on annual basis from the year 2005 until 2016.

A total of 342,909 seed was generated by the southern Africa sweetpotato support platform during 2017 from two sites, Gurue and Umbeluzi in Mozambique. Over the years 146,662 true seed has been disseminated widely to SSA and beyond, including Brazil, Asia and USA.

Three observational trials are under evaluation comprising 3,000, 2,667 and 1,695 new clones in the field and will be ready for harvesting in November and NIRS analysis to determine the beta-carotene, iron and zinc levels. A total of 450 clones have been selected and sent for verification of Fe and Zn through XFR in Lima in two batches. High Fe and Zn levels in these clones were identified through NIRS analysis in Maputo. More than 30 clones had higher Fe > 25 mg/kg dry weight (DW) basis.

3.4 Progress – Southern Africa sub-region

Sunette Laurie

The report covers national breeding programs of Mozambique, Madagascar, Malawi, Zambia, South Africa and Angola. Unfortunately, sweetpotato breeding information could not be obtained for Angola. The presentation highlighted specific objectives for each country, programs they are using for statistical analysis, funding source for sweetpotato breeding or foundation seed, some of the challenges they are facing and sweetpotato clones in the pipeline for official release.

High storage root yield, increased β-carotene content, and high dry mater content (>30%) were the key traits that are bred for by all the five countries in the southern Africa region. Some of the other traits under consideration include earliness, drought tolerance, weevil resistance, root processing qualities, high iron and zinc, Fusarium wilt resistance and root uniformity. However, there are some desirable traits, currently not under consideration due to limited resources and these include cold tolerance, water use efficiency and deep rooting. All the five countries were involved in participatory breeding activities at both on-station and on-farm. For the organoleptic assessment, all the programs were using farmer groups with only Madagascar and South Africa occasionally using a trained panel. Malawi had the highest number of sweetpotato breeders (4) and technicians (31), while Mozambique had the highest number of screenhouses in Southern Africa. All the five countries in the sub-region had received botanical seed from support platforms of either Uganda or Mozambique.

HIDAP and Genstat were the most widely used programs for data analysis by the national programs in the Southern Africa region, each used by at least three countries, while R, SAS and ANOVA Excel were the least used programs. Twelve promising sweetpotato clones have been earmarked for release in 2018, five by Mozambique and Madagascar and two by Zambia. The major challenge the breeding programs in southern Africa face, include decreased funding, power cuts in tissue culture laboratories, irregular rainfall pattern, prolonged droughts and procurement complications.

3.5 Progress West Africa Sweetpotato Support Platform

Edward Carey

Breeding focus for the West Africa sweetpotato support platform is on quality traits, non-sweet sweetpotato and reduced perishability. The Southern Zone of Ghana is forest and prone to virus, so it is difficult to move clones before they are released. Some good varieties exist in the northern regions/savanna but also succumb to virus when brought to the south, therefore wide adaptation becomes a goal. CIP-Ghana is involved in the initial breeding cycles (crossing blocks, seedling nurseries and observation trials (OTs) supported by SASHA. Despite non-sweet sweetpotato being the signature trait, the target is still unclear for instance:

Edward Carey explains how highly desirable but intricate the non-sweet sweetpotato ideotype is for West Africa

- Sugars in raw sweetpotato are not a good predictor of sweetness in cooked sweetpotato
- Sugars in cooked sweetpotato are not a good predictor of sweetness since other factors contribute (aromatic)
- Cooked sugars can be precisely measured with the NIRS, but they cannot accurately and routinely describe taste

So, a trained panel of 27 people has been recruited to precisely define sensory attributes and help with selecting contrasting genotypes (low and high sugar; low and high sweet). The panel has been used to develop lexicon for the fried sweetpotato. Low sweet, medium sweet and high sweet genotypes identified in comparison with yam. Amylase influences sweetness, but needs to be understood for a fair evaluation for the genotypes.

Some traits evaluated for postharvest perishability/storage include: transportability, cortex thickness, wound healing assessment, weight loss, rots and weevils. The support platform plans to use the B X T population for marker assays for storage traits.

In 2017, the first trial from the heterosis breeding scheme was conducted and the results show an average 98.2% heterosis increment for commercial root yield without separating genepools. Moving forward, DNA of parents has been sent to BecA, Nairobi, for genepool separation.

3.6 Progress West Africa sub-region

Some Koussao

The report covers the breeding programs of Ghana, Burkina Faso, Nigeria and Cote d'Ivoire. The key traits that are bred for include high yields, increasing β-carotene content, low sweetness, SPVD and weevil resistance, earliness and high dry matter. Some of the desirable traits that are currently not attempted because of limited resources include root shape and storage ability. All the four breeding programs are engaged in participatory breeding only at on-farm trials. Farmer groups are the most widely used way for organoleptic tests in West Africa even though Ghana has a trained teste panel. All the breeding programs received botanical seed from the support platform from Mozambique last year. SAS is the most extensively used program analysis and is used by Burkina Faso, Cote d'Ivoire and Nigeria. Fourteen sweetpotato clones have been earmarked for official release in 2018 in West Africa, Burkina Faso having the highest number of candidates, five. Some of the challenges encountered by the breeding programs include acute lack of funds, limited number of staff and lack of screenhouse space.

Discussion

It is great seeing platforms sharing seeds to NARS in Africa, however, there should be a framework and structure on how the families are evaluated and selected. The data sets could be put in Sweetpotatobase and comparisons of generated data made. This improves selection of parents. Jim Lorenzen suggested that it would be great to include the locations of the evaluation sites for these genotypes by GIS. Bode informed the meeting that the complete pedigree of progeny derived from polycrosses can now easily be traced with the help of genomic tools.

3.7 Progress East and Central Africa Sweetpotato Support Platform

Robert Mwanga

East and Central Africa is a high virus pressure region and the breeding milestones of the East and Central Africa sweetpotato support platform include:

- Studies demonstrating that significant genetic gain (2% per year in yield) can be achieved in 2 years in early generations and 4 years for selected varieties;
- At least 14 African sweetpotato breeders breed using the latest knowledge and efficient methods;
- At least 250,000 seeds with increased frequencies of resistance to SPVD (2–10%) disseminated to at least 10 NARS partners; and
- Selected hybrid progeny demonstrating yield jumps of 10–20% from populations with SPVD resistance.

Robert Mwanga highlights accomplishments of East and Central Africa sweetpotato support platform

During 2017, a total of 147,278 botanical seed were generated from two crossing blocks population Uganda A (50 genotypes) and Population Uganda B (80 genotypes). Of the total seed 113,047 were from polycrossses while 34,231 were from controlled crosses. Since 2014 a total of 303,047 (comprising 320 families) botanical seeds have been distributed to national program across SSA, largely for SPVD resistant variety development.

The agronomic performance of 130 sweetpotato genotypes that are currently used as parents were evaluated for 3 seasons (2016A, 2016B and 2017A) at three sites in Uganda. Results show that SPVD, the key trait for the sweetpotato support platform is negatively correlated with most traits associated with yield, like storage root yield (RYTHA), commercial root yield (CYTHA) and harvest index (HI).

Eight out of the 22 released sweetpotato varieties in Uganda were evaluated in genetic gain studies for two seasons across 3 sites (Namulonge, Serere and Kachwekano). Results reveal a 21%-106% increment in storage root yield over the farmer variety Kawogo which translates to a genetic gain 0.46 t/ha per year. A trial using a clean improved released variety as a base and the released varieties to measure genetic gain is planned.

Eight sweetpotato hybrids selections showing field SPVD resistance are currently under evaluation in advanced yield trials.

The capacity of sweetpotato breeders in Africa continues to be strengthened. Since 2009, 10 PhDs and three MScs have been trained in SSA. During 2017/2018, seven countries released 31 sweetpotato varieties in SSA; 16 (48%) of which are orange-fleshed.

3.8 Progress East and Central Africa sub-region

Benjamin Kivuva

The report covered six sweetpotato breeding programs of Kenya, Uganda, Tanzania, Ethiopia, Rwanda and Burundi. The key traits bred for in the Eastern African region are high root yield, high dry matter content, high β-carotene, continuous root formation and bulking, dual purpose utilization, SPVD, Alternaria blight and sweetpotato weevil (SPW) resistance. Some other desirable traits that are not advanced due to limited resources, include drought tolerance, processing quality, root shape, anthocyanins, herbicide resistance, starch quality, oxidation resistance, storability and earliness.

All the breeding programs engage farmers mainly through participatory on-farm trials with exception of Uganda which combines participatory on-farm trials with participatory on-station trials. All the breeding programs use farmer groups, paired taste tests or trained tasting panels for organoleptic assessment except Kenya. All the countries have received botanical seed from the support platforms in Uganda and Mozambique. GenStat is the most widely used programme for analysis in the region. Seven new sweetpotato varieties were released in 2017 and 13 promising varieties have been earmarked for release in 2018. Some of the challenges faced by the breeding programs include prolonged drought, shortage of human capacity, low funding, and the emerging non-traditional pests like the Army fall worm in Uganda.

3.9 RTB (Roots, tubers and bananas) project report for 2017 and planning 2018 and beyond.

Wolfgang Grüneberg

RTB is structured into five flagships, namely, 1) enhanced genetic resources, 2) adapted productive varieties and quality seed, 3) resilient crops, 4) nutritious food and added value and 5) improved livelihoods at scale. Each of the flagships is further broken down into clusters. This report focuses on cluster SW 2.6 which codes for "**User preferred sweetpotato varieties and seed technologies"** with five product lines, namely,

1. Trait capture and gene discovery (including a range of trait expressions such as min and max. temperatures)

2. Breeding methods and their implementation into applied breeding programs such as implementing the “accelerated breeding scheme” in various countries.
3. Varieties and breeding populations–the medium and long term genetic gain is driven by population improvement
4. Seed systems/implementation of new methods and modification
5. Capacity building

Some of the products that are due for reporting this year, including the innovation of shortening the breeding timelines using the accelerated breeding scheme (ABS) in which candidate varieties can be developed in 4 years when you compare with 8 years for the traditional breeding system. ABS has been adopted by 11 NARS, 10 of which are in SSA. Another product that is due for reporting is the summary documentation of OFSP varieties that are available by world regions.

3.10 Problematic Traits

Edward Carey

The purpose of the presentation was to prompt the speedbreeders’ CoP to start identifying traits, methods or tools that are no longer make sense and have a discussion on how to resolve them. The sweetpotato crop ontology has 206 traits described. These are mainly crop descriptors and breeding traits. However, some of the traits are described by different scales by different breeding programs, therefore, there is need for curation. One of the best ways to curate the traits is to link them to Sweetpotatobase and HIDAP where we can monitor their utilization. Using the examples of what is contained on the trait pages of marketable/commercial root yield, reaction to drought and maltose content the presentation highlighted the need for continuous curation of the traits. The breeders were urged as key stakeholders to sign up for the user group at GitHub/plant-trait-ontology.

Discussion

Craig Yencho informed the speedbreeders that all the 206 descriptors are in HIDAP and Sweetpotatobase and the only way we can share information is if we have a shared dictionary. Curation of traits is an ongoing process and Dorcus Gemenet is leading the process. One of the major traits that is conspicuously missing in the ontology is the CIP Color charts used to score for flesh color and urgently needs to be confirmed in the ontology

It seems most NARS were operating on very lean budgets for releasing varieties. It would be good to know how much the support platforms are using? From the reports there is clear disparities between the support platforms and the NARS.

The funding situation has been evolving over the years, previously many of the NARS were supported by AGRA grants. Unfortunately, AGRA has changed priorities from cultivar development to cultivar dissemination and this is beginning to affect the NARS breeding programs. The funds at the support platforms cover many shared services and equipment (such as freeze driers, real time PCR, NIRS) and reagents. Although the support platforms receive more funds than the NARS the budgets help in maintaining equipment and paying for reagents and services.

3.11 Panel discussion: understanding the characteristics of outstanding recent releases

Many sweetpotato varieties have been released in SSA, some are better than others. What makes varieties successful and more popular, which characteristics are important?

The spread of Olympia in Zambia, by Martin Chiona

In Zambian the consumer preferences for sweetpotato include its use as a vegetable, dry matter and yield. High dry matter comes before root yield.

The variety, 'Olympia', has roots that are white skinned with a light orange flesh colour when raw, but becomes deep orange after cooking. 'Olympia' yields 19 t/ha, but with application of fertilizer the yield can be more than 40 t/ha. When a variety has been adopted in the centre of Zambia, it gets easily spread. 'Olympia' was released along with 'Kokota' but the latter failed, because it is late maturing and the yield was low. However, there is a farmer who is growing only 'Kokota' because he markets it to an Indian community in Zambia.

'Olympia' is now replacing maize increasingly in many places. One of the practices that promote 'Olympia', is that before harvesting, the upper biomass is grazed by animals leading to less weevil and better storage ability.

The spread of 'Bophelo' in South Africa, by Laurie Sunette

'Bophelo' was selected from polycross breeding, it has sweet roots with very high yield and was released in 2011. The storage roots have an attractive smooth orange skin colour. The storage roots contain 6708 µg of beta-carotene, moderate dry matter content and an attractive colour when cooked. It is good for flour production. It has been promoted through multiple funding and private investment that has facilitated its spread. 'Bophelo' is used in school feeding programs in South Africa.

The spread of 'Kadyaubwerere' (meaning when you taste you will come back) in Malawi, by Obed Mwenye

'Kadyaubwerere' is a high yielder (28-30 t/ha), The storage roots have an attractive skin and deep orange flesh colour. It has high DMC (31%) and the roots are sweet. The roots can easily be stored for a long time under open air. The roots are oval shaped and can readily fit into bags for the transportation system. They are also easy to peel and mash (pound) so the variety has been well incorporated into various popular utilisation options and the industry likes it for making puree. ‘Kadyaubwerere’ has a high multiplication rate for seed business and is widely adopted across ecologies in the country. Because of the earliness and fast multiplication, its sweetness and good storage ability, appreciated by food industries, it has been widely adopted.

The spread of ‘Kabode’ in Uganda, by Robert Mwanga

HarvestPlus was popularising OFSP in Uganda to solve the problem of vitamin A deficiency. The varieties in the project at that time were ‘Ejumula’ [dry matter content (DMC) 33%, high beta-carotene (BC) 7,760-14,370 µ/100g fresh weigh basis (FWB) highly susceptible to SPVD] and ‘Kakamega’ (DM 32%, low BC, 3,760 µ/100g FWB]. When, ‘Kabode’ was released in 2007, with resistance to SPVD, high DMC (31%), it was well adopted and grown in all the East African countries and has reached West Africa (Côte d’Ivoire). ‘Kabode’ has a good shape when grown in sandy soil but the shape is poor in heavy soils. ‘Kabode’ was released along with ‘Vita’ but Kabode was easily adopted because of its good multiplication rate. ‘Kabode’ takes a short time to cook and has reached more than 60 districts in Uganda.

The spread of ‘Irene’ in Mozambique, by Maria Andrade

In Mozambique varieties are given a female name, because it is believed that sweetpotato is a woman’s crop. The variety was named ‘Irene’, after one of the best promoters of OFSP in Mozambique. The storage roots of ‘Irene’ have high DMC (29.5%), high yields of 29 t/ha. The leaves can be eaten as vegetable. Many farmers like it for this dual purpose for both storage roots and as a vegetable. Irene has now been released in Cote d’Ivoire, Kenya, Burundi and performed well in Abu Dhabi. Men like the juice from ‘Irene’. ‘Irene’ is very easy to multiply even in tissue culture. Currently, Irene is grown on 3,082 ha in Mozambique.

3.12 The development of potato genome analysis at the Max-Planck-Institute for Plant breeding research in the context of potato breeding in middle Europe

By Christiane Gebhardt

The breeding of potato has many similarities with sweetpotato like

- Both crops are polyploids with polysomic inheritance and difficult genetics.
- Both crops are non-inbred due to self-incompatibility and severe inbreeding depression
- Both crops are vegetatively propagated, with low multiplication rates and their planting materials propagate diseases (like viruses).

The breeding of potato in Europe is done by private sector, who produce and sell certified potato seeds. High investments are made for developing new varieties and it is essential for business that legislation protecting varieties and breeder’s rights is well enforced. Potato variety breeding takes at least nine years. Basic plant research over the last 70 years resulted into three concepts that have revolutionised traditional plant breeding. That is;

- Invitro cell and tissue culture (TC)
- Genetic engineering (gene therapy)
- Marker assisted breeding (gene diagnosis)

Potato research at ***Max-Planck-Institute has gone through various phases:***

- 1960-1990: Pre-breeding to introgress pathogen resistance gene and other traits from wild potato species
- 1970- 1990: Cell and TC: ploidy reduction to diploid level by another culture and somatic hybridization
- 1985-2005: genetic engineering (e.g. virus resistance)
- 2005-2016; genome analysis; molecular linkage maps, mapping and cloning of genes, QTL mapping, association mapping

There has always been a gap between an impact factor and the impact. For instance, in understanding the molecular basis of the natural variation of disease resistance and tuber quality is an impact factor that is driven by curiosity. This impact factor can be translated into another impact factor by developing DNA based markers for increased efficiency and precision selection (precision breeding). Impact is realised when the DNA based markers are applied in developing successful varieties using efficient and cost-effective selection methods. This concept was illustrated with various examples like the development and utilisation of the diagnostic DNA marker for resistance to the root cyst nematode, *Globodera pallida*, in potato. Some of the lessons we can learn from the potato research include;

- It took 15-20 years of potato research before in vitro culture and molecular techniques were adopted by the practical breeding business.
- Collaborative research projects with breeders were essential to narrow the gap between basic research and application
- For quantitative traits, associated mapping in populations of advanced breeding materials was superior to linkage mapping for narrowing the gap between basic science and application.
- It is important to have both phenotypic and genotypic analysis tools to introgress diverse genetic resources.

3.13 RTBFoods and Feedback from Marketing, processing and utilization CoP

Tawanda Muzhingi

The Food and Nutritional Evaluation Laboratory (FANEL) is a regional research support platform for advancing in nutritional biochemistry, food science and food safety analysis for CGIAR, NARS, NGO partners and the private sector in SSA that is linked to CIP projects. FANEL supports research and development of safe and nutritious food and breeding for quality traits and end user preference.

The marketing, processing and utilization CoP held their annual meeting on 23th -24th April 2018, in Blantyre Malawi. The theme was **'Orange-fleshed sweetpotato value chains for sustainable food systems in SSA**'. During the meeting, it was an opportunity for private sector players, regulators, small-to-medium enterprises (SMEs) and farmers to share experiences, challenges and opportunities of OFSP processing in Africa. This meeting was attended by 75 participants from 10 countries and was followed shortly by a USAID funded OFSP industry forum in Malawi on 25th April 2018, which was attended by 50 participants.

RTBfoods is a BMGF funded 5-year project to support ongoing efforts by breeders of roots, tubers and banana crops to develop new varieties that are better adapted to biotic and abiotic stresses (farm level) and agro-industrial value chains (postharvest). The project is structured into 5 work packages (WP) on

- Value chain preferences, product profiling and economic analysis (WP1)
- Biophysical characterisation of quality traits (WP2)
- High throughput phenotyping (WP3)
- End-user focussed breeding (WP4)
- Gender equitable positioning, promotion and performance (WP5)

The RTBfoods work package leaders recently had an exchange visit to HZPC in the Netherlands to understanding how breeding can address quality traits. HZPC is an innovative global market leader in potato breeding, seed potato trade and product concept development. Some of the practical lessons from the visit include 1.) setting up sensory panels for objective scoring and 2) linking sensory panel data to texture analysis of cooked product profiles.

3.14 Report excellence in breeding (EiB) and Roots, Tubers and Bananas (RTB) Breeding Community of Practice

Edward Carey.

The Excellence in Breeding (EiB) platform is manged by CIMMYT where all CGIAR breeding programs and some NARS are obliged to participate and provide services. The rationale is to create synergies to accelerate genetic gains of breeding programs targeting the developing world. EiB has increased emphasis on developing demand based products, increased need to measure breeding programs' success against a defined target. The strategy for product development should be to replace the market leading variety rather than releasing too many varieties;

Discussion

EiB is suggesting that breeders should not release too many varieties but you may never know which of the varieties will end up successful?

Markets and environment keep changing, that is the main reason some varieties are less adopted or drop off. Jim Lorenzen illuminated that releasing many varieties is the ideal scenario in the absence of market intelligence but with good market intelligence, releasing a few varieties that can replace the market leader should be ideal. Variety adoption can vary from district to district and from country to country, depending on usage. Variety release must satisfy specific demands from end-users.

3.15 Diversity analysis of sweetpotato for breeding dual-purpose varieties

Damien Shumbusha

This was part of the PhD research of the Africa Centre for Crop Improvement /University of Kwazulu Natal, South Africa. This research aimed to assess the level of phenotypic and genotypic diversity among Rwandan sweetpotato varieties, and to develop dual-purpose varieties for food and feed. The genetic diversity using nine SSR markers among 24 sweetpotato genotypes showed six clusters, high variability of 57 (mean total number of alleles); no relation between genomic allocation and geography, genotype position was independent of flesh colour. Eight genetically distant genotypes were found and used in a crossing block.

Closing Remarks

Dr. Craig Yencho, the GT4SP leader, thanked all participants. He learnt a lot from the discussions which were thoughtful and respectful and he urged the breeders to always reach out to the genomics team to work with them.

Dr. Robert Mwanga, who coordinated preparations for CoP meeting, thanked all the participants for coming despite their busy schedules and thanked, Dr. Jan Low, SASHA leader, who works tireless to make things work. He thanked Dr. Jim Lorenzen from the BMGF, for the assistance the BMGF has extended to the sweetpotato crop to improve livelihoods of the poor. He thanked Dr. Christine Gebhardt, a member of the Scientific Advisory Committee of SPHI, for accepting to come to the speedbreeders CoP meeting to share her invaluable experience on potato; Dr. Isaac Dramadri, from Makerere University, for demonstrating to the CoP how the PhotoSynQ tool works and Bernice Wairimu for managing all the meeting logistics. He encouraged the speedbreeders to build on the training that was offered by AGRA to overcome the lack of funds and make writing proposals a daily process for survival. Thanked the genomics team for tremendous progress achieved in developing markers for marker assisted selection and capacity building.

Dr. Jim Lorenzen, the program officer at the BMGF, thanked the participants and Jan Low for the nice program. The breeder's meeting is a nice meeting to come to and see all the NARS together. Difficulties were raised by AGRA when they changed the strategy but it takes creativity to move forward. He emphasized the importance of data and data management – engage more in HIDAP and Sweetpotatobase to make collective progress and assistance. He urged the CoP to identify champions using the example of community of practice for virus epidemiology in cassava in West Africa. Champions were identified and some are government ministers who serve as members of this network. The ministers have ability or political muscle to move things at a larger scale. Sustainability is key from champions. We have potential champions for the sweetpotato community of practice. He highlighted that donors will always be looking at variety adoption and breeders need to learn from success stories, mistakes and demands from consumers and farmers so that you target better. Thank you for your hard work. Jim also thanked Jan for keeping him well informed. Both the SASHA II and genomics project are coming to an end in the first half of 2019 and renewal of projects are under discussions.

Dr. Jan Low thanked several people that have been working hard behind the scenes. Bernice and Faith – thank you for making sure everything was in order and setting up recorders for taking minutes especially for the complex genomic discussions and presentations. Luka, Mercy, Robert for putting the program together. Jan was excited with the promise of new variety releases and wished everyone a safe trip back.

ANNEXES

Annex 1: Meeting evaluation

The evaluation form was completed by 40 participants, 42.5% of these were below 40 years; 37.5 % were between 40 and 50 years and 21% were above 50 years. Women comprised 21.6% of the participants while men were 78.4%. The main expertise of the participants were breeders (62.5%) and 25% of the participants had other expertise apart from breeding. Results of the evaluation are summarized in Table 1 to 5 and Fig. 2 to 5. Overall, most participants' expectations were met and no participant expressed disappointment concerning their expectation from the meeting.

Table 1. Distribution of age, gender and technical expertise among the participants of 17th edition of the speedbreeders' annual CoP meeting.

Participants	**Detail**	**Percentage**
Age (n=40)	Less than 40 years	42.5
	41-50 years	20.0
	Above 50 years	37.5
Gender (n=37)	Female	21.6
	Male	78.4
Field of expertise (n=40)	Breeder	62.5
	Other	25.0
	Missing	12.5

More than 20% of the participants testified that the meeting offered much more than they had expected (Figure 2).

Table 2. Evaluation of the meeting organization and quality of presentations

Aspect of the meeting	**Percent rating by participants**				
	Very poor	Poor	Alright	Good	Very good
Overall meeting organization		2.5	15	47.5	35
Overall quality of presentations content (n=40)	0	0	7.5	47.5	45
Quality of day 1 sessions on data management (n=40)	2.6	0	12.8	41	43.6
Quality of the day three sessions on Genomic resources (n=39)	0	0	10.3	43.6	46.2
Quality of the day four sessions on breeding progress (n=39)	0	0	5	50	45
Usefulness of the panel discussion on perspectives on applications of genomics to the NARs sweetpotato breeding programs (n=39)	0	0	12.8	46.2	41

Usefulness of the panel discussion on understanding the characteristics of winning varieties (n=40)	0	0	2.5	32.5	65
Quality and usefulness of the field trip (n=37)	0	0	22.2	47.2	30.6

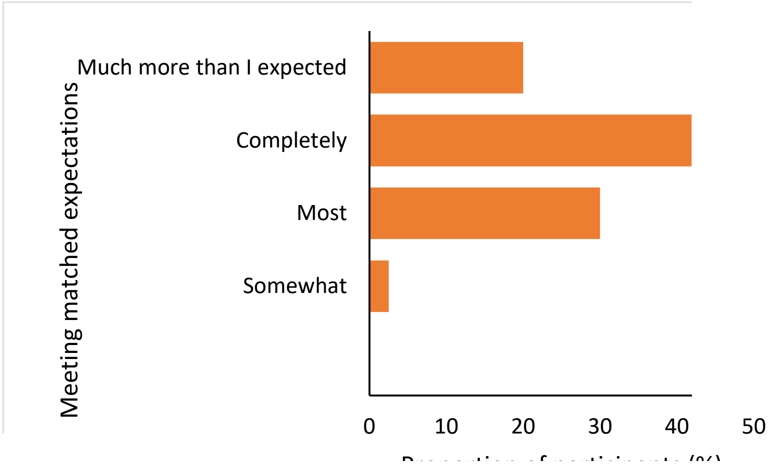

Figure 2.How much the 4-day breeder's meeting matched the expectations of the participants

Most participants (92.5%) rated highly the quality of all the presentations at the 17th speedbreeders' CoP annual meeting, except for 1 participant (2.6 %) who perceived the quality of sessions on data management to be very poor. Most speedbreeders' found the sessions on HIDAP and sweetpotatobase very rewarding and have expressed willingness to use them to manage, share and analyze their breeding data (Figure 3). However, many of them still expressed a desire for either backstopping through skype or email (42.1%) or personal training (44.7%) (Figure 4).

Requ

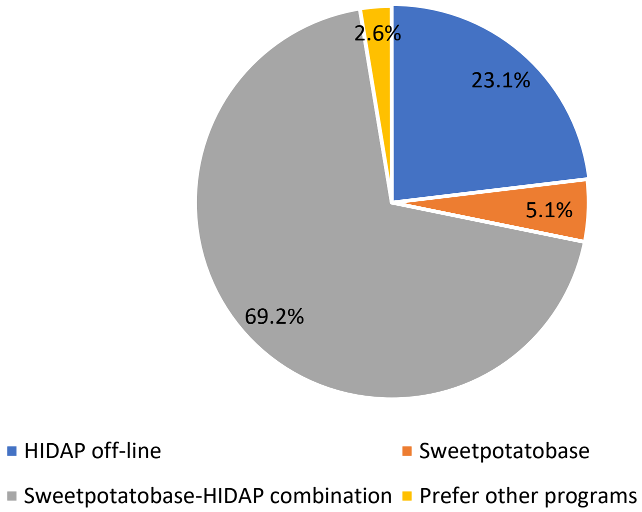

Figure 3. Data management tools that are most likely to be used by the participants

Figure 4. Training needs for data management tools

During this meeting, *speedbreeders'* were introduced to multspeQ's PhotoSynQ tool that can measure multiple photosynthetic measurements like quantum yields of photosystem two and non-photochemical quenching which could be used by breeders to select genotypes that have inherent abilities for photoprotection or can minimize photodamage. Most of the breeders appreciated the PhotoSynQ tool but considered it very expensive for their breeding programs (58.3%) and 22.2 % of the participants found it both useful and affordable (Figure 5). Most participants will also require backstopping through email or skype (40%) and in person training (44.7%) (Figure 6)

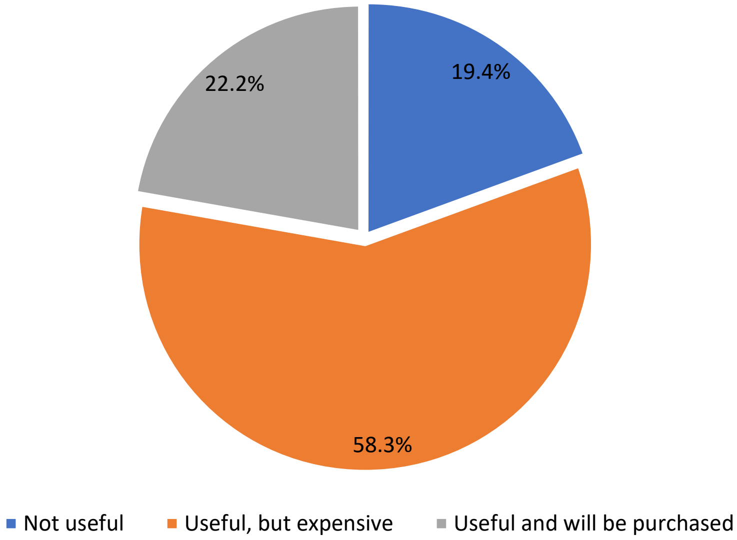

Figure 5. Participants perception of how useful the photosynq tool could be to their breeding objectives

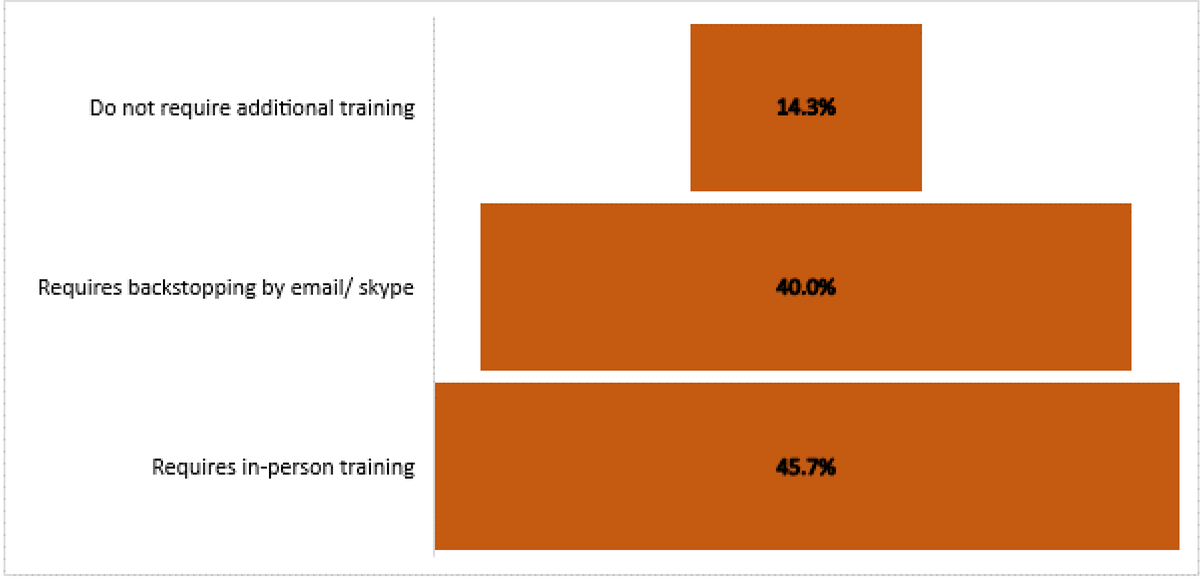

Figure 6. Training needs for the photoSynQ tool

All the topics covered during this year's meeting were considered very useful by at least one participant. The field trip and advances/application of genomic tools were the most appreciated parts of the meeting and each was mentioned 13 times as the most useful part of the meeting. On the contrary RTB reports was the part of the meeting that was considered least useful to the breeders with five mentions. The breeders emphasized the need for allocating more time to various topics of interest including experimentation research, data analysis, product profiling and market intelligence for sweetpotato varieties. Some participants also requested for parallel sessions so that they can be at liberty to choose the most relevant topics to them.

Table 3. Parts of the meeting that were most useful

Parts of the meeting	Frequency		
	First mention	Second mention	Third mention
1.Advances and application of sweetpotato genomic tools	13	10	8
2.Data management, analytics, storing and sharing	3	8	6
3.Field trip	13	7	2
4.Progress in Sweetpotato breeding	5	5	5
5.Undestanding winning varieties	1	5	6
6.Crop ontology	0	1	
7.Interaction of participants	0	1	2
8.Photosynq tool	1	1	5

Table 4. Parts of the meeting that were least useful

	Frequency	
Part of the meeting	First mention	Second mention
1.RTB reports	2	3
2. Advances and application of genomic tools	3	1
3.Breeding progress	4	0
4.Photosynq	3	0
5.Field trip	1	2
6.sweetpotatobase	1	1
7. IGSS	0	0
8. Understanding winning varieties	0	1
9.Data management	0	1

Table 5. Suggestions for improvement or topics that could be covered in the next meeting

Meeting aspect	Detail
Genomics	• Steps in QTL and linkage mapping • Molecular breeders from national programs need to be invited to learn from the sweetpotato advances • Genetics of Polyploids • More hands-on experience for genomics studies
Data management, analytics and storage	• More time for hands on data analysis • More time for data/experimentation research • More on applied statistics and data management
Breeding	• Product profiling • Market intelligence • Time to discuss on ontology issues and curation • Need to improve our efforts to network
Meeting organization issues	• Increase on the size of the meeting room • Separate participants into working groups with some parallel sessions • Improve on the time management • Get better hotel • Decongest the Agenda • Include half day for sight seeing • Meeting to should be hosted in other regions like south Africa

Annex 2: Meeting Agenda

17th Sweetpotato SpeedBreeders’ and Genomics Community of Practice Meeting:
Introducing the Next Generation Breeders’ tools and Understanding Winning Varieties
5-8 June 2018

Swiss Lenana Mount Hotel, Nairobi, Kenya

Coordinators: **Robert Mwanga** (r.mwanga@cgiar.org) -Speedbreeders and **Mercy Kitavi** (m.kitavi@cgiar.org) - Genomics

June 4 **Mon**	**ARRIVAL AND INSTALLATION OF NEW VERSION OF HIDAP**	***Bernice Wairimu & Luka Wanjohi***
June 5 **Tuesday**		
8:00 am	**REGISTRATION**	***Bernice Wairimu***
	Chair: Dorcus Gemenet	*Notetaker: Reuben Ssali*
8:30 – 9:00 am	Welcome remarks & Introductions	*Robert Mwanga, Craig Yencho, Jim Lorenzen*
9:00 -6:00 pm	**Theme: Data management, Analytics, Storing and Sharing**	*Supporting team: Dorcus Gemenet Mercy Kitavi, Benard Yada, Luka Wanjohi*
9:00 - 9:45 am	Stats update: The Westcott design.	*Raul Eyzaguirre*
9:45 -10:30 am	Introduction: HIDAP/SPBASE development, interaction and status	*Omar Benites* *Bryan Ellerbrock*
10:30-11:00	Official Opening	**Lusike Wasilwa, Director Crop Systems, KALRO**
11:00 – 11:30 am	**PHOTO AND HEALTH BREAK**	***Bernice Wairimu***
11:30-12:30 pm	HIDAP off-line training: Trial sites, create list of genotypes in HIDAP Offline	*Omar Benites*

12:30-13:30	HIDAP off-line training: Fieldbook management: Fieldbook creation, data quality of field data and statistical analysis in HIDAP Offline.	*Raul Eyzaguirre*
13:30-14:30 pm	**LUNCH BREAK**	***Bernice Wairimu***
	Chair: Dorcus Gemenet	*Notetaker: Reuben Ssali*
14:30-16:30 pm	SPBase and HIDAP on-line training: Import fieldbooks from SPBASE, check fieldbooks, descriptive plots and reports.	*Bryan Ellerbrock/Alex Ogbonna*
16:30-17:00 pm	User perspectives SPBase/HIDAP: CIP Ghana representing CIP's Support Platforms	*Jolien Swanckaert*
5:00 - 5:15 pm	**HEALTH BREAK**	***Bernice Wairimu***
5:15 - 5:45 pm	User Perspectives SPBase/HIDAP: NaCCRI Representing National Programs	*Doreen Chelang'at*
5:45- 6:15 pm	Introduction to Photosync	*Isaac Dramdri, Damien Shumbusha, Jean Ndirigwe*
June 6 Wednesday	**FIELD DAY**	***Coordinator: Mercy Kitavi: Eunice Wainaina***
8:30	Depart from Hotel for Field day at the University of Nairobi Kabete Campus	*Logistics: Frank Ojwang & Bernice Wairimu*
9:30 – 10:30 am	Field book app data collection exercise Barcode label printing	*Luka Wanjohi, Bryan Ellerbrock*
10:30 – 11:00 am	**BREAK**	***Bernice Wairimu***
11:00 – 12:30 pm	Photosync demonstration and practical exercise	*Isaac Dramdri, Astere Bararyenya*
12:30 – 1.30 pm	Depart for hotel and lunch	*Mercy Kitavi*
1:30 -2:30 pm	**LUNCH**	***Bernice Wairimu***
Afternoon	Chair: Ted Carey	*Notetaker: Bonny Oloka*
2:30 -3:15 Pm	Photosync - download data, processing	*Isaac Dramdri, Astere Bararyenya*
3:15 – 4:00 pm	Field book App	*Luka Wanjohi, Bryan Ellerbrock*
4:00 - 4:30 pm	Discussions & Field day wrap up: participants to tell of their experiences	*Isaac Dramdri, Astère Bararyenya* *Luka Wanjohi, Bryan Ellerbrock*
4:30 - 5:00 pm	Sweetpotato Knowledge Portal	*Faith Njung`e & Luka Wanjohi*

7:00 – 9:00	**COCKTAIL DINNER**	***Bernice Wairimu***
June 7 **Thursday**	Chair: Marc Ghislain	*Notetaker: Benard Yada*
	Theme: Genomic resources (Tools and Methods)	
8:15 – 8.45 am	Opening statement from the GT4SP **PI - Setting the stage for genomics-assisted breeding in sweetpotato**	*Craig Yencho*
8:45 – 9:15 am	The optimized GBS protocol for hexaploid sweetpotato and its application-highlight differences with other protocols e.g. DArT	*Bode Olukolu*
9:15 – 9:45 am	New methods for construction of genetic linkage maps in hexaploid sweetpotato	*Marcelo Mollinari*
9:45 – 10.15 am	New quantitative trait loci (QTL) mapping methods for hexaploid sweetpotato	*Guilherme Da Silva Perreira*
10:15 -10:45 am	**HEALTH BREAK & GROUP PHOTO**	***Faith Njung`e & Bernice Wairimu***
	Theme: Applications of the Genomic Resources	
10:45 -11:15 am	The potential of genomic-assisted breeding of sweetpotato in SSA given the new genomic tools	*Dorcus Gemenet*
11.15 -11:45 am	QTL mapping for RKN, quality traits and resistance to sweetpotato weevil (NKB and TB)	*Bonny Oloka*
11.45 – 12:15 pm	Population diversity and genome-wide association studies (GWAS) of Sweetpotato varieties in Burundi	*Gaspard Nihorimbere*
12.15- 12.45 Pm	Phenotyping and QTL analysis for storage root chemistry traits of sweetpotato (TB and BT)	*Victor Amankwaah*
12:45 - 2.00 pm	**LUNCH**	***Bernice Wairimu***
	Chair: Mercy Kitavi	*Notetaker: Bode Olukolu*
2:00 - 2:30 pm	Phenotypic and QTL analysis of the BT population in Ghana	*Obaiya Utoblo*
2:30 - 3.00 pm	SNP discovery and genome wide association study (GWAS) of continuous storage root formation and bulking traits in sweetpotato (*Ipomoea batatas*)	*Astère Bararyenya*
3:00 - 3.30 pm	Efforts made to genetically characterize the 100 best bet sweetpotato varieties in Africa	*Mercy Kitavi/Benjamin Kivuva*

3:30 – 4:00 pm	Integrated Genotyping Support and Service Platform at BecA Hub	Catherine Ziyomo
4:00 -4:15 pm		
	Chair: Craig Yencho	*Notetaker: Bode Olukolu*
4:30 - 5:50 pm	**PANEL** Discussion- Perspectives on applications of genomics to the NARs sweetpotato breeding programs - Panelists – Suggested composition: Obed Mwenye, Benard Yada, Wolfgang Gruneberg, *Gaspard Nihorimbere, Some Koussou*	*Craig Yencho, panel intervener*
5:50 - 6:00 pm	Discussions and wrap up	*Craig Yencho*
June 8 **Friday**	Chair: Martin Chiona	*Notetaker: Godwill Makunde*
8:00 - 8:30 am	Best bet catalogue	*Jolien Swanckaert /Edward Carey*
8:30 - 9:00 am	Progress Breeding at CIP HQ (including Hybrid Breeding)	*Wolfgang Grüneberg*
9:00 - 9:20 am	Progress - Southern Africa Sweetpotato Support Platform	*Maria Andrade*
9:20 - 9:40 am	Progress - Southern Africa	*Sunette Laurie*
9:40 - 10:10 am	Progress West Africa Sweetpotato Support Platform	*Edward Carey*
10:10 -10:20 am	Progress – West Africa sub-region	*Some Koussao*
10:20 -10:35 am	General discussion/Questions	
10:35 -10:55 am	**HEALTH BREAK**	***Bernice Wairimu***
	Chair: Maria Andrade	*Notetaker: Jolien Swanckaert*
10:55 - 11:15 am	Progress - East and Central Africa Sweetpotato Support Platform	*Robert Mwanga*
11:15 -11:35 am	Progress - East and Central Africa sub-region	*Benjamin Kivuva*
11:35 – 12:05 pm	RTB SW2.6 reports 2017 and planning 2018plus	*Wolfgang Grüneberg*
12:05 - 12:35 pm	Problematic Traits Discussion	*Edward Carey*
12:35 - 12:45 pm	General discussion/Questions	
12:45 - 1:45 pm	**LUNCH BREAK**	***Bernice Wairimu***
	Chair: Benjamin Kivuva	*Note taker: Some Koussao*

1:45 – 2.00 pm	Genetic studies on orange-fleshed sweetpotato for high dry matter content and resistance to sweetpotato virus disease	*Solomon Afuape*
2:00 -2:30 pm	Panel Discussion: Understanding the characteristics of outstanding recent releases (**Jan Low chair**)	Each to prepare slide but will only discuss (5 minutes each)
	The tale of Olympia in Zambia	*Martin Chiona*
	The tale of Bophelo in South Africa	*Sunette Laurie*
	The tale of Kadyaubwerere in Malawi	*Obed Mwenye*
	The tale of Kabode in Uganda	*Robert Mwanga*
	The tale of Irene in Mozambique	*Maria Andrade*
2:30 – 2:45 pm	General Discussion/Questions	*Jan Low*
2:45 - 3:05 pm	The development of potato genome analysis at the Max-Planck-Institute for Plant Breeding Research in the context of potato breeding in Middle Europe	*Christiane Gebhardt*
3:05 - 3:25 pm	RTBFoods & Feedback from Marketing, Processing and Utilization CoP	*Tawanda Muzhingi*
3:25 - 3 :40 pm	Report EiB and RTB Breeding Community of Practice	*Ted Carey*
3:40 - 4:00 pm	Diversity analysis of sweetpotato for breeding dual-purpose varieties	*Damien Shumbusha*
4:00 - 4:15 pm	General discussion	
4:15 - 4:30 pm	**HEALTH BREAK**	***Bernice Wairimu***
	Chair: Robert Mwanga	Notetaker: Godwill Makunde
4:30 – 5:00 pm	Wrap up session and Workshop evaluation	*Jan Low, Craig Yencho, Jim Lorenzen*
June 9 **Saturday**	**DEPARTURE**	***Bernice Wairimu***

The executive summary of the last breeder's meeting is provided in this folder. The full 16th Breeders CoP Meeting Report, 2017, is available on line:

http://www.sweetpotatoknowledge.org/files/breeders-cop-meeting-report/

Annex 3: Meeting participants

List of participants, 17th Sweetpotato SpeedBreeders and Genomics Community of Practice Meeting, Nairobi, Kenya, 5-8 June 2018

No	First Name	Last Name	Gender	Title	Institution	Address	City	Country	Telephone	Fax	Mobile	Email	Skype Address
1	Adofo	Kwadwo	M	Root Crops Breeder	CSIR - Crops Research Institute	CSIR, P.O. Box 3785	Kumasi	Ghana	+233-3220-60389/60395 / 60396	233 322060396	233 208198214	kinfodda@yahoo.com	adofof001
2	Anne	Mulwa	F	Assistant breeder	Kenya Agricultural and Livestock Research Organization (KALRO)	P.O. Box 340-90100	Machakos	Kenya			254 715504807	annmulwa@gmail.com	
3	Astèrè	Bararyenya	M	PhD Student, Makerere Univ.	ISABU-Burundi	PO Box 795	Bujumbura	Burundi	+257 22223390		257 79967257	barastere@gmail.com	bararyenja.astere
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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.

SASHA Sweetpotato Action for Security and Health in Africa

CIP INTERNATIONAL POTATO CENTER A CGIAR RESEARCH CENTER

CGIAR RESEARCH PROGRAM ON Roots, Tubers and Bananas

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