Sweetpotato SpeedBreeders and Genomics Community of Practice

Report of the 16th Annual Meeting

Integrating Modern Genomic Tools with Traditional Approaches

Held at Grand Legacy Hotel, Kigali, Rwanda

May 14 -19, 2017

Compiled by Robert Mwanga and Reuben Ssali; Edited by Christine Bukania

Report of the 16th Sweetpotato *Speed*Breeders' and Genomics Community of Practice Meeting

Theme: *Integrating modern genomics tools with traditional approaches*

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Photos: C. Bukania

***Cover photo:** Breeders participate in a taste test of sweetpotato varieties during a field visit to Rubona Research Station in Rwanda (Credit: C. Bukania)*

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LIST OF ACRONYMS

ABS	Accelerated breeding scheme
AFLP	Amplified fragment length polymorphism
ARC	Agricultural Research Council
ANOVA	Analysis of variance
AT	Advanced trials
BMGF	Bill & Melinda Gates Foundation
BTI-CU	Boyce Thompson Institute- Cornell University
CIP	International Potato Center
CoP	Community of practice
SRFB	Storage root formation and bulking
DArT	Diversity arrays technology
DMC	Dry matter content
EHP	Experimental heterosis populations
Fe	Iron
GAB	Genomics-assisted breeding
GBS	Genotyping-by-sequencing
GG	Genetic gain
GREAT	Gender responsive researchers equipped for agricultural transformation
GS	Genomic selection
GT4SP	Genomic tools for sweetpotato improvement
GWAS	Genome wide association studies
HEBS	Heterosis exploiting breeding schemes
HIDAP	Highly interactive data analyis and productivity
HQ	Headquarters
LSD	Least significance difference
MAS	Marker assisted selection
METs	Multi-environmental trials
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
PCR	Polymerase chain reaction
PYT	Preliminary yield trials
PVS	Participatory variety selection
QTL	Quantitative trait loci
RAB	Rwanda Agriculture and Animal Resources Board
RAPD	Randomly amplified polymorphic DNA
RCBD	Randomized complete block design

RDA	Recommended daily (or dietary) allowance
RRS	Reciprocal recurrent selection
RTB	Roots, tubers and bananas
SASHA	Sweetpotato Action Security and Health in Africa
SNP	Single nucleotide polymorphism
SPCSV	Sweet potato chlorotic stunt virus
SPFMV	Sweet potato feathery mottle virus
SPHI	Sweetpotato for Profit and Health Initiative
SPVD	Sweetpotato virus disease
SSA	Sub-Saharan Africa
SSP	Sweetpotato support Platform
SSR	Simple sequence repeat
SWCA	South West and Central Asia
WAE	Wide adaptation and early bulking
XFR	X-ray fluorescence spectrometry
Zn	Zinc

Executive Summary

Participants pose for a group photograph

The **16th Sweetpotato for Profit and Heath Initiative Sweetpotato *Speed*Breeders Annual** Meeting, held in Kigali, Rwanda, 14th to 19th May 2017, was officially opened on behalf of the Minister for Agriculture by the Director General of the Rwanda Agriculture and Animal Resources Board (RAB), Dr. Mark Cyubahiro Bagabe. In his opening address, Dr. Bagabe lauded the efforts that various governmental and non-governmental partners had made to promote sweetpotato in Rwanda. He stated that in the past, cereal crops had always taken center stage. However, recent challenges such as climate change, pests and diseases had made it necessary to consider alternative food crops even more.

Forty-three participants from 13 countries were engaged in practical sessions on how to integrate genomic tools into sweetpotato breeding work. These tools aim to make sweetpotato breeding more efficient, by enabling breeders to develop sweetpotato varieties that are adapted to the specific growth conditions, and which meet the preferences of consumers in a shorter time.

Sweetpotatobase overview and setting up accounts: Bryan Ellerbrock and Alex Ogbonna presented the five Ws of the Sweetpotatobase to highlight who is involved in developing and utilizing the Sweetpotatobase, what it is, when it can be used , where to find it and why the CoP should be using it and helped to set yup accounts.

Highly Interactive Data Analysis Platform (HIDAP): Raúl Eyzaguirre and Luka Wanjohi introduced the offline version of HIDAP to the *Speed*breeders. HIDAP, which is replacing CloneSelector, is easier to install, while continuing to be able to be used online. It easily produces reports with summary statistics in MS Word and PDF formats. From a development standpoint, HIDAP makes it easier to add new functions and update existing ones. To understand HIDAP functionalities better, participants participated in exercises using training data sets (provided by the trainers) and the breeders own data sets.

New statistical approaches: Wolfgang Grüneberg and Raúl Eyzaguirre conducted this interactive session on new statistical approaches consisting of three main points: Approaches to be used to analyze data from the PhD project of Mr. Astere Bararyenya, identification of genetic gain and suggestion of the topic for the next breeders' meeting.

RTB project reports: The presentation of Roots, Tubers and Bananas (RTB) project reports by Wolfgang Grüneberg focused on global reporting on 2016 sweetpotato progress cluster SW2.6 (2=Breeding, 6= Sweetpotato). This cluster SW2.6: "user preferred sweetpotato varieties and seed technologies" was in the past theme 2 "sweetpotato breeding".

In his **introduction of the session on genomic tools**, Craig Yencho was delighted that the sweetpotato breeders and molecular geneticists continued to meet. He stated that these meetings would teach the two groups to communicate better with one another. This session featured a session titled **Panning the gold: QTL mapping and genomic selection in hexaploid sweetpotato** in which Bode Olukolu, Dorcus Gemenet and Mercy Kitavi and Marc Ghislain covered i) Markers and next generation genotyping platforms, ii) Marker Assisted Selection (MAS) for sweetpotato improvement, iii) Linkage, quantitative trait loci (QTL) and genome wide association analysis and genomic selection (GWAS).

In the **reports from different regions,** participants heard the following presentations

- Breeding for Fusarium wilt resistance and vine dissemination of informal cultivars in South Africa by Whelma Mphela
- Genetic variability of continuous storage root formation and bulking in Ugandan sweetpotato germplasm by Astere Bararyenya
- GREAT training and implications for sweetpotato breeding in Ghana by Utoblo G. Obaiya
- Progress at the Southern Africa Sweetpotato Support Platform by Maria Andrade,
- Progress report of the West Africa Sweetpotato Support Platform by Ted Carey
- Progress at the East and Central Africa Sweetpotato Support Platform by Robert Mwanga,
- Sub-regional sweetpotato breeding progress reports for East and Central Africa 2016-2017 by Laura Karanja
- Sweetpotato breeding progress in Southern Africa by Martin Chiona
- West Africa breeding progress by Some Koussao
- Progress at CIP HQ by Wolfgang Grüneberg

The meeting also featured a visit to Rubona Research Station, to learn about the station's variety development, crossing block and germplasm maintenance, tissue culture laboratory and pre-basic seed production. These operations feed into the sweetpotato seed system, and help to ensure that farmers in Rwanda get supplies of disease-free planting material in a timely manner.

This report and reports from previous meetings and PowerPoint presentations and photographs are available at the Sweetpotato Knowledge Portal: http://www.sweetpotatoknowledge.org/.

1. Introduction and opening session

RAB Director General Dr. Mark Bagabe (second right) officially opens the meeting

The 16th Sweetpotato for Profit and Heath Initiative Sweetpotato *Speed*Breeders and Genomics Community of Practice (CoP) Annual Meeting was held at Grand Legacy Hotel, Kigali, Rwanda, from 14 to 19 May 2017. It was attended by 43 people from 13 countries, of which 13 were women.

The meeting was opened by Dr. Mark Bagabe, the Director General of Rwanda Agriculture and Animal Resources Board (RAB) on behalf of the Minister of Agriculture and Animal Resources.

Prior to the Director General's opening speech, Dr. Robert Mwanga of the International Potato Center (CIP), welcomed all the participants and thanked the Government of Rwanda for recognizing the importance of sweetpotato to the livelihoods of farmers and consumers. He further applauded the Government of Rwanda for investing in training sweetpotato breeders and offering them institutional support. The growth in sweetpotato production in Rwanda has largely been driven by the supportive policies adopted by the Government of Rwanda. "Many countries in sub-Saharan Africa depend on agriculture. While donors and governments talk a lot about investing in agriculture, Rwanda has translated this talk into actual investment in sweetpotato production," Dr. Robert Mwanga, co-leader of the *Speed*Breeders and Genomics CoP and one of the 2016 World Food Prize laureates said. Dr. Mwanga conveyed the apologies from Dr. Jan Low, Leader of the Sweetpotato Action for Security and Health in Africa (SASHA) project and co-leader of the SPHI and Dr. Jim Lorenzen of the Bill & Melinda Gates Foundation (BMGF) responsible for the SASHA and Genomic Tools for Sweetpotato Improvement Project (GT4SP) projects who were unable to attend the annual meeting due to other commitments.

Dr. Craig Yencho, the other co-leader of the CoP, leads the GT4SP project, hosted at North Carolina State University (NCSU), Raleigh. He stated that teamwork had been critical to the progressive development of sweetpotato breeding in sub-Saharan Africa. Today, this progress can be seen in 12 countries that have crossing blocks and are releasing varieties. He also pointed to the growing recognition of sweetpotato as a food and nutrition security crop. This led to three CIP sweetpotato scientists, Drs. Low, Mwanga and Andrade, along with Dr. Bouis (HarvestPlus) receiving the 2016 World Food Prize for their work on biofortification. Time Magazine named OFSP among the best 25 inventions of 2016. He expressed his pleasure of working with the CoP which was like a family.

In his opening address, Dr. Mark Bagabe welcomed participants to Rwanda and described the importance of sweetpotato for the food security and economy of Rwanda. He said introducing OFSP varieties had made the Rwandese staple more nutritious and more robust. He reminded the meeting that he had been out of the sweetpotato breeding world for about seven years and he was happy to be associated with the meeting of sweetpotato breeders again. He informed the meeting that Rwanda had been overwhelmed by requests for sweetpotato vines in 2017. This could be associated with the current climate change challenges like the recent outbreak of the armyworm, which made many farmers see sweetpotato as a fallback position. Rwanda is now looking at exporting sweetpotato in the near future. He assured the meeting that RAB would continue contributing to capacity building. He thanked the BMGF for starting the program and SASHA for choosing Rwanda as a place to host the meeting. He encouraged the participants to visit the RAB station at Rubona. He concluded by congratulating the 2016 World Food Prize Laureates and wishing the participants very good deliberations.

This report summaries the major topics covered during the meeting. The agenda for the meeting is provided in Annex 3 and a list of participants with their contact information in Annex 4. A list of publications made by SSA breeders during the past year is presented in Annex 1. The evaluation of the meeting is provided in Annex 2.

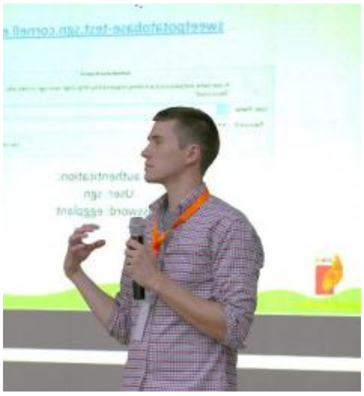
2. HIDAP and Sweetpotatobase training

2.1. Sweetpotatobase overview and setting up accounts

Bryan Ellerbrock and Alex Ogbonna

Currently, five programs have data in the database; these are BTI, CIP, Ghana, Uganda and NCSU. Sweetpotatobase is a central, web-based database and breeding management platform that can be used at every stage in the breeding process (round-tripping).

Bryan presented the **five Ws** of the Sweetpotatobase to highlight **who** is involved in developing and utilizing the Sweetpotatobase, **what** it is, **when** it can be used , **where** to find it and **why** the CoP members should be using it.



Bryan Ellerbrock (BTI) explains the 5Ws of Sweetpotatobase

CoP members can create accounts for their breeding programs using the links *sweetpotatobase.org and sweetpotatobase-test.sgn.cornell.edu*. The first link is for actual project database accounts while the latter is for training purposes.

Sweetpotatobase will enable the CoP to streamline data collection, curation, and analyses. Participants were engaged in several demonstrations and exercises on how Sweetpotatobase works, including creating accounts (login), and lists, searches (germplasm, trials), loading accessions, trial creation, phenotyping, data upload and download.

Discussion

Participants were concerned about how much control a person accessing the Sweetpotatobase has over the data. Bryan and Alex clarified that every user has a certain level of privileges under his control.

Craig Yencho requested Mercy Kitavi to set up some webinars as follow up trainings on Sweetpotatobase.

2.2. Highly Interactive Data Analysis Platform (HIDAP)

Raúl Eyzaguirre / Luka Wanjohi

Luka Wanjohi (CIP) instructs breeder Laura Karanja in using HIDAP analytical tools

Luka and Raúl introduced the offline version of HIDAP to the *Speed*breeders. The HIDAP program is expected to replace CloneSelector as the tool of choice for analysis of multi-locational trials. HIDAP has several already inbuilt lists like the table of locations and the CIP's institutional germplasm lists. However, there is still an option to add a location or genotypes that are not on the list. Using HIDAP, breeders can now generate materials list, create field books, compute derived traits, and transform and analyze data with HIDAP. The program also generates single and multiple trial reports with detailed model specifications, data descriptions, ANOVA tables, genotype means, Least Significant Difference (LSD) and Tukey tests (only if ANOVA is significant for genotypes) variance component estimations, and stability analysis (only if ANOVA turns out significant for interaction) can be generated from HIDAP. Exercises were conducted using training data sets (provided by the trainers) and the breeders own data sets.

2.3. New statistical approaches

Wolfgang Grüneberg and Raúl Eyzaguirre

The session of new statistical approaches was interactive and consisted of three main subjects: 1) Approaches to be used to analyze data (from the PhD project of Mr. Astere Bararyenya of Burundi); 2) Determination of genetic gain and 3) Topic suggestions for the next breeders' meeting.

Astere Bararyenya's project aims at identifying genetic variability of continuous storage root formation and bulking in Ugandan sweetpotato germplasm. The motivation of this study is understanding and adapting breeding practice to small-scale farmers' practice of piecemeal harvesting of sweetpotato. Ideally, farmers who piecemeal harvest would like earlier maturing varieties with continuous storage root formation and bulking. Understanding the difference between piecemeal and one-time harvesting is very important. Genotypes with the trait of continuous storage root formation and bulking are very important for small-scale farmers but the value of these genotypes given the changing climate is questionable because farmers tend to grow and harvest everything to avoid yield loss due to drought stress. For genetic characterization of Ugandan sweetpotato germplasm to identify parents to be used in breeding experiments, it was suggested to consider factors such as genotype, environment (locations), and harvesting time with repeated measurement design as the experimental design. The key features of such a design were discussed. In addition to yield data, the dry matter accumulation, and weevil damage should be recorded.

The determination of genetic gain obtained by breeding programs to improve quantitative traits requires data from regional trials and appropriate statistical methods for its estimation. Trials to estimate the genetic gain are carried out on-farm and on-station trials in West, East, Central, and Southern Africa. These trials are exceptional because the genetic gain is determined across environments and time (years). Errors could happen if the plant materials used are not clean, therefore it was suggested that all plant materials (even farmers' varieties) to be used in trials to determine the genetic gain should be virus-free (clean). In some cases, farmers' varieties still have high yields. I In this case, it is very difficult to measure the genetic gain on yield but with beta-carotene, positive genetic gain results are easily captured.


Participants Bonny Oloka (right) and Whelma Mphela during the meeting

The suggested topic for the next breeders' meeting is *the nearest neighbor design and heterosis.*

2.4. RTB project reports

Wolfgang Grüneberg and Raúl Eyzaguirre

The presentation of Roots, Tubers and Bananas (RTB) project reports focused on global reporting on 2016 sweetpotato progress cluster SW2.6 (2=Breeding, 6= Sweetpotato). This cluster SW2.6: "user preferred sweetpotato varieties and seed technologies" was in the past theme 2 "sweetpotato breeding". The reported cluster was divided into the following five activities/product lines:

1. User preferred sweetpotato varieties aligning the objective with six outputs
2. Accelerated sweetpotato selection schemes/methods and tools in earlier and later generation with five outputs
3. Improved sweetpotato population and true seed dissemination for farmers' needs with seven outputs
4. Guidelines, technologies and diagnostic tools for improving the sweetpotato seed system with four outputs
5. Capacity building for sustainable sweetpotato intensification with 11 outputs.

Each output is coordinated and reported by one scientist. Reports of all outputs were submitted and compiled. The compiled report can be requested from CIP.

3. Field trip to Rubona Research Station

On the morning of 17 May 2017, 39 participants went on a field trip to Rubona Research Station. Rubona is located in Rusatira sector of Huye district in the Southern Province. With a staff capacity of over one hundred scientists, it is the largest among the research stations of the Rwanda Agriculture Board (RAB). RAB is in charge of developing agriculture and animal husbandry through reform and using modern production methods, research, agricultural extension, and education and training farmers in new technologies. The Rubona Station has a large research component on root and tuber crops, including a sweetpotato program supported by the International Potato Center (CIP). The visit was coordinated by a team from Rubona, led by Dr. Jean Ndirigwe.

At the tissue culture lab, Julius Kagabo (RAB) led the SpeedBreeders and Genomics CoP on a tour to observe the transfer of material into nutrient media and how the growth room is maintained. Prior to this, they visited the plant pathology lab, where they found out how sweetpotato planting material is tested for viruses.

While it is not always possible to physically identify the virus symptoms on infected plants, the plant pathology team uses grafting on *I. setosa* to confirm whether the plantlets are completely free of virus infection before they are used for micropropagation in the tissue culture lab. Tissue culture plantlets provide the source of disease-free materials that are multiplied through different stages of the seed system.

Gaspard Nihorimbere and other participants at the tissue culture laboratory

These cuttings will be sold to about 50 registered decentralized vine multipliers to multiply in the open field and distribute to other farmers. The end-result is that farmers will receive planting material that are free from viruses and other diseases or have very low levels of infection. This is part of RAB's strategy to hand over seed production to the private sector, and concentrate on research and provision of pre-basic seed.

At the crossing block, Ndirigwe explained that the breeding focus in Rwanda is on high yield, high dry matter and resistance to sweetpotato virus disease. He explained that farmers in Rwanda particularly liked Vita, an orange-fleshed variety, which is high yielding and has high dry matter. Gihingumukungu, an orange-fleshed variety that was developed in Rwanda, was performing well in high altitude areas with low virus pressure. It is preferred particularly for puree processing because it has low dry matter.

Participants at the crossing block

Participants participated in a taste test of sweetpotato varieties, which included varieties developed in Ghana. This exercise was led by Dr. Ted Carey (CIP). The members of the SpeedBreeders and Genomics CoP used a 9-point scale to rate the cooked varieties based on appearance, fiber, cooked taste, aroma, sweetness and cooked texture. Apart from providing some data for the breeders from Ghana, the exercise also demonstrated the challenges of using consumer panels for taste tests. Based on the findings, he highlighted the need for calibration of the people participating in the panels, to ensure that the findings are consistent.

Bruno Michelin and other participants during the taste test

4. Aiming for the goal: genomic tools

4.1. Introduction statement from the GT4SP Principal Investigator

Craig Yencho

Craig Yencho was delighted that the sweetpotato breeders and molecular geneticists continued to meet. He stated that these meetings would teach the two groups to communicate better with one another.

He stated that sequence-based breeding involves generating big data sets which would require new skills on how to work with these large data sets. The starting point would be to learn the new language to be able to ask the right questions, for instance, how the populations would be like and how big they would be. He noted that polyploidy complicates analysis but it also brings a lot of diversity, and that diversity can be easily exploited to improve sweetpotato.

4.2. Panning the gold: QTL mapping and genomic selection in hexaploid sweetpotato

Bode Olukolu, Craig Yencho, Dorcus Gemenet, Mercy Kitavi and Marc Ghislain

This presentation covered i) Markers and next generation genotyping platforms, ii) Marker Assisted Selection (MAS) for sweetpotato improvement, iii) Linkage, quantitative trait loci (QTL) and genome wide association analysis and genomic selection (GWAS).

4.3. Markers and next generation genotyping

Bode Olukolu

Dr. Bode Olukolu reviewed a wide array of genetic markers that have been used over time, including morphological markers, protein markers, DNA markers based on hybridization and DNA markers based on polymerase chain reaction (PCR). He explained the pros and cons of each type of genetic marker. He then introduced the next generation genotyping using either single nucleotide polymorphism (SNP) chip/arrays or sequencing based genotyping (GBS).

He also explained the process entailed in developing SNP chips/arrays and the advantages; for example, that they require less bioinformatics analysis, have few missing data, and are cheap and easy to perform.

However, SNP chips/arrays also have some disadvantages like: It takes time to design an array and the initial cost is high; unreliable genotype call in highly divergent samples due to reduced probe-sequence hybridization (GBS can resolve this); and they could have uncertainties bias if SNPs are discovered in just a small set of samples (resolved by broad germplasm choice).

4.4. Genome-Assisted Breeding (GAB) for sweetpotato improvement

Dorcus Gemenet

This presentation by Dr. Dorcus Gemenet illustrated how GAB will enable sweetpotato breeders to save time and resources and hence achieve genetic gains faster. GAB is divided into MAS and genomic selection.

MAS involves tagging large effect QTL /markers for selecting a desired phenotype. Dorcus demonstrated the process of identifying the markers/QTLs using populations that have been developed by the GT4SP project. These include biparental mapping populations like:

1. Beauregard x Tanzania (BxT, CIP)
2. Tanzania x Beauregard (TxB, NCSU)
3. New Kawogo x Beauregard (NK x B, NaCRRI) population.

The parents of these mapping populations were selected on the basis of one or more contrasting traits. The GT4SP project is also developing multiparental populations for QTL mapping like the 8(A) x 8(B) Mwanga diversity panel. This multiparental population has been generated from two heterotic groups. This inter-group mating is likely to result into high within family variation while preserving the historical recombination within the design.

However, for polyploid crops like sweetpotato the following has to be considered during genetic linkage analysis for QTL mapping:

- Self-incompatibility, inbreeding depression - no homozygous parents
- Unavailability of good quality sequence information
- Multiple alleles at marker loci and at loci for traits of interest
- Different possibilities of allele dosages across homologous chromosomes
- Both bivalent and multivalent pairing during meiosis
- Possibility of preferential pairing of different homologs

Genetic analysis is further complicated by the absence of suitable linkage mapping software.

Genomic selection

Genomic selection uses all the available markers to predict the breeding values of a given genotype, which does not require prior QTL mapping. However, it requires high density markers to improve selection accuracy. Genomic selection has been proven to be most effective for quantitative traits with very low heritability. Two genomic selection strategies have been proposed for the GT4SP project. Both strategies aim at maximizing diversity while reducing the time required for phenotyping.

Discussion

The discussion revolved around differentiating traits that are most suitable for either MAS or genomic selection. One of the guiding principle to consider is the heritability of the trait. Traits that are controlled by large (major) QTL effects could readily be introgressed by MAS. Genomic selection will be most beneficial for traits that have low heritability values that require several seasons for evaluation. The genomic tools under development need to prioritize traits that are difficult to breed for, such as drought tolerance, resistance to sweetpotato weevil and sweetpotato virus disease (SPVD) and culinary attributes like taste. The breeders and molecular geneticists were urged to also consider processing attributes of the sweetpotato for distinct user groups such as rural households, restaurant patrons, and the processing industry. There was consensus that the traits should be well understood if genomic tools are to be applied effectively.

4.5. Ipomoea trifida and I. triloba – why the reference resource for sweetpotato improvement

Robin Buell

This presentation aimed at highlighting the progress on sequencing of the sweetpotato genome, identifying the remaining technical challenges and illustrating how genome information can be used to facilitate breeding efforts and the utilization of untapped allelic variation.

The guiding principle for utilizing a reference genome in breeding is that if the region of the genome that is responsible for a trait is known, simple biotechnology methods can be used to select progeny from a cross that has that region of interest. Robin demonstrated how genomics has been used to reveal alleles associated with important agronomic traits in recalcitrant breeding systems like potato.

Sweetpotato is a hexaploid and heterozygous. Thus, it requires extensive effort to generate its sequences. For several species (such as strawberry, potato), and it has been shown that a related wild species with reduced ploidy can be highly robust to serve as a reference genome. Two diploid relatives of sweetpotato *Ipomoea trifida* and *I. triloba* were selected and sequenced as the reference genomes for sweetpotato. Currently, 15 chromosomes are assembled for both diploid species; 15 chromosomes each. *I. trifida* and *I. triloba* genomes can be used as proxies for *I. batatas* and sweetpotato breeding. Robin illustrated how to discover variants using 16 hexaploid sweetpotato clones (parents of the Mwanga diversity panel).

5. Reports from different regions

5.1. Breeding for Fusarium wilt resistance and vine dissemination of informal cultivars in South Africa

Whelma Mphela

This study aimed at confirming the resistance levels of imported cultivars and exploring their utilization as parents in breeding for resistance to local pathogenic Fusarium isolates. Two resistant clones (Bonita and Murasaki) imported from Louisiana State University, USA, were crossed with seven Agricultural Research Council (ARC) sweetpotato cultivars to generate 92 progenies that were screened for Fusarium wilt response in the glass house along with their parents. Seventy-four of these progenies were also screened in a field along with their parents. Fusarium wilt rating for both glasshouse and field experiments was on a scale of 0-3 (where 0 = no disease symptoms and 3 = complete wilting due to Fusarium). Twenty-one and 48 genotypes showed no Fusarium wilt symptoms in the glass house and in the field experiment, respectively. These resistant genotypes could be disseminated among commercial producers or used as a source of resistance for Fusarium wilt.

Whelma also shared experiences of successful vine dissemination of new varieties in South Africa involving commercial and smallholder farmers, government and NGO programs on large scale, communities, schools and hospital gardens. The key for successfully expanding the production of new sweetpotato varieties is the availability of vines for production.

5.2. Genetic variability of continuous storage root formation and bulking in Ugandan sweetpotato germplasm

Astere Bararyenya

Mr. Bararyenya presented his PhD study, which aims at improving yield through continuous storage root formation and bulking. Piece meal harvesting is a very common practice among many smallholder farmers in sub-Saharan Africa, although the mode of piecemeal harvesting varies among communities. Farmers tend to harvest only what is sufficient for home consumption at any given time. Some of the key questions the study is attempting to answer include:

1. What variation of continuous storage root formation and bulking (SRFB) exists in the Ugandan sweetpotato germplasm?
2. What are the most useful parents in breeding for continuous SRFB in sweetpotato?
3. How heritable is the trait?
4. What is the gene action pattern and to which extent can the trait be exploited to improve yield of sweetpotato in Uganda?

One hundred and thirty diverse clones have been assembled and are being characterized for SRFB at three sites in Uganda in an Alpha lattice with two replicates. The dry matter accumulation is measured (repeated) at four harvest times: harvest 1: 90 days after planting; harvest 2: 120 days after planting; harvest 3: 150 days after planting; and at harvest 4: 180 days after planting. Preliminary results have revealed variation in storage root formation and bulking. The genotypes can be characterized into four categories; those exhibiting: i) delayed storage root formation and bulking, ii) early storage root formation and bulking, iii) early and continuous storage root formation and bulking and iv) late continuous storage root formation and bulking.

Discussion

Due to the variation in the way piecemeal harvesting is done across various communities, the discussion revolved around defining piece meal harvesting in various contexts. This ranged from harvesting only part of the plot to harvesting only the sizable roots while allowing others to continue bulking. Some breeders wondered at the relevance of the study given the various production constraints of sweetpotato (like drought, weevil infestation and SPVD) that will not allow the farmer to continue harvesting once the constraints set in. However, since this is a practice widely in use by farmers, there is need to develop varieties that allow farmers to maximize the yields and ensure food security (either harvesting sweetpotato for a long time or harvesting early storage roots before the onset of the constraint such as weevil).

5.3. Breeding of sweetpotato for drought tolerance and high dry matter content in Rwanda

Placide Rukundo

This presentation was based on results from Rukundo's PhD study, which aimed at breeding sweetpotato for improved drought tolerance and dry matter content by determining genetic diversity of germplasm for these traits and investigating genetics in relation to yield.

Fifty-four genotypes were assembled as parents for this study including accessions from East and Central Africa. The phenotypic characterization of these genotypes was conducted at two sites, with three replications in a 9x6 alpha lattice design. The genotypes were screened for drought tolerance in both greenhouse and *in vitro.* Eight genotypes (*K513261,* Kwezikumwe, 2005-020, Otada24, SPK004, Ukerewe, 2005-110 and 2005-034**)** were selected as potential parents for genetic enhancement of DMC based on high yield, high DMC and flowering rate. Genotypes, 2005-146, 4-160, 8-1038, Karibunduki, Kwezikumwe, Purple 4419, Nsasagatebo, Karebe, IMBY 3102, Mwanakumi, and 97-062 were identified as drought tolerant from both greenhouse and *in vitro* experiments. These parents were crossed to generate 2,768 clones, which were evaluated and 72 clones were selected as potential candidates for new varieties. The target is to release the best of these genotypes in Rwanda.

5.4. GREAT training and implications for sweetpotato breeding in Ghana

Utoblo G. Obaiya

Utoblo started the presentation by explaining to speedbreeders the meaning of GREAT, as an acronym for Gender-responsive Researchers Equipped for Agricultural Transformation. This is a certificate program delivering applied gender training for agricultural researchers to offer tailored skills development in gender-responsiveness along the design, implementation, evaluation, and communication of agricultural research. Utoblo was one of the fellows of the recently concluded GREAT course for breeders of Roots, Tubers and Bananas (RTB). Part of the course entailed conducting a gender responsive research project and this presentation was aimed at disseminating findings to the sweetpotato breeder's CoP.

The gender responsive research project was titled *'Gender differentiated sweetpotato traits preferences by men and women producers in Northern Region and Upper East Region of Ghana'*. The quest was to identify gender differentiated sweetpotato traits preferences by men and women producers, consumers, processors and traders. Some of the key findings of the study include

- Sweetpotato is not the number one crop in terms of production in both the Northern and Upper Volta Regions but it still plays vital roles in the communities where it is produced.
- Market access and perishability of sweetpotato are the major limiting factors for men and women in selecting sweetpotato as a commodity for production.
- Obaari is the most cultivated sweetpotato cultivar in Upper Volta Region, where it is marketed in Bitou market of Burkina Faso, while Apomuden dominates the farms of both men and women in Northern Region.

- Women farmers preferred varieties associated with good cooking and quality traits, nutrition and health while men preferred varieties with good agronomic performance that are readily marketable.

5.5. Progress at the Southern Africa Sweetpotato Support Platform

Maria Andrade, Godwill Makunde, Abilio Alvaro, Jose Ricardo, Joana Menomussang and Wolfgang Grüneberg

The Southern African region is prone to natural disasters and effects of climate change such as drought, floods and cyclones. Malnutrition is still a challenge in many Southern Africa countries. Breeding sweetpotato for drought tolerance in Southern Africa took on another dimension when the Accelerated Breeding Scheme (ABS) was introduced by Grüneberg *et al.* 2005.

The objectives/milestones of the Southern Africa Sweetpotato Support Platform include:

- 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 10-20% in hybrids from populations with drought tolerance 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

In 2016, three observational trials were planted in Umbelúzi (OT2820), Gurue (OT1868) and one from purple-fleshed crossing block at Gurue (OT1820) with six check clones, namely, 199062.1, Resisto-Mozambique, Tanzania, Namanga, Irene and Delvia. In all the observational trials, the storage root weight of the test clones was significantly higher than the check clones. In the OT2820 at Umbelúzi, when Tio Joe and Resisto were the male parents many progenies were with the orange-flesh color while families with Xiphone as a male progenitor had more progenies with white or yellow flesh.

Field trials were also established at five sites with the objective of documenting sweetpotato breeding progress made by the Southern Africa breeding platform over the past decade. All varieties in these trials were cleaned and indexed in tissue culture. These included 34 varieties with seven varieties released in 2016; 15 varieties released in 2011; five varieties released in 2006 and seven varieties released in 2000. This was a random complete block design (RCBD) experiment with 2 to 3 replications. Means for storage root yield on dry matter basis were highest (6.7 ton/ha) in the varieties released in 2016 and least (4.1 ton/ha) in varieties released in 2000. There was a clear increase of 0.4 t/ha between 2011 and 2016 releases.

Three crossing blocks were established in January 2016. In Umbelúzi, the crossing blocks had 68 parents (8 males and 60 females); and 56 parents (6 males and 50 females). These parents were selected based on drought tolerance, beta-carotene content, dry matter levels, and iron and zinc contents. The crossing block at Gurue has 35 parents (5 males and 30 females) selected based on drought tolerance with purple-flesh. A total of 43,769 seeds were generated by 30th December 2016. Thirty-six thousand OFSP seeds were distributed to 12 NARS and 11,400 seed from purple-fleshed parents were distributed to five countries.

The Southern Africa Sweetpotato Support Platform had established 8,012 seeds as observational trials at Umbelúzi and Gurue by June 2016. Harvesting and selections in the observational trials were done in late November. The heterosis trial has been planted under two treatments for the third season in Mozambique. Results so far show that the hybrid population AxB had superior means under both drought and irrigated conditions in 2016. The drought tolerance trials were planted also for the third season at Umbelúzi and data collection is in progress.

More than 2,808 samples were washed and processed from observational trials at Umbelúzi and Gurue, 1,808 of which were read in the NIRs lab in Mozambique. The mean beta-carotene content for the test clones in the observational trials was of 27.43 mg/100g DW and 26.73 mg/100g DW for check clones (Irene, Delvia, 199062.1, Namanga and Resisto). Two hundred clones were identified in Maputo NIRS lab as high in iron and zinc levels (> 20 mg/kg DW and >10mg/kg DW, respectively) and sent for verification of iron and zinc through XFR in Lima.

5.6. Progress report of the West Africa Sweetpotato Support Platform

Ted Carey

The West Africa Support Platform is involved in population improvement at a sub-regional level which links with participatory varietal selection at the national level towards releasing - less sweet sweetpotato (unsweetpotato) varieties with reduced perishability. The Platform is using the Accelerated Breeding Scheme.

Unsweetpotato, consumer acceptance, and breeding for quality attributes

In 2016, the West Africa Sweetpotato Support Platform made 49,743 controlled crosses in a screen house among 34 parents and produced 22,373 seeds. Of these 12,772 seeds from 606 families were germinated for establishing a seedling nursery in southern Ghana. A total of 9,500 seeds from 125 families is available for distribution to the national programs in the region. A panel of 28 genotypes has been assembled for processing and storage evaluation in West Africa.

5.7. Progress at the East and Central Africa Sweetpotato Support Platform

Robert Mwanga, Girisom Bwire, Jan Low, Wolfgang Grüneberg, and Jan Kreuze

The focus for East and Central Africa sub-region is resistance to sweetpotato virus disease (SPVD). Milestones of the East and Central Africa Sweetpotato Support Platform include:

1) *Studies demonstrating that significant genetic gain (2% per year in yield) can be achieved in two years in early generations and 4 years for selected varieties.*

Population improvement aims at exploiting heterosis and a combination of 6x8 B and A parents controlled crosses generated 48 families. These families were evaluated at Namulonge and Serere in Uganda. Overall heterosis increment of 16% for storage root yield over the mid-parent performance was observed and 55 clones were selected and established in a preliminary trial.

2) *At least 14 African sweetpotato breeders breed using the latest knowledge and efficient methods.*

African sweetpotato breeders are constantly embracing the latest knowledge and efficient methods. For instance, 12 countries (Burkina Faso, Ghana, Nigeria, Uganda, Kenya, Ethiopia, Rwanda, Tanzania, Mozambique, Ethiopia, Malawi and Zambia) have crossing blocks. Three countries (Cote d'Ivoire, Burundi and Madagascar) now have sweetpotato evaluation/ selection activities. All these countries are using the ABS or implement part of the ABS and can have their samples analyzed for quality traits using near infrared spectroscopy (NIRs) at the regional support platforms.

3) *At least 250,000 seeds with increased frequencies of resistance to SPVD (2–10%) disseminated to at least 10 NARS partners.*

The East and Central African Sweetpotato Support Platform used the established crossing blocks from two distinct genepools (Population Uganda A and Population Uganda B, separated by 18 SSR markers), to make controlled crosses for population improvement and generating botanical seed for national programs in the region. The Platform has disseminated 361,316 botanical seeds to eight national programs.

4) *Selected hybrid progeny demonstrating yield jumps of 10–20% from populations with SPVD resistance. Milestone 1 above feeds into milestone 4.*

Rationale for the sub-regional sweetpotato breeding

The rationale for sweetpotato breeding at the three sweetpotato support platforms in Ghana, Mozambique and Uganda was presented, using data of experiments of trials of 12 OFSP drought tolerant varieties released in Mozambique in 2011. The OFSP varieties were grown at Femesua in Ghana, Maputo in Mozambique, and Namulonge in Uganda. These sites were different in agro-climatic conditions and different viruses (12 viruses, some with different strains) were prevalent at the representative sites where the OFSP varieties were planted. Performance of the OFSP genotypes was poor to very poor at Namulonge and Femesua, respectively, indicating the need for breeding targeting specific agro-climatic conditions and specific viruses in the sub-regions.

5.8. Sub-regional sweetpotato breeding progress reports for East and Central Africa 2016-2017

Laura Karanja

This presentation highlighted the progress achieved by sweetpotato breeders in East and Central Africa. The specific objectives for each country is shown in Table 1. This covers six countries in East and Central Africa, namely, Tanzania, Uganda, Kenya, Burundi, Rwanda and Ethiopia.

All the six countries in the region have crossing blocks composed of 6 to 35 parental clones. During the year 2016/2017 observational trials were conducted in Tanzania, Kenya, Rwanda and Ethiopia. Preliminary yield trials were also conducted in Burundi, Rwanda and Tanzania. All countries had clones evaluated at advanced yield trial with the exception of Burundi. The largest advanced yield trial was conducted by Rwanda with 102 clones. Twenty-eight on-farm trials were conducted by the six countries. Breeders in Tanzania, Kenya, Uganda and Rwanda used CloneSlector for data analysis in observational trials, preliminary trials, advanced trials and on-fam trials. Four sweetpotato varieties were released in 2016 in the region, three by Tanzania and one by Ethiopia. Most of the countries were maintaining foundation seed with the number of plantlets available ranging between 455

(Tanzania) and 55,000 (Ethiopia). The breeders also highlighted exciting varieties for each country and these included Kabode in Tanzania, New Dimbuka in Uganda, KENSPOT 4 in Kenya, 97062 in Burundi, Vita in Rwanda and TIS-8250-1 in Ethiopia.

Table 1. Specific objectives for sweetpotato breeding programs for countries in East and Central Africa

Country	Objectives
Tanzania	To carry out participatory varietal selection at the national level to enable long-term production of new locally adapted varieties that significantly improve farmers' income and deliver nutritional benefits to consumers
Uganda	To increase sweetpotato productivity and utilization by smallholder farmers in Uganda through development of improved multipurpose varieties for food and nutritional security
Kenya	1. Breeding for cold tolerant dual purpose sweetpotato varieties 2. Breeding for drought tolerant OFSP for arid and semi arid lands in Kenya 3. Characterization of the best bet sweetpotato varieties from the Eastern, Western and Southern Africa platforms
Burundi	To develop high yielding sweetpotato varieties, with high beta-carotene content, resistance to diseases and high dry matter content
Rwanda	1. To assess the available genetic diversity through phenotypic characterization of sweetpotato varieties 2. To determine gene action and inheritance of root and vine yields and to select dual purpose sweetpotato varieties
Ethiopia	Breeding for high root yield, high root dry matter content, resistance to SPVD and high beta-carotene content

5.9. Sweetpotato breeding progress in Southern Africa

Martin Chiona

The progress report covers five countries, including Malawi, Mozambique, Madagascar, Zambia and South Africa. The presentation highlighted specific objectives for each country as shown in Table 2.

All the countries in Southern Africa have crossing blocks with the exception of Madagascar. In 2016/2017 observation trials were conducted in Mozambique, Madagascar, Zambia and South Africa. The largest observational trial was in Zambia with 1,806 clones. Five preliminary yield trials were established in Malawi, Mozambique, Zambia and South Africa. Ten advanced trials were conducted in the region in ten locations with Mozambique having the largest number of clones (58) in advanced trials. Only Zambia and Malawi conducted uniform yield trials. Malawi also had a multilocation trial with 13 test clones in six locations and 16 on-farm trials at eight sites. Zambia, Mozambique and Madagascar used CloneSelector for data analysis in 2016 for their preliminary trial, advanced trial and on-farm trials.

Mozambique released seven white-fleshed varieties in 2016. Overall, 15 clones have been earmarked to be released in 2017 by the national programs of the region (Zambia (3), Malawi (3) Mozambique (5) and Madagascar (4)). Only South Africa, Madagascar and Malawi have ongoing breeding projects in the southern region.

Table 2. Specific objectives for sweetpotato breeding programs for countries in Southern Africa

Country	Objectives
Malawi	• High stable yield • Vitamin A • High dry matter • Disease/pest resistance: SPVD, weevils, Alternaria • Root quality:sweetness, acceptance • High root yield • Drought tolerance • High dry matter • Disease/pest tolerance
Madagascar	• Disease/pest tolerance • Consumer acceptance • Wide adaptation
Zambia	• High root yield • High beta-carotene content • High dry matter(≥30%) • Disease/pest resistance: SPVD, • Consumer acceptance
South Africa	• High root yield • High beta-carotene content • Medium to high dry matter (>23%) • Disease/pest resistance:nematode, stem blight, Fusarium wilt, virus • Maintenance of disease-indexed material • Root quality: long storability,smooth appearance, low oxidation and latex

5.10. West Africa breeding progress

Some Koussao

This presentation was for the progress achieved by sweetpotato breeders in West Africa (Burkina Faso, Cote d'Ivoire, Ghana and Nigeria) as per the objectives of each country (Table 3). During 2016 one observational trial was conducted in Burkina Faso and five clones have been earmarked for release in 2017. OFSP clones with high dry matter content, BF59XCIP-4, Apomuden and Mother's Delight were the most exciting varieties in Burkina Faso, Ghana and Nigeria, respectively.

Table 3. Specific objectives for sweetpotato breeding programs for countries in West Africa

Country	Objectives
Burkina Faso	To develop and release high yielding sweetpotato varieties with: (1) high beta-carotene (2) high dry matter content (3) drought tolerance (4) early maturity (5) good storage ability (6) resistance to weevils.
Cote d'Ivoire	• Collect, characterize and conserve local sweetpotato germplasm • Introduce and evaluate sweetpotato varieties for local adaptation • Test the adaptability and acceptability of advanced material through farmer participation.
Ghana	• Collect, characterize and conserve local and introduced sweetpotato germplasm. • Hybridize adapted parental genotypes to introgress desirable genes into adapted genoypes for high yield, weevil and SPVD resistance, and root quality to meet different end users' needs. • Test the adaptability and acceptability of elite sweetpotato genotypes through farmer participatory approach across the five different agroecological zones. • For Northern Ghana, develop and release drought tolerant, high vine establishment, and early root bulking, with quality traits such as dry matter, beta-carotene and good storage quality.
Nigeria	• To develop new sweetpotato varieties that combine high yield, high dry matter, high carotenoid, SPVD resistance, and good storage root quality traits. • To assess the commercial processing potential of released OFSP varieties. • To enhance farmers' access to clean planting material of OFSP varieties.

5.11. Progress at CIP HQ

Wolfgang Grüneberg, Federico Diaz, Maria David, and Raúl Eyzaguirre

This presentation reviewed progress of experimental heterosis populations (EHP), genetic gain studies and SPVD resistance breeding at CIP headquarters.

Experimental heterosis populations

The objective of EHP is to determine the genetic gain (GG) for one complete reciprocal recurrent selection (RRS) cycle using heterosis exploitation breeding schemes (HEBS). The main traits are wide adaptation and early bulking (WAE), non-sweet sweetpotato (NSSP) after cooking and high Fe and Zn (HIFE). The RRS cycle involved S**tep 1:** Crossings for partial inbred populations (PJ x PJ, PZ x PZ – completed), **Step 2**. Partially inbred populations field evaluation (PJ and PZ – completed), **Step 3**. Crossings for H1 population (PJ x PZ – completed, for NSSP after cocking), **Step 4.** H1 population field evaluation (with parents selected in partially inbred and 80 base line clones).

Wide adaptation and early bulking (WAE)

The 23 x 23 PJ and 17 x 17 PZ parents were recombined to develop new PJ and PZ pools for WAEA – 9324 PJ partially inbred and 2152 PZ partially inbred clones were under field evaluation. A total of 50 PJ’ x 50 PZ’ parents were selected for H1 WAE. The target is to finally select 3-4 WAE varieties with less than 90 days from planting to harvest.

Non-sweet sweetpotato (NSSP) after cooking

A set of 5 x 5 PJ and 5 x 5 PZ parents were recombined to develop new PJ’ and PZ’ pools for non-sweet sweetpotato (NSSP). Seven hundred and two PJ’ partially inbred and 379 PZ’ partially inbred clones were under field evaluation. A total of 25 PJ’ x 28 PZ’ parents were selected for H1 NSSP. The target is to finally select two NSSP two varieties.

High Fe and Zn (HIFE)

The 5 x 5 PJ and 5 x 5 PZ parents were recombined to develop new PJ’’ and PZ’’ pools for high iron (HIFE). One thousand and six PJ’’ partially inbred and 711 PZ’’ partially inbred clones were under field evaluations. The 28 PJ’’ x 28 PZ’’ parents were selected for H1 HIFE. The target is to finally select two HIFE varieties with more than 28 ppm Fe.

Genetic gain (GG) studies

Eighteen released sweetpotato genotypes and two common check clones were evaluated at two locations of the arid Pacific coast (Huaral, Canete) and three locations of the Humid tropics of the Amazon basin (San Ramon, Satipo, Puero Ocopa), with harvests at 90 and 120 days after planting. The test genotypes, included Huambachero [CIP-42265], Jonathan [CIP-420014], Costanero [1992 CIP-187016.2], Yarada [1992 CIP-187018.1], Nacional [1992 CIP-187003.1], Tacna [1992 CIP-187019.1], Caplina [1992 CIP-187016.1], Atacama [1992 CIP-187020.1], Milagrosa [2000 .], INIA-100 [2001 CIP-192033.50], Adriano [2010 CIP-105228.1], Alexander [2010 CIP-105240.1], Arne [2010 CIP-105086.1], Benjamin [2010 CIP-105085.2], Abigail [2014 CIP-194540.5], Isabel [2014 CIP-189153.18] and Sumy [2014 CIP-105523.1]. The common check clones across regions were Daga (CIP-199062.1) and Cemsa-74-228 (CIP-400004).

In the first harvest at the Pacific coast (90 days), the slope of the regression line from 1992 up to 2014 is +0.18 t/ha for storage root yield per year and +0.026 commercial roots per plant per year. In the harvests at the Pacific coast (120 days) the slope of the regression line from 1992 up to 2014 is +0.36 t/ha for storage root yield per year and +0.042 commercial roots per plant per year.

Sweetpotato virus disease (SPVD) resistance breeding

The problem of SPVD is being approached from four different sides:

(i) Identification of marker associations and marker validation
(ii) Pre-breeding with germplasm resources exhibiting confirmed SPVD resistance, but exhibiting poorly in agronomic performance
(iii) Search for less SPVD susceptibility in advanced breeding lines and varieties with good agronomic performance

(iv) HEBS – more inbreeding in two pools and offspring testing (not at HQ – this is at Namulonge by an 80x50 cross)

Identification of marker associations and marker validation

Two small sets of VJ08 clones (a resistant set and susceptible set of clones, each comprising 12 clones) were used to identify markers associated with resistsnce/susceptibility (four AFLP markers - E44M34.533, E33M48.460, E36M34.400, E33M48.343, and E39M32.440) associated with *Sweet potato chlorotic stunt virus* (SPCSV) have been identified. These AFLP markers were absent in the resistant bulk but present in the susceptible bulk. One AFLP marker (E39M34.156) was present in the resistant bulk and absent in the susceptible bulk. Seven SSR markers associated with susceptibility to SPCSV (IBS204-172, IBS169-162, Ib-286-125, IbJ559-262, IbJ559-269, IbJ116a-229, and IBS149-225) have also been identified. Also five DArT markers associated with SPCSV 758044, 7563062, 7572542, 753123, and 7574925 have been identified.

The next steps are to validate these markers with about 500 clones of population VZ08, which is related to population VJ08 (same male parent) and explore testing them in applied breeding material at Namulonge.

Annexes

Annex 1 List of Publications from SSA sub-regions 2016/2017

East and Central Africa

Tanzania

Lukonge, E., Gibson, R.W., Laizer, L., Amour, R. and Phillips, D.P. (2015). Delivering new technologies to the Tanzanian sweetpotato crop through its informal seed system. Agroecology and Sustainable Food Systems, 39, 861-884.

Uganda

Journal papers

1. Sseruwu G., P. Shanahan, R. Melis, G. Ssemakula 2016. Genetic analysis of resistance to Alternaria leaf petiole and stem blight of sweetpotato in Uganda. Euphytica 210 (3): 393-404
2. Mwanga R.O.M., Kyalo G., Ssemakula G. N., Niringiye C., Yada B., Otema M.A., Namakula J., Alajo A., Kigozi B., Makumbi R.N., Anna-Marie Ball A., Gruneberg W.J., Yencho J.C., Low J.W. 2016. 'NASPOT 12 O' and 'NASPOT 13 O'. Sweetpotato. HORTSCIENCE 51(3):291–295.
3. Adikini, S., S.B. Mukasa, R.O.M. Mwanga, and R.W. Gibson. 2015. Sweet potato cultivar degeneration rate under high and low sweet potato virus disease pressure zones on Uganda. Canadian J. f Plant Pathology, 37(1):136-147.
4. Adikini, S., S.B. Mukasa, R.O.M. Mwanga, and R.W. Gibson. 2016. Effects of Sweet potato feathery mottle virus and Sweet potato chlorotic stunt virus on the yield of sweetpotato in Uganda. Journal of Phytopathology, 164(4):242-254.
5. Tumwegamire, S., P.R. Rubahiyo, W.J. Grüneberg, D.R. LaBonte, R.O.M. Mwanga and R. Kapinga. 2016. Genotype x environment interactions for East African orange-fleshed sweetpotato clones evaluated across varying ecogeographic conditions in Uganda. Crop Science 56:1628-1644.
6. Yada, B., G. Brown-Guedira, A. Alajo, G.N. Ssemakula, E. Owusu-Mensa, E.E. Carey, R.O.M. Mwanga and G.C. Yencho. 2017. Genetic analysis and association of simple sequence repeat markers with storage root yield, dry matter, starch and β-carotene content in sweetpotato. Breeding Science. Doi:10.1270/jsbbs.16089.
7. Yada, B., A. Alajo, G.N. Ssemakula, R.O.M. Mwanga, G. Brown-Guedira and G. C. Yencho. 2017. Selection of simple sequence repeat markers associated with inheritance of sweetpotato virus disease resistance in sweetpotato. Crop Science, 57:1-10. Doi: 10.2135/cropsci2016.08.0695.
8. Sefasi A., M. Ghislain, A. Kiggundu, G. Ssemakula, R. Rukarwa, R. Mwanga, J. Kreuze, and S. Mukasa. 2017. Embryo-like structures and root regeneration induced by 2, 4-dichlorophenoxyacetic acid in twenty African sweet potato cultivars. African Journal of Agricultural Research, 12(14):1190-1195.
9. Yada B., A. Alajo, G. Ssemakula, R. Mwanga, G. Brown-Guedira, and C. Yencho. 2016. Selection of simple sequence repeat markers associated with inheritance of sweetpotato virus disease resistance in sweetpotato. Crop Science, doi: 10.2135/cropsci2016.08.0695.

Conference proceedings

10. Ssemakula G., J. Akol, T. Alicai, B. Yada, M. Otema, B. Kigozi, J. Namakula, Makumbi, R.O.M. Mwanga, M. Ghislain, J. Kreuze, M. E. Halsey, M. Soto and P. C. Anderson (2016). Reaction of transgenic sweetpotato lines expressing siRNAs to sweetpotato virus disease. National Agricultural Research Organisation-Makerere joint agricultural dissemination conference 21st - 24th November, 2016. Book of abstracts pg 2
11. Ssemakula G., A. Kizito, J. Namakula and C. Kigozi (2016). Improving sweetpotato seed systems in Uganda through an innovative technology that keeps clean vines closer to farmers. Paper presented at the 17th International Symposium for Root and tuber Crops. Nanning Guangxi, China; Jan 18-23, 2016

12. Ssemakula G., J. Akol, T. Alicai, B. Yada, M. Otema, B. Kigozi, J. Namakula, Makumbi, R.O.M. Mwanga, M. Ghislain, J. Kreuze, M. E. Halsey , M. Soto and P. C. Anderson (2016). Reaction of transgenic sweetpotato lines expressing siRNAs to sweetpotato virus disease. National Agricultural Research Organisation-Makerere joint agricultural dissemination conference 21st - 24th November, 2016. Book of abstracts pg 2
13. Mwanga R.O.M, R.N. Makumbi, M. Andrade, G.S. Makunde, J. Ricardo, J. Low, J. Kreuze, W.J. Grüneberg, G.N. Ssemakula, B. Yada, K. Adofo, E. Carey. 2017. Rationale for sub- regional sweetpotato breeding in sub-Saharan Africa. Paper Presented at the ISTRC-AB conference, Dar es Salaam 5-10/3/2017 pg 137 book of abstracts.
14. Kiddo Mtunda, Everina Lukonge, Gorrettie Ssemakula, Haji Saleh, Gration Rwegasira, Mary Yongolo, Stephen Merumba, and Geraldina Mushema (2017). Novel delivery strategies for improved sweetpotato varieties: Experience from the fast track the improved varieties. Paper Presented at the ISTRC-AB conference, Dar es Salaam 5-10/3/2017. Book of abstracts pg 309.
15. Kpaka M.H., Manyong V., Mtunda K. Ssemakula G., Mirembe J. 2017. A phenotypic Approach to get better estimates for adoption rates of improved sweetpotato varieties, and predicting factors that influence farmer decision to adopt and intensify adoption: A logit and Tobit Model. Paper Presented at the ISTRC-AB conference, Dar es Salaam 5-10/3/2017. Book of abstracts pg 346

Kenya
Journal papers

1. Kiarie, S.M., L.S. Karanja, M. Obonyo and F.N. Wachira. (2016.) Application of SSR Markers in Determination of Putative Resistance to SPVD and Genetic Diversity among Orange Fleshed Sweet Potato. Journal of Advances in Biology and Biotechnology 9(2): 1-10.
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3. Ochieng L.A., Githiri S. M., Nyende B.A. and Karanja L. (2015). Analysis of the genetic diversity of selected East African sweet potato *(Ipomea batatas [L.] Lam.*) Accessions using microsatellite. African Journal of Biotechnology Vol. 14(34), pp. 2583-2591.
4. Rosally A., Wilson M., Karanja L. and Joseph O. (2016). Assessment of Sweet Potato Propagules for Re-infection by Various Viruses in East Kamagak Location – Homa Bay County-Kenya. American Journal of Experimental Agriculture 11(1): 1-9.

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5. Karanja, L., Joyce Malinga, John Ndung'u, Ann W. Gichangi, David Lelgut and John Kamundia. Five sweetpotato varieties for alleviating food and nutrition insecurity in Kenya. Proceedings APA conference, 2016, Addis Ababa
6. Ndung'u, J.N., Joyce Maling'a, Laura Karanja, Ann Gichangi, Rosemary, Cheboswony and David K. Lelgut. Retention of zinc, iron and vitamin a in highland sweet potato (ipomoea batatas) varieties after different cooking methods in Kenya, Proceedings APA conference, 2016, Addis Ababa.
7. Ann W. Gichangi, Joyce Malinga, Laura Karanja, Patrick Yegon, John Ndung'u, Rosemary Cheboswony and David Lelgut . Influence of seed sources on varietal adoption by sweetpotato farmers in the Nakuru and Bomet counties of Kenya. APA Conference proceedings, 2016, Addis Ababa Ethiopia
8. Kivuva et al. screening cold tolerant dual purpose sweetpotato in Kenya. Proceedings APA conference, 2016, Addis Ababa.
9. Kivuva, B., Mwanga, R., Low, J. and Agili, S. (2015) Screening cold tolerant dual purpose sweetpotato in Kenya. International Potato Center (CIP). Screening cold tolerant dual purpose sweetpotato in Kenya. www.sweetpotatoknowledge.org/.

Rwanda

Journal papers

1. Rukundo Placide, Shimelis Hussen, Mark Laing, Gahakwa Daphrose (2017). Combining Ability, Maternal Effects, and Heritability of Drought Tolerance, Yield and Yield Components in Sweetpotato/ Front. Plant Sci., 10 January | https://doi.org/10.3389/fpls.2016.01981.
2. Shumbusha D, Shimelis H, Laing M, Asiimwe T. 2017. Phenotypic diversity analysis of sweetpotato for breeding dual-purpose varieties. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science 67: 340-351.

Ethiopia

Journal papers

1. Fekadu Gurmu. 2017. Stability Analysis of Fresh Root Yield of Sweetpotato in Southern Ethiopia Using GGE Bi-plot. International Journal of Pure Agricultural Advances 1(1):1-9.
2. Fekadu Gurmu, Hussein Shimelis, Mark Laing. 2017. Combining Ability, Heterosis and Heritability of Root Dry Matter, ß-Carotene and Yield Related Traits in Sweetpotato. Frontiers in Plant Science. Accepted.
3. Fekadu Gurmu, Hussein Shimelis, Mark Laing. 2017. Evaluation of candidate orange-fleshed sweetpotato clones for nutritional traits. Acta Agriculturae Scandinavica, Section B - Plant Soil Science. Accepted.
4. Shiferaw Mekonen, Berhanu Bekele, TesfayeTadesse and Fekadu Gurmu. 2016. Evaluation of exotic and locally adapted sweetpotato cultivars to major viruses in Ethiopia. Greener Journal of Agricultural Sciences 6(2):69-78.

Burkina Faso

Journal papers

1. Hema, A., M. Koala, K. Somé, E. Palé, A. Sérémé, J. Simporea nd M. Nacro, 2016. Orange-fleshed sweet potato: a potential source of antioxidants and provitamins“A” for the fortification of a local infant food flour. J. Soc. Ouest-Afr. Chim. 042:8-15.

Ghana

Journal papers

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Nigeria

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Annex 2 Workshop evaluation

The evaluation form was completed by 24 participants 37% of these were below 40 years; 42% were between 40 and 50 years and 21% were above 50 years. Results of the evaluation are summarized in Table 4 to 7 and Fig. 1 and 2. Women comprised 25% of the participants while men were 75%. The main expertise of the participants were breeders (92%). Only 8% of the participants had other expertise apart from breeding

Figure 1: How much the 4-day breeder's meeting matched the expectations of the participants

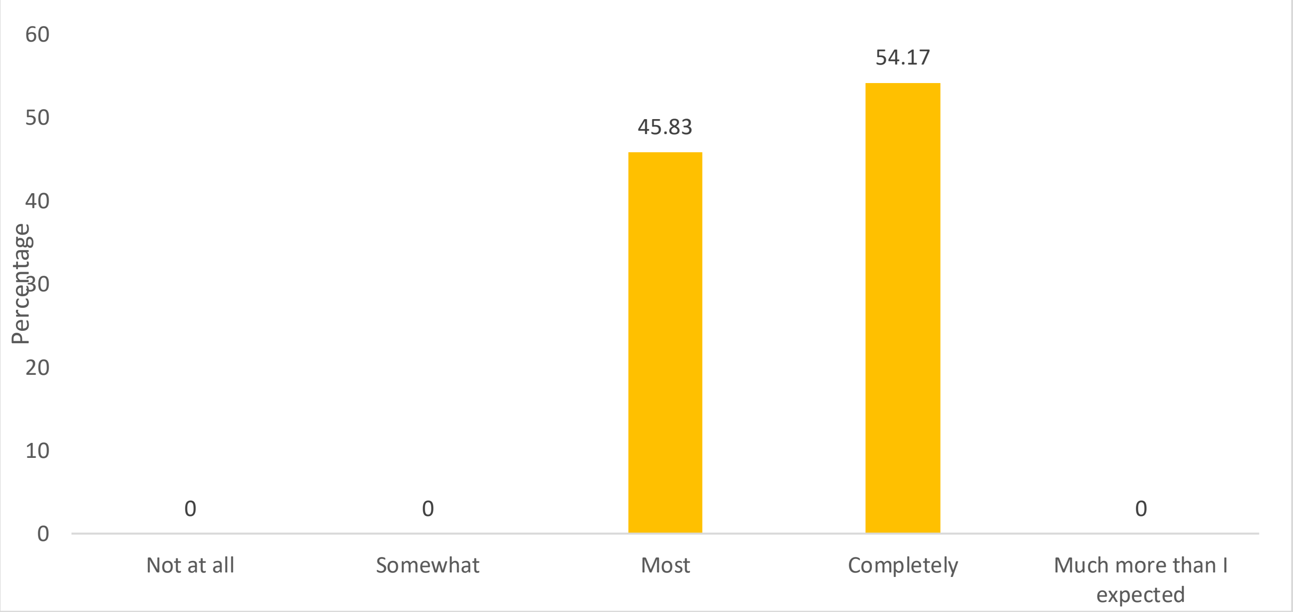

Table 4: Evaluation of the meeting organization and quality of presentations

Evaluation measure	Rating (%)				
	Very poor	Poor	Alright	Good	Very good
Quality of presentations in terms of content	0.00	0.00	4.17	25.00	70.83
Rating in terms of organization (logistics, communication)	0.00	0.00	8.70	21.70	69.57
Rating on quality of the day 1 sessions on Sweetpotatobase	0.00	4.17	4.17	50.00	41.67
Rating on quality of the day 1 and 2 sessions on HIDAP	0.00	0.00	0.00	50.00	50.00

Figure 2: Quality and usefulness of sessions, in percentage

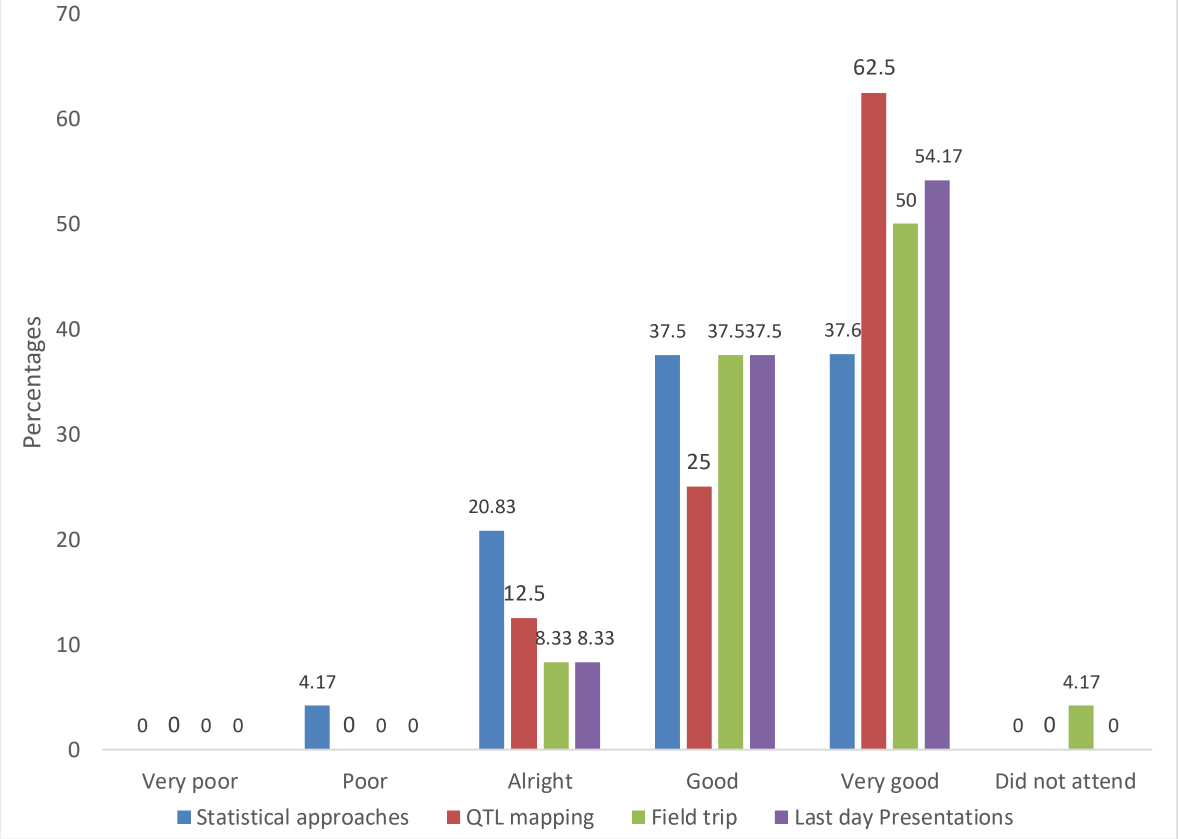

Table 5: Parts of the meeting that were most useful

Parts of the meeting	Frequency of mention		
	First mention	Second mention	Third mention
HIDAP	13	6	2
QTL mapping	2	2	6
Sweetpotatobase	3	2	2
GBS	0	3	1
Interaction with colleagues	1	0	0
MAS	1	0	0
Genomic selection*	1	2	0
Panning the gold	1	1	0
Field trip	1	2	4
Progress on sweetpotato work in different regions of the World	1	0	0
Breeding progress reports	0	1	3
New statistical approaches	0	0	1
Molecular markers	0	0	1
Presentations	0	0	1
GT4SP	0	0	1
Presentation on genetic gains and populations	0	0	1
I. Trifida and *I. Triloba*- Why the reference genome is a reference resource for sweetpotato improvement	0	1	0

On genomic selection mention is made on hexaploid sweetpotato, and tools for deployment in breeding.

Table 6: Parts of the meeting that were least useful

Parts of the meeting	Frequency of mention	
	First mention	Second mention
Demonstration on serology	1	1
Availability of reference genome	1	1
Statistical approaches	3	2
Field trip	1	1
None	9	13
HIDAP training	1	1
Last session presentations	1	2
Genetic gain	1	0
Sweetpotato base	1	0
Soft wares	1	0
PROGRESS-CIP HQ	1	0
RTB reports and evaluations	1	3

Table 7: Suggestions for improvement or topics that could be covered in the next meeting

Aspect	Detail
Genomics	• Cover one specific topic in genomics in detail instead of covering many things • Include Genomics tools and relation to breeding genetic gain and heterosis analyses • More time on QTL and genomic selection (2 responses) • Practical exercises for difficult concepts like QTL mapping
Breeding	More discussions on breeding goals, e.g. breeding for a specific purpose
HIDAP practice	• More time • More time (whole week)
Planning purposes	• Resource persons should travel to the countries and do practical sessions with scientists there • What do members of the community think about the breeding work? • Each country should be given at least 10 minutes to report progress • More time for interaction • Training period too short (3 mentions) • Bad internet connection in Mirror hotel • More time for progress reports
Other aspects	• How to overcome hybridization constraint • Sweetpotatobase need to be presented better and presentation slides shared (hardcopies) • Genome wide association, Genetic mapping

Annex 3 Workshop agenda

Time	Activity/Session	Responsible
May 14 Sunday	**Arrival**	*Tassy Kariuki*
2:00 pm	**HIDAP Installation** *(All afternoon inside main meeting room)*	*Raúl Eyzaguirre / Luka Wanjohi*
May 15 Monday		
8-8:30	**Registration**	Tassy Kariuki
	Opening remarks	*Jean Ndirigwe, Kirimi Sindi, Robert Mwanga, Jan Low, Craig Yencho* (15 minutes)
8:45-9:30 am	**DG RAB on Behalf of Minister of Agriculture**	
	Chair: Craig Yencho	**Note taker: Goodwill Makunde**
	HIDAP and Sweetpotatobase Training	
9:30 am	Welcome and introductions	*Bryan Ellerbrock, Alex Ogbonna*
9:40 am	Sweetpotatobase Overview and Setting up accounts	*Bryan Ellerbrock, Alex Ogbonna*
10:00 am	Lists and Loading Accessions	*Bryan Ellerbrock, Alex Ogbonna*
10:30 am	Break	
10:45 am	Trial Creation and UPload	*Bryan Ellerbrock, Alex Ogbonna*
11:45 am	Phenotyping	*Bryan Ellerbrock, Alex Ogbonna*
12:00 am	Data Upload and Download	*Bryan Ellerbrock, Alex Ogbonna*
12:40 pm	**Lunch**	
	Chair: Jean Ndirigwe	***Note taker: Benjamin Kivuva***
2:00 p.m.	HIDAP Installation	*Raúl Eyzaguirre / Luka Wanjohi*
3:00 pm	Offline creation germplasm lists & fieldbook files in HIDAP	*Raúl Eyzaguirre / Luka Wanjohi*
May 16 Tuesday	**Chair: Jose Ricardo**	***Note taker: Benard Yada***
8:15 am	Using analytical tools in HIDAP offline	*Raúl Eyzaguirre / Luka Wanjohi*
10:00 am	Health Break	
10:20 am	HIDAP Final Exercise	*Raúl Eyzaguirre / Luka Wanjohi*
12:30 pm	Lunch Break	
	Chair: Gorrettie Ssemakula	***Note taker: Placide Rukundo***
2:00 pm	New statistical approaches	*Wolfgang Grüneberg / Raúl Eyzaguirre*
4:00 pm	Health Break	
4:20 pm	RTB Reports	*Wolfgang Grüneberg*
5:00 pm	Feedback/Discussion/next steps	*Wolfgang Grüneberg / Raúl Eyzaguirre*
May 17 Wednesday	**Field Trip/Less sweet sweetpotato breeding taste test & discussion on quality assessment work**	*Jean Ndirigwe/Edward Carey/Tassy Kariuki*
May 18 Thursday	Sweetpotato breeding- Let's talk about the now and take a look into the future	
	Chair: Dr. Edward Carey	***Note taker:*** *Alex Ogbonna*

8:15 am	Introduction statement from the GT4SP PI	*Dr. Craig Yencho*
8:30 am	Panning the gold-QTL mapping and genomic selection in hexaploid sweetpotato	*Dr. Bode Olukolu* *Dr. Dorcus Gemenet*
10:00 am	**Health Break**	*Tassy Kariuki*
10:20 am	Continue session; Panning the gold - QTL mapping and genomic selection in hexaploid sweetpotato	*Dr. Bode Olukolu* *Dr. Dorcus Gemenet*
11:20 am	*I. trifida* and *I. triloba* -why the reference genome is a reference resource for sweetpotato improvement	*Dr. Robin Buell*
12:30 pm	Wrap-up	*Dr. Mercy Kitavi*
	Chair: Bode Olukolu	*Note taker: Reuben Tendo Ssali*
2:00 pm	Breeding for Fusarium wilt resistance and vine dissemination of informal cultivars in South Africa	*Whelma Mphela*
2:15 pm	Genetic variability of continuous storage root formation and bulking in Ugandan sweetpotato germplasm	*Astere Bararyenya*
2:30 pm	Breeding of sweetpotato for drought tolerace and high dry matter content in Rwanda	Placide Rukundo
2:45 pm	GREAT training and implications for sweetpotato breeding in Ghana	*Obaiya Utoblo*
3:00 pm	Progress Southern Africa Sweetpotato Support Platform	*Maria Andrade*
3:20 pm	Progress West Africa Sweetpotato Support Platform	*Edward Carey*
3:40 pm	Progress East and Central Africa Sweetpotato Support Platform	*Robert Mwanga*
4:00 pm	Health Break	
4:20 pm	Progress – West Africa sub-region	*Some Koussao*
4:35 pm	Progress - East and Central Africa	*Laura Karanja*
4:50 pm	Progress - Southern Africa	*Martin Chiona*
5:05 pm	Progress – CIP HQ	*Wolfgang Grüneberg*
5:20 pm	Wrap-up and meeting evaluation	*Robert Mwanga, Craig Yencho & Luka Wanjohi*
May 19 Friday	**Participants Depart**	*Tassy Kariuki*

Annex 4: List of participants

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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

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