NEXTGEN CASSAVA

Next Generation Cassava Breeding Project Annual Meeting 2019

Kampala-Uganda
February 18-22, 2019

Disclaimer

This report documents the Next Generation Cassava Breeding Project Annual Meeting that was held from February 18-22, 2019 at Speke Resort Munyonyo in Kampala, Uganda. The report is not a thesis, but a documentation of the proceedings and outcomes of the meeting without interpretation. It serves as a reference document for NextGen project management and meeting participants by providing details of meeting proceedings reported as they were presented with slight or no modifications. The opinions expressed herein are those of meeting participants and do not reflect the views of the compiler—they are a compilation of participants' contributions.

Compilation:

The contents of this report were transcribed by Pamella Ingabire and Carol Rugaba. The report was compiled, edited and designed by Joshua Raymond Muhumuza from Uganda Biosciences Information Center (UBIC). A final edit was performed by Canaan Boyer (Cornell University).

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List of Acronyms

AYT	Advanced Yield Trial
ACWP	African Cassava Whitefly Project
BMGF	Bill and Melinda Gates Foundation
BTI	Boyce Thompson Institute
CBSD	Cassava Brown Streak Disease
CET	Clonal Evaluation Trial
CIAT	International Center for Tropical Agriculture
CMD	Cassava Mosaic Disease
CoPP	Community of Partners and Practice
DFID	Department for International Development
EiB	Excellence in Breeding
Embrapa	Brazilian Agricultural Research Corporation
EPAC	External Project Advisory Committee
GBS	Genotyping By Sequencing
GWAS	Genome-Wide Association Studies
IITA	International Institute for Tropical Agriculture
KEPHIS	Kenya Plant Health Inspectorate Service
NaCRRI	National Crops Resources Research Institute (Uganda)
NIRS	Near Infrared Spectroscopy
NRCRI	National Root Crops Research Institute (Nigeria)
SNP	Single Nucleotide Polymorphism
SOP	Standard Operating Procedure
TARI	Tanzania Agricultural Research Institute
TRICOT	Triadic Comparisons of Technologies
UYT	Uniform Yield Trials

Introduction

The NextGen Cassava Breeding project (NextGen Cassava) seeks to modernize partner cassava breeding institutions in Africa and use cutting-edge tools for efficient delivery of improved varieties of cassava.

The project, currently in its second five-year phase, held its annual meeting in Kampala-Uganda from February 18-22, 2019. The meeting was an opportunity for project management and staff to take stock of accomplishments and challenges from the first year of NextGen Phase 2, deliberate on key issues and brainstorm on a strategic way forward for the project.

Meeting Participants at Speke Resort Munyonyo - Kampala

Welcome and Introductions | Richard Ofei & Canaan Boyer

Richard Ofei from IITA welcomed delegates to the NextGen Cassava 2019 Annual Meeting, an intensive five-day meeting of presenta-tions, work planning, and workshops. "The objective of the meeting is to improve the lives of farmers and seed producers," he announced.

Meeting participants included representatives from NaCRRI, Makerere University, TARI, IITA, NRCRI, Embrapa, CIAT, BTI and Cornell University, among others. The project management team: Chiedozie Egesi, Hale Ann Tufan, Jean-Luc Jannink and the project PI, Prof. Ronnie Coffman, were in attendance. The EPAC team- David Meyer, Steve Rounsley, Carlos Iglesias as well as representatives from BMGF and DFID, the project's main sponsors, were also present.

Canaan introduced project collaborators present. Representatives from IITA, EiB, NRCRI, AbacusBio, RTBfoods (a NextGen partner project), ACWP, Institute for Bio- and Geosciences (IBG-2), Syngenta, Leibniz Institut DSMZ, Kansas State University and Cornell University were introduced.

Members of the COPP (community of practice partnership) countries who were joining the team this year were also introduced. Martin Chiona (Zambia), Isata Kamanda (Sierra Leone), Bonnnie N'ZUE (Cote d'Ivoire), Ruth Pempreh (Ghana), and Athanase Nduwumureymi (Rwanda) comprised this group.

Canaan shared a summary of the program.

Three kinds of presentations were to be expected: executive summaries where the heads of divisions would share updates of the research in their respective divisions; roadmap talks where different project groups would present overviews of their accomplishments and roadblocks from Year 1 and, goals for Year 2. Project groups were also asked to 'Challenge the room' and "we hope that these talks will inform the work planning sessions that will take place later," Canaan said. During world café sessions, collaborators would present to smaller groups which would create a more intimate environment for interaction and discussion. Side meetings and a COPP work planning session with the breeding teams complemented the program.

"The objective for these meetings is to get together every year to work together in person, discuss the previous year, plan for the next while learning from the challenges and opportunities we've encountered," added Canaan. She hoped the meeting would come up with some clear action items for the coming months and adjustments that the project might want to make to Year 2 plans, keeping in mind the bigger picture and mission statement in everything that was being done.

"Please take advantage of the opportunity we have being together to plan to meet those you need to catch up with, say hello to the new people. This is a great group and it is fantastic to see a room with so many familiar and friendly faces. Welcome everyone!" she concluded.

Executive summaries

Chiedozie Egesi | Breeding division.

The project manager informed the participants that NextGen is funded primarily by Bill and Melinda Gates Foundation and DFID and is starting the second year of Phase 2. The project runs in the USA, Colombia, Brazil, Ghana, Nigeria, Tanzania and Uganda. "We

have 12 institutional partners across 3 continents and we have 8 more countries as COPP members—a force of many combined to lift up the cassava crop and by that the livelihoods of the populations who depend on it," Chiedozie stated.

"We call ourselves by the nickname Cassava Breeding Inc. to remind ourselves to run optimally like a seed company with breeding at the centre and all the other divisions working toward the objectives of delivering improved varieties," he added.

In the executive summaries, Chiedozie talked about the implementation of breeding, Jean-Luc talked about breeding research and what was being done to make breeding more efficient, while Hale discussed the surveying aspect and showed where the interdependencies and linkages happen in making Cassava Inc. deliver improved varieties.

"Our ultimate purpose is to develop a sus-

> " **Our ultimate purpose is to develop a sustainable cassava breeding scheme with accelerated genetic gains...**

tainable cassava breeding scheme with accelerated genetic gains leading to the release of improved cassava cultivars that satisfy the agronomic and end user needs of small holder farmers in Africa," Chiedozie noted. This is being done by continuously improving and refining germplasm to get the best varieties to the farmer, improving understanding of farmers' needs and whether these have changed over time and locality, improving the technologies used to deliver this. Institutional capacity is also being improved for effective collaboration across disciplines, divisions and organisa-

tions.

NextGen's expected outputs are to deliver effective improvement through optimal breeding schemes, research integration, demand-led breeding goal identification within a sound organisational structure.

Chiedozie encouraged outreach to national breeding programs throughout sub-Saharan Africa to urge them to adopt similar breeding program organisation. This would lead to release of improved varieties that meet farmers' criteria of improved yield and resilience.

The project is designing sustainable means for identification and quantification of cassava breeding goals based on evidence of the needs of smallholder farmers. This is meant to generate improved diverse cassava populations with a solid foundation for future genetic gains and, greater understanding of the genetic architecture of traits to improve the efficiency of future breeding.

The meeting learned that the project team had been challenged by EPAC in 2018 to provide a vision statement; to think about what steps could be taken to ensure the sustainability of Cassava breeding programs in Africa; what could be done to communicate our common goal / vision to ensure we were working as a team. The team was also posed with the scenario of a CBSD outbreak in west Africa with 40% of the farmers affected and asked; what would you wish you had done differently NOW in the face of such a disaster?

The project vision is to empower farmers through innovative, sustainable Cassava breeding. Variety development pipeline with

stage-gates denoting the stages from product design to release and deployment is being incorporated.

Below are updates on breeding work at different project partner institutions.

IITA

We did the research and product design in conjunction with NextGen survey division, RTBfoods and participatory evaluation to determine what the market needed. In the discovery phase, where we do the parent selection and produce the seedlings, right now we have 15,000 seedlings in the field. In the early development phase, we have 1760 C4A AND 1580 C4B in clonal evaluation trials, and 276 C3 in PYT. In the pre release phase we have 14 clones in the NCRPs, 8 of them through this project, hopefully by the end of 2020, there should be at least one variety released from Nigeria. IITA was running a one year breeding cycle as opposed to two year cycles in the other projects, so this speed will reflect as we look at other projects.

NRCRI

NRCRI has over 8,000 C2B seedlings from 2018 and is going on to plant 18,000 seedlings for C3A this year. Over 1000 seedlings in clonal evaluation trials in C2A, 59 clones in advanced evaluation trials across 4 locations, and because of the mandate for regional trials they are entering 14 clones, but are hoping to release more after 2022 from their own population.

TARI

Tanzania joined the project in 2017 but has moved on to have over 23,000 seedlings in their C1. In their C0 they have 120 in PYT, 85 in AYT and 19 in UYT which they're hoping to release in 2022.

NaCRRI

One of the best programs on the project. They have over 6,000 white root seedlings, 640 pVAC (pro vitamin A) C1 in CET, 63 C1 white root clones in AYT, 24 C0 pVAC clones in AYT. They're adapting TRICOT to their national performance trial and because they've done the farmer participatory evaluations they hope to release this year or early next year.

EMBRAPA

Material has gone on to CET, 823 seedlings in C1.

The above is an overview of the progress made in stage gating breeding work and a big improvement has been observed right across the breeding programs.

In response to the EPAC challenge last year to put emphasis on breeding for resistance to CBSD including pre-emptive resistance breeding for West Africa, a few sources for the material have been identified. Edward Kanju's work and 5CP project identified some material that has been distributed to southern and central Africa already. The materials have been received in Nigeria and are being grown for crosses.

Some materials were identified from Stephan Winter's lab-some CIAT material from the core collection that was resistant to CBSD. These are under evaluation in Uganda, Tanzania, and West Africa in preparation for field planting this season. Materials were also shared with Rwanda and Burundi.

Edward Kanju has also developed some really interesting lines that are being cleaned up for distribution at KEPHIS. Project management felt Stephan Winter should be part of this process so that comparisons can be made. Some material from west Africa is being tested in Uganda and Tanzania. Progeny testing is being done by an MSc student from Nigeria studying

at Makerere and doing evaluation for resistance to CBSD at NaCRRI.

Ismail and his team's work on marker validation and usage in Cassava breeding, is now a resource being used by breeding programs in Africa, Asia and Brazil as work continues on other markers.

Regarding germplasm exchange, material from the project's international nurseries in Hawaii is currently under evaluation in Nigeria and being prepared for Asia because of their CMD problem at the moment. Peter Kulakow has shared CMD resistant clones with Vietnam and Thailand. 150 clones from the advanced training population at EMBRAPA are being shared with Africa. Stephan has already done some cleaning and distribution of these clones will be discussed at this meeting. Stephan is also preparing some wild species and C1 clones for sharing. This is good progress because of the difficulty in getting germplasm material out of Brazil.

"We have in the room Excellence in Breeding project partners, who we're all working with to continually improve the process to sustain our accelerated genetic gain goals," the project manager announced. Meetings were held in Ibadan in November 2018 with NextGen project partners, some COPP members and IITA.

Project concepts were developed, breeding pipeline nomenclature for stage gates adapted, and variety development strategies defined, so we can track progress and resource expenditure. Each of the breeding teams developed product profile contracts. Product advancement meetings were also worked on and later this week a mock up going through the process and motions will be conducted.

Some studies have been done in Nigeria from which 5 varieties were identified that are well spread out that need replacement. The key things in the product profile contract are the variety that you want to replace; the basic,

"must-have" traits; the value added traits, and the estimated annual cost of replacement program.

We worked with EiB to develop a continuous improvement plan. IITA was put through the Breeding Program Assessment Tool (BPAT) commissioned by the BMGF, and the report that was generated was shared with both IITA and non-IITA institutions so they could make contributions and also to be able to adapt it to their operations.

Chiedozie also discoursed on the project quality management system. A taskforce called Quality Champs (QChamps) was set up. This will work across all the programs. "We're working with BTI and Cassavabase. Our vision is for regular collaborative meetings and directed development and implementation of improved procedures working with EiB and facilitated by the Cassavabase team," he told the meeting.

As an achievement so far, all the project's phenotyping, genotyping etc. is managed in Cassavabase which means the SOPs set there are complied with. More SOPs are being developed for each organisation. These will be peer reviewed at regular meetings. Plans are underway to include COPP partners in this process.

Participants were informed that 5 of 8 representatives of the project COPP members were at the meeting. NextGen is supporting them with field management, peer reviews, training workshops and most importantly, germplasm exchange. The COPP members have also had data management training which is still ongoing. They have been supported with tablets and barcodes. 32 breeders and technicians have been trained. Barcoding for all field plots in the countries that have had the training has been accomplished. All trials have been uploaded to Cassavabase and all historical data has been submitted to the team for curation and uploading to Cassavabase.

NextGen is working with a sister project—Basics seed and Best seed, both funded by BMGF—to address the bottleneck that is Cassava multiplication. Semi-Autotropic Hydroponics (SAH), which is less intense than using tissue culture, is being employed, so the materials in late regional trials are already being bulked up to produce planting materials for this year's trials. IITA and NRCRI also have seed companies purely specialising in business marketing foundation seed. In COPP countries NextGen is working with a project called Technologies for African Agricultural Transformation (TAAT)—an African Development Bank funded project—which is going to provide SAH labs to 3 or 4 of the project's COPP partners.

The project manager challenged the room to think about what is being done to ensure that the process of continuous development is happening; there is a steady rate of genetic gains; the gap between maximum impact and targeted output is being bridged; that we have strategies for product development and rigorous metrics for success; and that variety replacement strategy is efficient and resources are efficiently managed.

Jean-Luc Jannink | Research Division.

Jean-Luc opened his remarks by stating that the overall mission for NextGen Cassava research division is to translate current breeding research to applications breeders want.

He presented research going on at the Cornell hub rather than what has already been distributed throughout the project. "The big thing for us the research division is to have a genotyping tool that is going to work for you," he said.

The research team's tool was tested at IITA in 2018 and it was determined that the imputation accuracy was not good enough. The team reverted to the old tool and have made some improvements like properly matching imputation reference panel with imputation targets, and filtered out duplicated region SNPs that may have fixed heterozygosity, which poses problems for most bioinformatics platforms.

The Buckler lab and his students have long had this insight and have helped develop a method that helped weed out what looked like SNPs but were not actually SNPs. "So now we can pick the best version of the filtering pipeline and move forward with the confidence that we can do as good a job as with the full set of SNPs," Jean-Luc asserted. All the breeding programs on the project had been encouraged to move and set up these imputation reference panels.

One of the things planned for Phase 2 is to have a look at the genetic gains that we were obtaining on an annual basis. Using data from a number of locations in Nigeria as a whole, similar to analysis that Alfred Ozimati did in 2018 for NaCRRI, it was observed that CMD, FYLD and DM did what was hoped for. "I think we need to do these analyses on an ongoing basis for all the other programs too and also to develop better methods for doing them," he suggested.

One of the other projects that has been going on at Cornell has been Cassavabase: the improved digital ecosystem which has helped implement rigorous sample collection protocols, with better genotyping process interfaces and improved tracking of pollination. The Cassavabase team has also been superb at organising workshops to ensure that breeders know how to use these tools in practice.

The team is also figuring out how to organise its network for multi-environment trials. NaCRRI had a shot at this with Alfred's work using 10 locations across Uganda in two planting seasons. Alfred collected weather variables across these locations, planting dates, and check phenotypes. These environments can be clustered using either weather variables or check phenotypes to get a 'plants-eye' view of these environments. There's a stronger clustering among the check phenotypes between the different planting seasons; it doesn't cluster so neatly when weather variables are used. The team is working on how to analyse these data and develop this improved multi-environment trial.

To optimise breeding schemes it is important to know what the error variances are for different types of trials. Moshood Bakare, a second year graduate student, has been working to curate data and estimate the residual variances for locations across IITA and a number of traits. Data comparison revealed that the uniform yield trials don't necessarily give lower error variances. Marnin, Moshood and Jean-Luc will look all their different analyses to try and figure out why this is. This is a first step for optimising breeding schemes. The second step will be figuring out what resources are available across the breeding programs. Jean-Luc and his team have started working with Tanzania where because of CBSD, the breeding programs in the coastal region and the lakeside region have been segregated for a number of years now. They were surprised that on plotting principle component axis, the data from Uganda is intermediate between the two Tanzania programs. The first principle component is about the introgression on chromosome 1. The team is figuring out how to work with these data to get maximum prediction accuracy for the two Tanzanian breeding programs.

Hale Ann Tufan | Survey Division.

The survey division within Cassava Inc. interfaces with the users of the varieties that

developed on a project. Hale talked about how her division engages farmers to understand what they need and feed that back into

the product profiles for the breeders. Her team also does on farm testing to understand how project varieties are doing.

In most public breeding programs, the breeding objectives are set by demography vs geography i.e. trying to understand how where they grow crops affects adaptation but Hale's team is looking to also understand what the end user needs. A recent survey found that over 90% of projects follow formal procedures to define breeding objectives and priorities by mostly consulting other experts. Therefore, consultation with farmers is relatively weak. Her team is looking for ways to strengthen that, and is working to understand trait and varietal differences that can complement and inform NextGen product profiles.

The survey division's mission statement is to define actionable breeding targets that satisfy diversity and demand. The three main components of trait descriptors—understanding the traits that matter, the relative importance of these traits to the different end users, on farm trialling to see how they perform.

A lot of work was done in Phase 1 to define the traits, thus production traits across NextGen member countries are already known. The Survey division's focus is now on the knowledge gap in the quality traits. They are partnering with RTBfoods project which is already doing a lot of work in this area. Their 'work package 1' is concerned with capturing traits and preferences for quality of product through

consumer surveys and processing evaluation. The project is also developing high throughput methods to measure these quality parameters, methods to screen breeding populations and for on farm trials.

Outputs for NextGen.

Within the RTBfoods work package 1, Next-Gen is focussed on looking for high quality characteristics and indicators, low quality characteristics and indicators, prioritisation both simple and pairwise, mapping good and bad varieties for each characteristic to get at what end users define as quality. Differences in traits can also be analysed by region, by sex, ethnicity, marital status etc.

The output for NextGen is a list of product quality traits and their prioritisation across different countries. Other activities like processing documentation and consumer studies will build on these activities.

Year 1 accomplishments.

Data collection and digitisation in Nigeria and Uganda has been completed. Data analysis will be completed in time for the next annual RTBfoods meeting in March 2019. A workshop will be held before that to analyse these data together and with the developers' permission, these tools will be applied to work in Tanzania which is not an RTBfoods country.

It was realised that the team were not doing a good enough job with systematic quality analysis of breeding lines. The IITA quality lab will be interacting more with RTBfoods for routine screening of breeding lines.

Regarding NIRS calibration development and screening of breeding lines, more coordination and thoughts are needed on how the survey division can work with RTBfoods on this.

For on-farm trials, Hale's team used some of the data from Phase 1. The survey division has

done expert processing using people who are very informed on how to make good product to inform them on what is good or bad using 20 different varieties, three of which were NextGen varieties while the rest were local checks or released/improved. Fufu or Eba was made from all of them and the champion processors asked to rank them in relation to each other.

In the top 10 varieties ranked for Fufu and Eba across two states, there were perhaps unsurprising differences in preference as people may have different requirements. What was interesting however, was that even within states, there was e a difference in ranking between Gari and Eba. Something therefore happens in the process of adding water to make the product for consumption. What this indicates is that it isn't as straightforward as just breeding for good Gari. "So this the data we're starting to accumulate and understand to feed back into the breeding programs. The good news is our NextGen varieties were consistently near the top in these trials!" Hale noted.

She added that the next step was to understand the relative ranks and economic weights of the traits - to understand which ones are the most important, and by how much.

The survey division is also starting a collaboration with AbacusBio. Bruno Santos and Ireti Balogun attended the NextGen meeting as part of this initiative. Ireti is a PhD student who will be working with Hale's team for the next 3 years. She informed participants that, "The good news is together we have a lot of data on traits. We will distill and review these data and that will form the basis for the survey design for the 1000 minds software."

The meeting also learned that there is a lot of baseline work that has to happen this year on equivalence, direction of trait improvement, direction of trait trade-off and definition of traits in terms farmers understand so the team can focus on choosing the most important

traits as only 8 traits can be used to do this survey.

What the survey division hopes to achieve is absolute ranks for all identified traits in order of importance. Further, they will look at the typologies of farmers, work out which types of farmers prioritise certain traits and by how much. Hopefully product profiles will be teased out from these results.

The questions Hale's team seeks to answer include: which key traits to include in our product profiles; which traits to emphasize for different types of farmers; how to build them into our breeding priorities; are there explanatory factors that influence prioritisation of these traits by the end user? By assigning economic value to the traits, NextGen breeding objectives are beginning to be tailored to the different customer segments.

Achievements, 1000 minds.

Ireti Balogun from AbacusBio has recently joined the survey team and was at the meeting to learn more about the project. A pre-meeting was held, and key informants had interviews with breeders to understand Cassava and the dynamics of economic breeding.
Hale thought that it would be a good opportunity for EiB to facilitate the linkages with AbacusBio as this would reduce costs.

The meeting was informed that the survey division decided to use the TRICOT for on-farm testing. "We are using this method because traditionally field testing is expensive, limited in scale and number of varieties you can work with which leads to low data quality and limited opportunities to learn," Hale said.

TRICOT offers a solution which from first indications simplifies the trials as the farmers manage their own trials, lead farmers rather than researchers to collect the data, and involves little supervision or training.

The survey division's approach will be to give each farmer three varieties, use ranking to collect the data, define the farms as incomplete blocks, use balanced data depending on stratification whether geographically or by plant type. Variation in environment, crop management is expected and will have to be embraced.

Jacob van Etten published a paper in PNAS last month (January 2019) where weather data was used to look at climatic models and how that affects different crop prioritisation in three countries. They worked with 10,000 farmers in India and 1,000 farmers in Ethiopia and Nicaragua. It was found that without heat stress, the local check variety outperformed all other varieties, but with heat three varieties outperformed the local check. Doing this with thousands of farmers and with relatively small errors, they could go on to prescribe replacement varieties for the various regions at the national level.

NextGen has two TRICOT trials in Nigeria and Uganda. In Nigeria, the trial involves 44 farmers in pilots in two states. Data was collected over the phone, bundles labelled with ribbons to overcome challenges with literacy and minimal compensation for land preparation, weeding and harvesting done.

Preparations are in high gear to move on to the main trial. 30 varieties have been identified including the replacement target as defined in the EiB product profile contract. The trial will include 250 farmers over four states and the target is small scale Gari production.

In Uganda, the pilot is also ongoing with 30 farmers across two sub counties. The survey team is providing a bundle of three varieties including the local check to be planted separately on each farm. Data collection will be on paper through extension workers, bundles will be labelled alphabetically and, minimal compensation for land preparation, weeding and harvesting will be done.

For the main trial in Uganda, 12 NextGen candidate for release varieties, a local check and replacement target will make up the bundle. 50 farmers' groups have been identified comprising 200 farmers across three regions. The target segment is fresh consumption.

In Tanzania, trials will start this year, focussing on the coastal region and fresh consumption and links to the urban market.

All in all, the pilots are ongoing, farmer groups and varieties have been identified, varieties for the main trials are being multiplied and trait lists are ready.

Challenges.

In discussions on the ranking vs scoring challenge, it has been suggested that absolute scores should be given on top of ranking. The team resolved to give an absolute score and an open ended question for each farmer for each variety. In addition, anchoring observations will be done at 10% of the sites by breeders and food scientists.

The problem of how to stratify farmer selection will be dealt with by using geography and use in the first instance.

All traits across all partners and all datasets will be reviewed. These will be crosschecked with trait lists to ensure all product profile traits are present.

Hale's challenge for this meeting was how to get all this together into one selection index for the breeding program.

Roadmaps

Ismail Rabbi - IITA

Year 1 Accomplishments.

Continued population improvement work, par-

ticipated in first national collaborative trial planting with NR-CRI over 10 locations, quantitative assessment done for Gari and Fufu, TRICOT trials implemented in Nigeria, improvements in quality management, engagement with EiB initiatives. The breeding division harvested 5,375 plots, with 35 data variables, all uploaded onto Cassavabase. There are also clones in stage 4 UYT; data was collected from over 10 locations, phenotypes assessed in the selection index for CMD resistance, dry matter content, fresh root yield and processed food yield. A good number of clones which outperformed the local check for dry matter content were identified.

Improvements in Quality Control Management.

- Phenotyping:
  - Trial layouts designed on Cassavabase
  - Metadata and row-col information included in trial file (so that more sophisticated mixed models can be built to mitigate field variability)
  - All data recorded using PhenoApps
  - All plots barcoded
  - Plot images uploaded to Cassavabase
- Genotyping:
  - Selected seedlings and clones genotyped using either 18 or 36 QC/fingerprinting SNP panel. Over 280 trait-linked and fingerprinting SNPs converted from GBS to Allele Specific PCR assay with support of High Throughput Genotyping (HTPG) project

- Data Quality Control:
  - Plot-basis Heritability calculated by trial/location/trait
  - PhD student (Moshood Bakare) analyzing historical data for breeding pipeline optimization. Data curated for Cassavabase; 11,000 accessions genotyped using QC and trait linked markers to establish a database for fingerprint data.

Markers linked to traits discovered in historic populations that are now performing well in new populations have been generated. For example, fairly accurate accessions that will be resistant or susceptible can be predicted, we can also plot the distribution of vitamin A in white roots, intermediate and higher yellow root, and the interaction between the markers.

Germplasm exchange and pre-breeding.

- Germplasm exchange:
Seedling nursery of IITA and CIAT crosses (43 parents) in Hawaii was moved for clonal evaluation after a full season. 5607 seeds from 353 HS families—all genotyped using MAS and QC SNP panel—grown in seedling nursery have been advanced to CET

- Pre-breeding:
  - CBSD resistant clones from CIAT/Winter's Lab shared with Rwanda, Burundi, Tanzania, Uganda (February 2019).
  - CMD resistant clones sent to Vietnam and Thailand
  - Virus elimination in 46 priority East African breeding lines ongoing in collaboration with KEPHIS
  - Other sources of CBSD resistance available in Ibadan; 5CP used in crosses in Nigeria and all East African partners; CIAT/Stephan Winter's clones presently in multiplication (SAH); West African clones

screened in East Africa

Engagement with Excellence in Breeding

- Breeding Program Assessment Tool implemented (BPAT survey conducted with George Kotch and Eng Hwa from EiB)
- Received recommendations and responded (shared with all NextGen breeders)
- Hosted EIB Module 1 breeders' meeting (IITA [all hubs], NaCRRI, NRCRI, TARI, November 2018)
- Developed Breeding Program Improvement Plan. This will be shared across programs in the NextGen community

Goals for Year 2

- Implement the Breeding Program Improvement Plans
- Continue population improvement using GS
- Genotype GS C4B using DArTseq
- Harvest CET in June and generate GEBV for both phenotyped and unphenotyped cohorts
- Establish crossing block with top selections
- Re-evaluate our breeding/training population with emphasis on Product Profile Contracts and pre-breeding for CBSD resistance
- Work towards variety release (on-farm trials)
- Advance partnership collaborations (RTB-Foods, CASS, ACWP…)

Roadblocks encountered and solutions found

Roadblocks	Solutions found
Genotyping bottleneck	• DArTseq platform agreed on • Establish large new TP
Field quality issues	Carefully consider field history before planting
Grazing and security	Run trials in better locations (Ikenne and Ago-Owu instead of Ibadan)

Challenging the room

• Seamless and coherent integration of breeding program improvement plans from NextGen Cassava and Excellence in Breeding initiatives.

• Communicate all experiences and new knowledge in cassava breeding, genomics, phenotyping, genetics, food science etc. (in the form of a book?).

Joe Onyeka - NRCRI

Joe's talk focussed on variety development pipelines/progress on key traits, population development and improvement, progress on key mandate to deliver varieties, collaboration with the flowering team and, work done with the survey division.

Regarding variety development, there are 29 clones in UYT in late development phase across 4 locations in Nigeria. In 2020, some candidates will be identified from these for NCRP trials and release.

For sampling for genotyping, the populations of Latin American and Nigerian accessions at NRCRI were passed through QC and marker selection platforms to look for CMD2 chain. Sample sheets were delivered to Intertek for further analysis.

Results from GBS are being used to base breeding predictions for C3A population. The C3A population has 25 parents based on the modified selection index focusing on dry matter content, fresh root yield and CMD severity. Approximately 18,000 seedlings were generated from the 25 parental combinations for C3A population for 2019.

Because NRCRI works for the federal government of Nigeria, there is an expectation to release varieties. Regional trials fast tracked by GS are taking place across 10 agro-ecological zones managed by NextGen collaborators—NRCRI and IITA. Product pipeline contracts for traits were also developed after the EiB training.

Improvements in QC and management.

Jean-Luc did an analysis and recommended a few key steps be undertaken: Implementation of full barcoding for all trials and sampling operations; improving plot management; improved data management and curation in Cassavabase; reduced work load on key field actors to enable them give full attention to whatever they were managing. Improvements have since been observed in heritability in all key traits.

Experiments were also conducted with the flowering team this year. Using red light, pruning and hormone treatment, results from

CIAT's light experiments were replicated. Naturally flowering varieties had enhanced flowering and non-flowering varieties did not. Similarly, in the PGR, the combination of STS and BA either by spraying or petiole treatment enhanced flowering. In the pruning experiment, flowering in non-flowering varieties was observed. The study will be continued next year.

In terms of working with the survey division, some farmer participatory trials are being done to assess varieties for release. Currently three NextGen varieties have been released to farmers.
In terms of Gari yield, they compare favourably with all local checks and outperformed local checks in terms of peel loss.

Goals for Year 2.

Identify a candidate variety from the UYT for regional trails, maintain the observed heritability trajectory through improved quality control and, continued population improvement and testing for variety identification.

Roadblocks encountered and solutions found

Roadblocks	Solutions found
Delay on the decision and logistic associated with the DartSeq platform for genotyping	Decision to make use of GBS pending the resolution of the challenge
Lack of timely access to sufficient barcode sheet	Temporary reliance on the IITA NextGen team for bailout
Occasional encroachment by the herders in some locations	Engaging the community leaders

- When you have over 8,000 individuals comparable in terms of plant vigour and pest and diseases in the seedling nursery, how do you make a decision on what to select for genotyping when you have resources for genotyping?

- Following advice not to release more many varieties at the same time and yet national programs are usually judged by the number of varieties they release, how do we satisfy these two disparate approaches?

Questions.

Concern/Issue	Response
We know that CBSD resistance is not a trait. In the context of CBSD pre breeding, if you had a lot of varieties making it through your selection for the national trails, assuming there's a yield hit on a CBSD resistant variety, how would you convince the government to release that variety?	A couple of our sister programs in Nigeria are doing CBSD research. In a recent meeting with government officials in Abuja, we updated them on the progress of our CBSD pre breeding program in East Africa, and they are fully supportive of releasing some of these varieties in Nigeria.
Plant type and architecture are not included in your selection index. Have these been considered to be included as advantages for mechanised farming and adaptation to climate change?	This point was raised in a recent meeting with our breeders and we are going to review our selection index.

Challenging the room.

Robert Kawuki, NaCRRI.

Robert started off with a brief history of cassava use in Uganda from 1860 to date. He noted that project work at NaCRRI is about reorganising the breeding program, keeping in mind what is known, what has been learned from history, and the opportunities presented by the tools available today. "So we're working with the results from the survey in Uganda, the trade associated with those products, and profiling their basic traits, value added traits or future value added traits," he reported.

"We've been exploring ways to phenotype CBSD. The Makerere team developed a tool that computes a percentage of the cassava root covered by necrosis." Ways to improve phenotyping for end-user traits are also being explored. It was discovered that when NIRS is used to phenotype DMC, the estimates got depend on the part of the root sampled. Furthermore, when waxed roots are scanned after 3 days the results are very biased, it is advisable to use fresh or waxed samples not older than three days.

Increased use of Cassavabase, for example for tracking parental lines, was reported. In terms of germplasm exchange, germplasm from Latin America and West Africa has been received. In both materials, a reasonable amount of clones with CMD resistance have been identified. However, the CBSD results so far are inconclusive, so they will be tested again in the pilot phase.

Improvements in Quality control and management.

Barcodes are now being used in field plots, sample processing in all the steps from field to lab to data collection in NIRS, and dramatic improvements in heritability have been registered.

Goals for Year 2.

▪ Research Division
  • Continued refinement/validation of flowering technologies
  • Completion of metadata submission to Cassavabase (exploring ways of its practical use)
  • Upscale use of NIRS for critical end-user traits
  • Upscale prediction/validation studies

▪ Breeding Division
  • Product advancement (C2 to CET; C1 pVAC to AYT; C1 to UYT;)
  • Generation of C3 (white-fleshed) and C2 (pVAC) population
  • Genetic gain assessments
  • Refine product profiles and traits
  • Develop frameworks to guide pre-breeding

▪ Survey Division
  • Implement TRICOT
  • Explore 1000 minds study (typologies and trait rankings)

▪ Others
  • Fast-tracking procurement plans
  • Fast-tracking graduate thesis work
  • Communication plans (publications)
  • Continued retooling (scientists, students and technicians)

Roadblocks encountered and solution found.

Roadblocks	Solutions found
Sample processing in preparation of NIRS predictions	Mini experiments to guide decisions undertaken (plant position and storage effects)
Virus titre quantification in breeding trials	Discussions on titre quantifications still on-going; mini experiments proposed
Changes in genotyping platform	For Cassavabase, now working with three local persons with support from Cornell
Optimal utility of barcodes in field book	Retooling courses
Cassavabase support function (local staff departure)	

Challenging the room.

In our desire to "**Empower farmers through innovative, sustainable cassava breeding**"
1)   What don't we know about the farmer?
2)   What do we have to learn or re-learn?
3)   What can we do very well?
4)   What have we failed to do?

Questions

Concern/Issue	Response
In your process of continuous improvement, what tools or technologies don't you have at the moment that you think will help going forward?	Insufficient barcoding material for all the trials

Heneriko Kulembeka, TARI.

Heneriko provided updates

from the Tanzania program which joined NextGen in 2017.

Accomplishments.

▪ Cassava botanical seeds generated by TARI FOR Cycle 1 planting

▪ Introduction and preliminary field screening of five CBSD immune genotypes from CIAT. These have also been transferred to hotspot area to further test CBSD resistance in the field

▪ Capacity Building: Three PhD and 1 MSc. students recruited, conducted short term trainings on R, Cassavabase, Optimization of flowering. Two units of tractor and associated implements procured. Vehicle procurement nearing completion.

Improvements in quality control and management.

▪ Designing cassava trials and Field layout using Cassavabase

▪ Deployment of barcoding in cassava breeding trials for quality control

▪ Perfection and Routine Collection of all field data using Field Book

▪ Uploading data in Cassavabase

▪ Development and use of SOP for all stages in variety evaluation from Planting to harvesting.

Plans for Year 2.
▪ Establishment of Cycle 1 Seedling Nursery

▪ Genotyping of 55 parents for Quality Control

▪ Genotype, Phenotype Cycle 1 F1 progenies and GS (support on analysis)

▪ Improving breeding population for CBSD resistance using five CBSD immune clones from CIAT

▪ Evaluation in Advanced yield trial of 15

promising lines from Cycle 0.

▪ Import superior breeding lines Cycle 1 to cycle 3 from NaCRRI

▪ Establishment of pilot TRICOT (on-farm) trials

Roadblocks encountered and solutions found.

Roadblocks	Solutions found
Delay in drying of botanical seeds after maturity due to cool weather at Maruku	Synchronization of time of planting crossing blocks
Flooding at Chambezi caused loss of data	
Mole rats infestation in crossing block at Maruku damaged plants	Trapping
Poor sprouting rate of some CBSD immune clones (PER556, PER 226, COL2182)	

Challenging the room.

▪ Do we actually have CBSD markers ready for deployment?

▪ How soon do we start applying new phenotyping methods for CSBSD root necrosis and DMC determination?

Questions

Concern/Issue	Response
On phenotyping, does interaction with Module 1 and EiB help with your challenge?	Yes, we're interacting, my concern is about how soon we can perfect the methods currently in use to make them effective

Regarding field management, there's also been a fair amount of discussion in IITA. It highlights to us that there is an opportunity to improve research station management.	A word of caution regarding CBSD markers, there could be so many independent causes of resistance and we may have no markers for CBSD.
We have had so many presentations on marker validation. The topic of validation is as big as the QTL detection, we need to develop a strategy and have resources devoted to it as well other research on CBSD.	Stephan Winter suggested that instead of selecting perhaps the selection should focus on eliminating as soon as possible for susceptibility, so we focus more effort on what is left over.

Opening Ceremony

Titus Alicai, Program Leader-National Root Crops Program | NaCRRI

Titus welcomed all the guests and thanked the organizers for organizing a great meeting. He appreciated Cornell University for the support to the project and thanked the leadership at Cornell for choosing to work with NaCRRI. He noted that cassava is a very important crop to Uganda as majority of Uganda's population consume cassava. The crop also has a very bright future as a cash crop for example Titus informed participants, cassava is being manufactured into beer (Engule) as a way to improve its value chain.

At this "assembly of the best cassava breeders in the world", he highlighted a number of challenges to be addressed:

Pests and diseases was one the challenges he called the attention of the meeting to. Cassava Mosaic Disease (CMD) which had been a problem from the 1990s was now under control.

However, Cassava Brown Streak Disease (CBSD) spread by whiteflies is still widespread. The disease is very prevalent everywhere cassava is grown. He informed the meeting that there was stabilization of national incidents due to the tolerant and resistant varieties distributed by NARO.

The young and weak cassava seed system was the other challenge underscored. "There are many players who would want to help farmers but they inadvertently spread the disease," he said. To counter this, a seed system has been instituted. Standards for cassava and manuals for seed inspection and production have also been produced.

"NextGen has made a great impact through capacity building and developing systems for breeding and tools for data capture," he noted. The project has also helped in data capture, digital migration, and large scale data collection. This has helped cut the time it takes to develop a variety.

Titus concluded by reiterating the importance of the meeting and urged participants to reflect on the achievements and challenges and be clear on the way forward.

Prof. Ronnie Coffman-NextGen Project Principle Investigator | Cornell University

Prof. Coffman noted what a privilege and an honor it was for him to be present at this 7th annual meeting of the Next Generation Cassava

Breeding project.

He welcomed the chief guests: Prof. Joseph Obua, NARO Governing Chair representing the Minister of Agriculture; Dr. Godfrey Asea, Director, NaCRRI; and Dr. Titus Alicai, Head, National Root Crops Program, NaCRRI. He also welcomed all the distinguished scientists and students from NextGen. "I am impressed by your dedication and the progress you have made together over the last 6 years. You are all doing a great job for cassava, for Africa and for humanity," he praised.

The project PI extended a special welcome and vote of thanks to Jim Lorenzen, the program officer from the Bill & Melinda Gates Foundation (BMGF). He appreciated Jim's commitment and depth of understanding of a complex crop like cassava. "It is my understanding that the Bill & Melinda Gates Foundation has identified the NextGen Cassava project as one of the five things that makes them optimistic about Africa. That is a really nice commendation and we appreciate it," he said.

He further acknowledged the support of the Department for International Development and UK aid who were unfortunately not represented as they were urgently trying to honor commitments prior to BREXIT. Representatives from the media were encouraged to look out for the many great stories about cassava that deserve telling.

"The NextGen Cassava Breeding project—now in its 7th year—is a remarkable example of a successful collaborative partnership in agricultural development," Prof. Coffman stated adding that, "NextGen works with 11 institutional partners across seven countries on three continents and, to that—through the COPPs—we have added seven more African countries. Congratulations!"

The meeting learned that Cornell University and the other partners involved in NextGen Cassava celebrate this global partnership

of people who are working to generate the agricultural innovations for cassava that are needed to meet Africa's pressing food security challenges.

He commended Chiedozie Egesi for his leadership of this project along with Jean-Luc Jannink at Cornell, and the many scientists in the US and Africa who work on this project. He applauded the many students who study cassava today, who will inherit the breeding platforms going forward to improve cassava even further. Prof. Coffman also appreciated Canaan for facilitating this meeting and her leadership on the new project website which was getting launched that day.

Prof. Coffman shared briefly on plant breeding and its importance. "Many years ago, for a large conference of economists, I was asked to describe plant breeding for an audience who knew nothing about it. To prepare for it, I approached an economist friend and asked him what economists really hoped to achieve, what really makes them salivate? His reply was, we hope to improve total factor productivity (TFP)," he related.

TFP reflects the total economic cost of production per unit of output. It accounts for subsidies (transfers within the economy) and price changes (inflation). Improving TFP involves raising output per unit inputs (per hectare, per worker, per cubic foot water, etc.), reducing inputs per unit output, and adding value with constant prices.

Plant breeding contributes to all of this by manipulating the plants that collect radiant energy from the sun. Plant breeding is probably the foremost profession in TFP and is an essential public/private investment. Prof. Coffman asserted that it is important for the team to remind themselves of the value of the work they do as plant breeders, and to stand up for this profession as there are many people who do not understand its importance.

"One of our current challenges as plant breeders is to communicate the fundamental societal need for adapted genotypes developed through plant breeding, but based on the power of a genomics and systems-biology approach. Those concepts are difficult to understand for people who are not biologists. We should recognize that," he counseled.

He noted the expanding use of transgenic crops (which not everyone is happy about), anticipated 'edited' cultivars through CRISPR-CAS9 technologies, and the rising public skepticism and fear for the latter technology. "As plant breeders, please make sure you take every opportunity to defend the rights of people everywhere—especially in developing countries—to access the innovations you, as plant breeders, bring about. The future of food in Africa should not be decided by 'elites' in developed countries," Prof. Coffman advised.

Regarding the project, the meeting was informed that NextGen has been tasked with reimagining cassava. Cassava breeding is a lengthy process which in the past has taken up to a decade to release new varieties. "We are in the business of shortening breeding cycles. NextGen is succeeding at that," he said. Many cassava genotypes flower poorly which makes it difficult to make crosses. There is need for improved flowering and seed set. Limited germplasm exchange also necessitates greater integration of Latin American germplasm into African cassava breeding. NextGen is succeeding at both these things.

> **We are in the business of shortening breeding cycles. NextGen is succeeding at that.**

He noted that gender dynamics among stakeholders are important to consider in cassava

breeding and variety selection. NextGen is a leader in surveying stakeholders—both men and women—and incorporating feedback in the selection and delivery process.

"Data management is fundamentally important. We are succeeding at that through Cassava base," he reported.

Information exchange within the cassava research community is critically important. The project PI voiced the need for international platforms to facilitate communication and data exchange. "NextGen is succeeding with internal and external communications. And after 6 years, there is now a vibrant, internationally connected cassava breeding community that you should all feel a part of. So keep up the good networking," he added.

Guests were informed that NextGen is an important global network based on shared values around plant breeding and sustainable food production.

Prof. Coffman continued, "Norman Borlaug, the father of the Green Revolution, winner of the Nobel Peace Prize, and another one of my mentors, said: 'Take it to the farmer.' Today, Dr. Borlaug would include a gender component in that exhortation so it is more inclusive and effective: Make sure you survey the farmers—both men farmers and women farmers independently—to develop and distribute new varieties of cassava that can withstand biotic and a biotic stresses, that are high-yielding, and that incorporate various other characteristics deemed valuable by your stakeholders so that everyone equitably participates and shares the benefits."

He concluded by thank the NextGen team for listening to input from stakeholders and for addressing their priorities. He further appreciated the team for contributing to the project's shared mission as a plant breeding initiative, and looked forward to another great meeting and another great year.

Jim Lorenzen, Senior Program Officer | BMGF
Jim acknowledged all the delegates, scientists and invited guests present. He thanked the organizers and leaders of the NextGen project for the good work done and for recognizing the support of the Gates foundation, UK aid and DFID.

He urged the breeders to focus on coherent programming. He acknowledged that breeders face a lot of distractions from the donors and all stakeholders but encouraged them to focus on bringing products that have an impact on society even in the face of so many distractions like the chase after money.

"Be your own champion, of your own program," he advised. Jim urged the team to communicate where the incentives are not helpful, where they need help to do their job. He informed the delegates that the donors are willing to fairly fund projects that focus on impact.

Dr. Godfrey Asea, Director | NaCRRI

The NaCRRI director welcomed delegates to the 7th meeting of the NextGen Cassava Breeding Project. He also recognized and welcomed members of the EPAC. All delegates were appreciated for accepting the invite to come to Kampala.

He was excited to learn that the small holder farmer was the major beneficiary of the NextGen project. He thanked the scientists for the genetic gains on the project but also tasked them to put productivity gains into consideration.

He informed the meeting that as of November 2018, the Genetic Engineering Regulatory bill

had been passed by parliament and was only awaiting endorsement by the president. This is a success story for the NextGen project which has supported biosafety and biotechnology communication through the Uganda Biosciences Information Center (UBIC).

He challenged Barbara Zawedde and her team (UBIC) to continue educating people on the importance of biotechnology as a way of facilitating acceptance of new varieties of products of modern biotechnology that will be released onto the market.

Members were informed that Uganda is one of the four pilot centers for NIRS Programme. This is appreciated because it boosts Uganda's capacity for research and development.

He thanked all the donors especially BMGF for their commitment and support to NextGen and agricultural research and development in general.

Professor Joseph Obua, Chairman NARO Governing council.
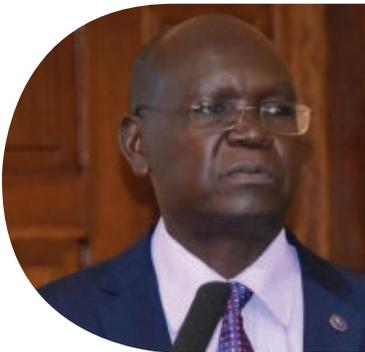
The NARO Council chair welcomed all the delegates to Uganda on behalf of the NARO governing council. He noted that Uganda has world class scientists, who are encouraged to participate in collaborative research. This, he said, increases on their knowledge and experiences hence making them better. He remarked that international collaboration gives international credibility to the agricultural research done in Uganda. He informed the delegates of NARO council's support for such collaborations.

Prof. Obua commended the NARO team, the scientists in Uganda for the good work in researching into methods of dealing with the challenges faced by farmers in the country. He thanked the delegates for gathering to discuss ways of improving food security in Uganda, and urged the partners to continue the good relationship.

He then delivered remarks from the Minister of Agriculture Animal Industry and Fisheries who he was also representing.

Remarks from the Minister of Agriculture Animal Industry and Fisheries

The Minister welcomed all delegates to the 7th NextGen Project annual meeting and thanked IITA, NARO and Cornell University for organizing the meeting. He recognized the long term partnership of Cornell and IITA and asked that it continues. He thanked the BMGF on behalf of the Government of Uganda for funding the project.

"The meeting provides a platform to look back and celebrate the successes of the project, and to look at developmental challenges affecting farmers. It also provides for the need to find realistic solutions to the challenges in the cassava industry," his speech

"The meeting provides a platform to look back and celebrate the successes of the project, and to look at developmental challenges affecting farmers. It also provides for the need to find realistic solutions to the challenges in the cassava industry

read in part.
Cassava is very important to Uganda because

it is consumed by majority of the population, but it has been greatly affected by CBSD. The Minister noted that he was informed that the project was intending to produce improved varieties that would help to deal with CBSD. He informed the delegates that the government has prioritized cassava as one of the crops to improve food security and nutrition, and applauded NextGen's efforts in dealing with constraints in cassava production.

The Minister acknowledged the support and contribution of UBIC in championing biosafety education in Uganda. He also reiterated that he has benefitted from the education campaigns carried out by UBIC.

He asked the delegates to ensure that their work ultimately should help improve cassava seed system, reduce postharvest losses and drag along the cassava value chain.

He wished meeting participants successful deliberations and officially opened the 7th NextGen Cassava Breeding Project Annual meeting.

NextGen Cassava Product Design and Management (Changing our views on how this works) | George Kotch, EiB

George's discussion was centered on providing a fundamental understanding of EiB's initiative on product design and management. He expounded on why the top five donors of the CGIAR support this initiative; what can be learned from high performing organizations; fundamental shifts in our ways of working including greater transparency, discipline and accountability; how products are designed as part of a variety replacement strategy; and a continuous improvement philosophy.

Use of tried and tested techniques to increase productivity and variety turnover thus greater impact, increased funding opportunities, collaborations, reduced stress, improved understanding, and formal linkages between different generations of product profiles were listed as expected outcomes of Module 1.

"Module 1 is about product design and product management, and also the transmission of the good work that is siloed in one centre to all the nodes in the network," George stated. He praised the good work he had seen in all the divisions and compared the survey division to product management teams in seed companies that take the output of the later stages of the breeding process to the early adopter and feed responses back to the breeders to improve their product profiles.

On the product profile process, the meeting learnt that the product profile functions as a contract between all stakeholders in a network to design and deliver market-focused products. The product profiles that have been put together are going to be reviewed in March by the donors and they will be highlighting areas for improvement. He explained that stage gates are decision making points of reference, and are therefore linked to product profiles and not independent of them.

He then spoke about variety replacement strategy in which variety replacement drives variety development. The market leading variety should be used as a benchmark for this process. "Breeding for the agro-climatic zone is not what the market seeks," he asserted. Variety Replacement Strategy is a product design and breeding strategy to replace the leading variety within the marketplace, in contrast to breeding for an agro-ecological zone.

George explained that EiB has been tasked with initiating product managers and is keen to see some within the CG system: people to assess traits and value returns. "There aren't any

dedicated product managers in the CG system at the moment and the cross-functional teams will take up that role," he announced.

In this scheme, the cross-functional team will set the product profile because they're closest to the customer, not the breeders. Breeders will be akin to an engineering team working on blueprints produced by the architectural team. It was important to realise that this system is designed to maximise breeding for variety replacement, to maintain a steady turnover of varieties and hence a significant upsurge in in economic value.

He also explained that when cross-functional teams set the profiles, it helps to mitigate the bias that a breeder might have to work within his expertise and ignore the opportunity to work on other traits. He defined a few key terms including product profile commitment, must-have traits, value added traits and future value added traits.

A product profile is an agreement that a breeder will come up with product to replace the leading variety in the marketplace with a specified period, usually 5 years. The EiB product replacement strategy tool was discussed. The meeting was informed that donors are interested to see product profiles; basic traits, target varieties, value added traits. The decision to fund depends on the overlap between project impact goals and donor impact goals.

The commitment to deliver a product within a timeframe also introduces a new level of accountability because the advancement process is linked to a product profile and the value is in using the stage gates to measure progress from design through to product release. It is a conceptual and operational model to move products from idea to launch. Ultimately, the process is also important when developing investment strategies, as it provides a one stop snapshot of where every variety is in the product profile pipeline. This also helps make decisions to allocate resources appropriately.

Questions.

Concern/Issue	Response
This model is good due to the independence of the decision making. So often in commercial seed companies the breeders and other divisions clash over what gets released on to market. The other point is that the stage gates have to relate to KPI's to measure advancement. It is the next step after implementing the stage gates approach.	
How does this approach fit in with national programs where there maybe already established procedures and priorities with regard to variety release?	The role of the product manager will be to communicate to the national programs the shared goal of impactful release. It doesn't make much sense to devote the resources we do, if we have no impact and this is same for all crops and all national programs.
Why do some of the stage gate pipelines have 5 stages and others 6?	Some crops have more stages than others and at the moment we're refining the system to include corn, potato and cassava. We intend to publish once we get through system outlets.
Why isn't assessment of variety performance and acceptability after release included in the pipeline?	After stage 6, the product is with the farmer, but all the stages have a checklist that will ultimately ensure that by release we will have a fair idea about performance and acceptability. Also if our donors can see the assessment we're doing at each of the stage gates, it is easier for them to release funds because it gives a snapshot of a highly functional organisation.
What is the importance of the profile to market access and how important is it that the varieties developed reach the farmer?	This system is all about achieving maximum impact by increasing variety turnover. It is about demand and market led breeding. Its real value is in designing what the end user requires.
On the differentiation of breeding for agro-climatic zones vs geographic zones, we're currently collecting a lot of information on farm types, can you share any ideas or experience that can help us fit this information into this model?	It has been suggested Module 1 is about behavioural modification.
By relinquishing power, the breeder increases his probability of designing impactful products.	
We have spoken about product replacement, are there opportunities to explore new market opportunities?	The focus now is on establishing the brand that drives sales and establishing a standard way of working. Then incrementally, we will think about our next generation of products.

The use of mixed models in clonal crop breeding | Hugo Campos

Hugo talked about the use of mixed models to analyse breeding data. Mixed models increase the heritability in a breeding program by 8-10% when compared with traditional statistics, and can be achieved with relatively little money. Issues raised from a traditional statistical approach to dealing with breeding data were; pervasiveness of unbalanced datasets, GxE noise confounded with genetic signal, overly simplistic assumptions, inability to use genetic insight from relatives, statistical stances somehow dissociated from genetic ones, and inability to extract full value for money from very expensive field datasets.

On Linear Mixed Models (LMMs), Charles Henderson laid the bases in the 1950s, animal breeders started using LMMs to assess generic merit in the 1970s, tree breeders in the 1980s, plant breeders in the 1990s. Hugo stressed that this was a very important learning topic for meeting participants.

Fixed and random effects of LMMs were explained at length. Whether a genotype is a fixed or random factor has very profound consequences on the information extracted from data using LMMs. If the overall objective is to select superior individuals, then the genotype is best treated as a random factor.

The main consequences of declaring a genotype as random effect is that genotypic predictions are obtained through Best Linear Unbiased Predictor (BLUP). BLUPs were developed for ranking and breeding in animal genetics. When BLUPs are used, one always gets shrinkage (abbreviation to the mean). The degree of shrinkage is closely related to heritability, a concept close to breeders' hearts.

"BLUPs is a tool we cannot do without because using BLUPs any breeder can make comparisons of populations and genotypes assessed in different environments and years. Using all the data available for a genotype enriches the information going into your prediction model," Hugo said. It also enables exploitation of information from relatives. The information on genetic variance and genetic parameters can be obtained from previous breeding trials which saves time and other resources. Currently, software and hardware to run BLUPs and mixed models is available for purchase.

Meeting participants were shown some examples from a single trial analysis for a trait in potatoes, where comparison of the results of traditional modelling missed some the best genotypes which were only captured thanks LMM. Modelling via LMM also impacts selection.

Multi Environmental Testing (MET) which aims to evaluate test genotypes and predict their expected responses to selection in a Target Population of Environments (TPE)—a subset of farms, future seasons and environments/geographies where new cultivars will be planted—was discussed.
The extension of this modelling to MET and TPE as they're becoming more relevant is key as focus shifts to product profiles. Hugo cautioned about the likelihood that all GxE, and therefore MET and TPE analyses, carry a substantial, unintended shortcoming; The default variance/covariance matrix—called Compound Symmetry—assumes that the genetic correlation between any pair of environments is the same, and that the genetic variance is constant across environments; but data sets hardly, if ever fulfill such expectations. Hugo informed the audience that mixed models maximize response to selection and

contribute to maximizing genetic gains within given TPEs. "Ceteris paribus, the use of mixed models will increase the likelihood of replacing current cultivars. Genetic prediction is the next application of LMMs," he said. The importance of getting a good grasp of LMM if one wanted to avoid a mechanistic approach to the work of genomic prediction was stressed.

He urged the project join forces to handle all cassava and RTB foods crop breeding data using MMLs because it will reduce costs and increase prediction efficiency.

He also recommended a book, "Genetic data analysis for plant and animal breeding" by Fikret Isik, James Holland and Christian Maltecca, which shares perspectives on how to use MMLs and other data analysis for breeders.

Regarding measuring genetic progress and gains, a few issues with genetic gains from historical sets of cultivars (ERA-like studies) were raised: performance of older genetics under current conditions may be misleading, and environmental conditions might have changed, confounding the impact of GxE thereby requiring specialized trials, at the expense of breeding resources.

Hawaii intercontinental nursery Roadmap | Peter Kulakow, IITA

Peter updated the meeting on accomplishments of the inter-continental germplasm exchange in Hawaii: A seedling nursery of 3,500 surviving plants was completed in Nigeria to

validate SNP markers for CMD2 resistance

and carotenoids. The plants are currently in clonal trial in Ikenne. Clones from IITA and CIAT are in quarantine in the USA. Planting of a crossing block for hybridization is expected in 2020. 30,000 seeds are ready for distribution to Vietnam, Thailand, Colombia, Nigeria and Uganda.

"This complements the work that has been done with Stephan Winter's lab except that in addition to moving germplasm under good phytosanitary conditions, we also have a virus free hybridization block, so we're moving botanical seed between continents which has been difficult in the past," he noted. Collaborators in Hawaii are the University of Hawaii, the USDA-ARS plant germplasm center in Hilo and the USDA APHIS plant quarantine in Beltsville, Maryland.

In the first year, over 12,000 seeds were produced from over 450 seedlings, and a significant portion of it moved to Nigeria. The rest is still in Hawaii ready for shipment to Colombia and Asia.

A seedling nursery was also built under screen house conditions in Ibadan, where all importation protocols were satisfied. Seed was also grown in it as an extra procedure. Plant observations were done before they went out to the field. The plants were established in June 2018, and 3 months after planting, some plants had developed CMD but a good number of healthy plants remain.

Basing on the CIAT open pollinated plants as an example, a high proportion of these had a disease rating of 4 and 5, mostly outcrosses to IITA genotypes in Hawaii. IITA open pollinated material was mostly CMD resistant and some evidence of hybridization with CIAT materials was observed. Peter reported that his team have some pedigrees with interesting material in terms of CBSD tolerance. This study did not use the most elite materials because it was a proof of concept.

He also showed some drone images which were part of the CASS project. IITA x CIAT full sibs were mostly doing well for CMD resistance. CIAT half sibs had a bit of infection while IITA half sibs were doing well.

Ismail Rabbi and his team have done the CMD and biofortification marker validation work for over 3500 seedlings, confirmed value of CMD markers for CMD resistance, and that trial has been advanced to clonal evaluation phase.

From the 2017-18 clonal crossing block seed harvest, 68 selected seedlings were plant-ed as clones in 2017. 2,677 full-sib family seeds have been produced from 151 unique cross combinations representing 66 of the 68 selected clones. Open pollinated seed was collected from 47 of the 68 clones: 15,113 seeds collected from 24 IITA-derived clones; 7,756 seeds collected from 23 CIAT-derived clones. Harvested seed is ready for distribution to NextGen partners in Africa, Asia and Latin America.

Phase 2 Status –Hawaii

USDA has worked with APHIS to determine regulatory parameters for introducing clones. Clones were identified at CIAT and IITA for introduction • Four CIAT clones were received in Beltsville, MD USA on July 13, 2018: GM4512-5 (High Carotenoids); SM3767-10 (High Carotenoids); COL1107 (CBSD Immune by Stephan Winter Lab); ECU183 (CBSD Immune by Stephan Winter Lab).

The following clones were received on July 6, 2018: IITA-TMS-IBA070593 (high carotenoids, CMD resistant); IITA-TMS-IBA061635 (high carotenoids, CMD resis-tant); IITA-TMS-IBA972205 (high starch, high NextGen breeding value, high flowering, highest group for CMD resistance); IITA-TMS-IBA980505 (highest group for CMD resistance).

On improvements to quality control and man-agement, Peter and his team plan to make use of Cassavabase's crossing management tool for all crossing working in Hawaii and also for barcoding of plots.

Goals for Year 2.

▪ Phytosanitary testing of clones begins in March 2019 in Beltsville, MD USA

▪ Potential provisional release to Hawaii for confined multiplication prior to completion of testing

▪ Target planting of Hawaii crossing block in December 2019 or January 2020

▪ Replant 30 selected clones from selected seedlings in April 2019

▪ Use these as additional CMD resistant parents when introduced clones are planting in December 2019 or January 2020.

▪ Consider introduction of additional seedling families from NextGen selection cycles for additional parents.

Roadblocks encountered and solutions found.

Roadblocks	Solutions found
Slow rate of introduc-tion of clones from African and Latin America through the APHIS System	Solution is patience and persistence, how-ever the process will result in streamlining for future introductions
Labor needed to make controlled crosses in Hawaii	Consider option of having a CIAT or IITA person stay during the crossing season to provide additional assistance

Challenging the room.

▪ Unique opportunity to rapidly help Asia manage the emerging CMD pandemic by providing a source for large amounts of CMD

resistant botanical seed. Patience is needed to achieve long term results. Not everything is fast.

▪ Analyze the most efficient, cost effective and rapid methods of germplasm exchange, accessibility and introgression

Questions.

Concern/Issue	Response
Have you learned anything in your studies about when CMD2 is not effective in predicting the value of your seedlings?	Ismail: We analysed the data on CIAT seedlings. We could predict susceptibility very well in the CIAT half sibs. Without the CMD2 allele, all the genotypes score 5 or 4. There were also a few from the CIAT subset that had the homozygous CMD2 for heterozygotes. These clones are in clonal trials right now, so we need a year's worth of validation data to determine if the clones are susceptible or resistant.
Is botanical seed from Africa accepted in Asia?	No.

Website Launch | Canaan Boyer and Samantha Hautea, Cornell University

Canaan and Samantha unveiled the new NextGen website developed with John Bakum, the project web designer. Key new features on the new site were highlighted. Guests were informed that a few changes can be made to the website and one of the great things about the new design is it is easier to update.

"We updated the website because the old website was mainly focussed on Phase 1 of the project and didn't reflect Phase 2 well. It was difficult to add new information to the old site because of the way it was built. It was also hard to find information, our partners we're not visible," reported Samantha.

Before the new website was built, a survey was conducted to gather input from the NextGen community with an aim of designing a more modern and mobile-friendly site. The survey also revealed that a lot of people use the site to tell people about the NextGen project. The old website had a lot language from the proposal document for Phase 1 of the project. Therefore, to make it more outward facing, more public-friendly language has been used on the new site.

"On the new homepage, we have tried not to use a single image from the old website. Our cache was somewhat limited. Ideally we'd like to have pictures of healthy cassava in a slideshow on the homepage," Canaan added. She requested the team to share any high quality, high resolution photos and information about where they were taken, who took the photos and these would be added to the gallery and, some used on the homepage.

On the main menu, there are a couple of subsections about what the project does. The developers wanted the main page to be a one stop shop, where visitors could access a lot of information without clicking on another page, with top down menus with a list and information where visitors can link to the areas of the site they're interested in.

To keep the site more active, a couple of

things were added: a section called cassava in the news, where stories are automatically generated and updated by a server; updating the project blog with the most recent entry; a section for project newsletters; and a link to the NextGen Twitter feed.

The header on every page has a link to media, a panel for Cassavabase and a link to their website. The footer on every page will show NextGen partner institutions and a link to their website. There's also a link to subscribe to the project newsletter.

The "what we do" top down menu introduces the sections with small blurbs about what each one is about. The text is taken from the project narrative showing what is hoped to be accomplished in Phase 2. This section also defines why cassava is a crop worth investing in.

The impact section describes project outputs to date, how GS has been implemented, and capacity building with students and partners. This will also be updated with new developments in the future.

A section on project structure and objectives, which describes the three divisions and gives a brief description of their functions is also included. There is a section for project documents where all documents on best procedures, learnings and any white papers developed will be shared.

"The 'who we are' section is our people page, reorganized so that people are no longer listed by institute and people have different tags now. So although you can still search by institute, we no longer have the traditional biographies attached. We decided to focus on the project and what everyone's role is in the project," Canaan announced. "What we have also done is when you look up a person, it will provide you with a link to their articles and we're going to add the option so you can have a URL linking to their bio from their institutional website," she added.

The 'where we work' section is different from the old version because it highlights the institutional partners NextGen works with. Each institutional partner will have a short blurb about the institution, link to their website and give a sense of what they do within the cassava family. This was done to ensure project partners are visible.

The media page is a one stop shop for resources to learn about our project. It will direct users to the project YouTube page for videos. One can also be able to access the NextGen photo archive and journal articles. Journal articles can also be searched by year of publication and subject matter. There are also quick links to the project blog.

Wrapping up, Samantha urged the team to try the different features and give feedback. "There's a link to an online form on the website, but you can also email us directly and let us know what you think," she said.

CBSD Roadmap | Edward Kanju, IITA

Edward started his talk by giving a brief history of breeding for CBSD in Uganda. "We started breeding for CBSD in 2004, when CBSD was first reported in Namulonge. The prevailing wisdom at the time was CBSD didn't spread to mid-altitude areas but was confined to coastal zones. Robert Kawuki from NARO asked for CBSD resistant germplasm from Tanzania and 5,000 seeds were sent to NARO and IITA," he narrated.

Out of 5,000 seeds introduced from Tanzania in 2004 (IITA Uganda), only three clones

combined high resistance/tolerance to CMD and CBSD along with moderately high yield and good cooking qualities. Only one (MM 2006/0130) was officially released in 2015 (NARO-CASS 2).

His presentation was centred on breeding for CBSD resistance at IITA-Uganda, CBSV and CBSD resistant lines, promising 5CP and Nigerian germplasm, CBSD immune cultivars from CIAT, BPAT recommendations and next steps as well as revised CBSD scoring for foliar symptoms.

Accomplishments.

In 2015, Robert Kawuki released NARO-CASS1—one of the best promising first generation CBSD tolerant lines for the mid-altitude areas. Out of the IITA breeding program, three clones—MM 2006/123, MM 2006/128 and MM 2006/130 were selected.

A new breeding program was started with the three clones and in 2015 seeds from these families were sent to Tanzania to test performance in the coastal zones. Five lines that were CBSV negative were identified. These were sent to Stephan Winter in Germany for challenging by grafting, and to Morag Ferguson at BeCA for cleaning, virus indexing and in-vitro conservation. They are now being evaluated under AYTs across 6 sites (two in eastern Tanzania and 4 in Lake Zone).
12 promising lines—all derivatives of the three clones, all CBSD resistant lines—which are due for virus testing by Robert Kawuki later this year were identified. One or two of the accessions are also showing promise for dry matter content and fresh root yield.

With the 5CP project, funded by BMGF, that run in 5 countries for 6 years, with trials in Malawi, Mozambique, Uganda and Tanzania, four clones were selected for national performance trials in Tanzania and are scheduled for official release. Also the material from Ibadan has been challenged by Stephan Winter's lab

and 2 clones have been identified as very good.

In Uganda, of the 500 lines introduced in the 1990s, the best two for CBSD resistance have been selected for breeding.

Improvements in quality control and management.

BPAT recommendations on virus screening:

- The cassava team should consider complementing the current field based virus resistance/tolerance screening methods with improved field and controlled environment screening methods and diagnostics

- Identify germplasm with resistance to white fly infection in the absence of virus. For this purpose, use should be made of CIAT material that is reported to have resistance to whitefly.

Plans for Year II.

- Send best CBSV resistant breeding lines to Stephan Winter's lab in Germany for challenging by grafting.
- Field and screenhouse grafting trials for CBSV resistant lines
- Develop semi-inbred lines and F1s among the CBSV-resistant lines
- Develop F1s between CIAT cultivars and CBSD resistant/tolerant lines
- Identify germplasm with resistance to whitefly. (Use both CIAT material and African cultivars that are reported to have resistance) Regional distribution of best CBSV resistant lines and seed families, especially to interested CoPP member countries
- Genetic and environmental factors that influence CBSD Symptoms were discussed. These included different QTLs for root

necrosis and foliar symptoms. Also, the strong influence of the environment on the expression of CBSD root necrosis can be attributed to variety susceptibility levels, predominant virus species, and climatic factors that influence the abundance of the whitefly vectors (OkulValentor et al., 2018).

Roadblocks encountered and solutions found.

Roadblocks	Solutions found
High cost of quantifying virus titre	
Drought –poor flowering and seed set (Serere, Uganda)	
Molecular markers need validation	
Drought –poor flowering and seed set (Serere, Uganda)	
Lack of financial resources for virus cleaning and indexing –important for regional exchange of germplasm	
Inadequate human resources	

Challenging the room

▪ CBSD markers for CBSD tolerance have been developed but not validated. Virus resistant lines are now a reality. Should we go ahead and validate the markers?

▪ We need to elucidate if the virus resistant QTLs are unique. This falls under discovery. Should we go ahead and do it?

Questions.

Concern/Issue	Response
Routine field screening is very important because there are quite a lot of viruses circulating at Namulonge. There is need to prioritize screening at Namulonge.	Some promising lines are being trialled in whitefly hotspots in Tanzania. In just a season it will be possible to tell if a variety is resistant or not.
Is it possible to send some staff for training in grafting techniques so samples don't have to be sent to Germany?	Discussions are ongoing and a new PhD student who will hopefully backstop at this end has joined the team. However, Kanju's team are eager to maintain the relationship with Stephan Winter's lab as it afforded them access to very advanced technological solutions.

Image Phenotyping Roadmap | Joyce Nakatumba

Joyce began by explaining that the broad strategy for the AIR lab was to integrate cutting edge computational tools/techniques with good impactful problems. The lab is currently focused on two main issues, lack of expert labor which brings about the need to automate, and scarce quantities of actionable data.

She also explained how AIR fits in with NextGen Phase 2. 'Increased efficiency and quality of NextGen breeding programs leads to improved genetic gain for target pipelines' was listed as a primary outcome for Next-

Gen Phase 2. The secondary outcome will be adoption of technological advances, increases breeding efficiency in the partner breeding programs.

The major output from AIR lab will be PhenoApps - Cassavabase integration. This will ensure communication between Cassavabase and PhenoApps developers with breeders match tool development to meet breeders' needs.

Accomplishments in Year 1.

The main tasks were to automate cassava necrosis phenotyping more efficiently than current methods and also to seamlessly integrate this into Cassavabase.

Data was collected using android phones with the FieldBook application over two phases. The FieldBook application was used to capture two traits i.e. a picture of the cross-section of each root and the respective CBSD scores given by an expert from NaCRRI. 6,777 images of cassava root cross-sections and their respective CBSD scores were collected. The data collection process was explained to the audience. A summary of the data analysis and results were also presented.

On a technology development front, mobile phone and desktop versions of phenotyping applications (whitefly count, necrosis detection, PPD detection) have been built. The lab is experimenting with web online "as-a-service" models of offering services to improve the computer vision models. Working prototype scripts to connect to Cassavabase are also ready. The team participated in a hackathon where they updated BrAPI spec to include images (https://brapi.docs.apiary.io/#reference/images) in BrAPI V1.3. so that images can be uploaded onto Cassavabase.

Improvements in Quality control and management.

The team integrated their standalone application to work seamlessly with FieldBook, made app content BrAPI spec compliant for taking plot field images and their upload and integration to Cassavabase.

Goals for Year 2.

▪ User training, field tests and deployment on new routines for uploading image data.

▪ Process mining of app usage logs - to understand the structures that support phenotyping - track PhenoApps field usage (are there routines that can be made redundant by application of technology ?)

▪ Better computing models for automated and semi-automated phenotyping through collaborations with different stakeholders.

▪ Image upload and integration with Cassavabase/BrAPI

▪ Use GPS-RTK to enable mobile device identification of plots being phenotyped.

▪ Automatically detect disease viral load in new plant traits in the breeders garden.

Roadblocks encountered and solutions found.

Roadblocks	Solutions found
Difficulty ensuring efficient image capture of necrotic cassava root images taken in situ, i.e. with a noisy background.	Better deep learning algorithms for segmentation of cassava root cross-section images (Mask-RCNN with tensorflow and keras)
Distinguishing between a CBSD root affected with necrosis and dirty/muddy root. Yellow background vs. white background	Use of a common background, we tried placing the root cross sections onto black background.

Challenging the room.

▪ Are there any repetitive tasks that the breeders feel we can animate?
▪ How can phenotyping workload in the breeding program be refined based on integration of technology?

Questions.

Concern/Issue	Response
How are you doing with detecting viral load from images of the whole plant? And have you tried using saliency analysis shown where CNN has learnt?	We have done some work in Cassavabase on based on leaf colour and roots for CMD. We have also done some work in spectrometry to tell viral load in the plant before it manifests. We've also infected healthy plants and then studied the course of infection using spectrometry. Because of low spectrometry our studies were confined to the leaves only.

We're also using deep learning to study DNA sequences. There are now tools to figure out where the machine is learning and inform us where we should be looking. |
Is it possible to send some staff for training in grafting techniques so samples don't have to be sent to Germany?	Discussions are ongoing and a new PhD student who will hopefully backstop at this end has joined the team. However, Kanju's team are eager to maintain the relationship with Stephan Winter's lab as it afforded them access to very advanced technological solutions.
Considering the variations in how disease manifests across genotypes, how do you use this data?	The tool at the moment will measure the concentration of the necrosis in the tuber. That has to be what the breeder wants to measure. But that is something worth thinking about.
Is your platform starting to show you things like polymorphic variation or it just classifying things better?	At the moment it is just helping the breeder classify better but the end goal is to have deep learning incorporated into as many aspects of the breeder's work as possible.

Biotechnology and biosafety Roadmap | Barbara Zawedde:

Barbara presented on biotechnology and biosafety education, efforts to ensure a positive environment for scientific work and education of young scientists in Uganda through stakeholder engagements.

Accomplishments for Year 1.

One key accomplishment was passage by Parliament of Uganda, of the Genetic Engineering Regulatory (GER) Bill, 2018. Significant effort was invested in engaging policy makers to apprise them of the relevant legislation critical to the advancement of science and technology in Uganda. Barbara voiced the need for continued effort to build more grassroots champions

to educate their fellow citizens about the benefits of NextGen work. The various strategies used to achieve this milestone were discussed.

Over 300 champions were empowered to support policy, and accelerate adoption of improved varieties/agricultural technologies.

Barabara reported progress towards integration of modern biotech into the national agriculture curriculum for secondary schools. Her team has been working to integrate modern biosciences into the secondary school curriculum and have been asked to develop teaching materials. To this end they also hosted a week-long internship course for teachers to learn on such topics molecular biology, sampling techniques, and field work. Furthermore, a booklet was published about the experiences of all the people that have been engaged through such internships describing their experience and how they intend to use the knowledge gained.

Over 300 champions were empowered to support policy, and accelerate adoption of improved varieties

Other publications highlighted included an article by Nassib Mugwanya in the breakthrough journal. This article made a case for why traditional agricultural practices cannot transform African agriculture. Also, working in collaboration with colleagues at the Science and Technology ministry, the National Council for Science and Technology, and the Program for Biosafety Systems, another paper was published in the Frontiers in Bioengineering and Biotechnology journal. The article entitled 'Readiness for Environmental Release of Genetically Engineered (GE) Plants in Uganda' scanned the environment in Uganda to understand how the country could best prepare itself for environmental release of GE crops.

Goals for Year 2.

▪ Engagements with the Ministry responsible for GER Act (2018) and other relevant MDAs

▪ Focus most efforts to support the commercialization pathway for NARO biotech products

▪ Continuous engagements of built champions to increase appreciation and support for agri-biotech applications for national development

▪ Support developing and piloting a modern biotechnology training manual for secondary schools

Roadblocks encountered and solutions found

Roadblocks	Solutions found
Strong activism against use of agri-biotech	High policy-level engagement Building grassroots champions
Semi-functional legislative environment (e.g. the GER Act was passed with a strict liability clause)	Continue engaging relevant legal fraternities, MDAs and development partners to work together towards an amendment of the Act.

Challenging the room.

Science communication is critical to technology uptake. All scientists are challenged to become champions for their work, especially to non-scientific audiences.

Questions.

Concern/Issue	Response
About the title of the article in breakthrough journal; agroecology is not old science. It is just as vibrant and cutting edge a science as molecular genetics with great promise for increasing the efficiency in agricultural production, representing it a such may make detractors rather than allies of those scientists.	The main argument of the article is centred around the classic definition of agroecology which models itself explicitly on traditional farming methods.
Is your work limited to Uganda or do you coordinate with other countries?	We also work with other countries through programs like ISAAA and the Alliance for science.
On the agroecology article: Agroecology is a science which often incorporates the best available technology and information to address modern agricultural challenges including climate change. Communicating our relationship is key. Similar issues were experienced while communicating biological genetics which led to decades of problems. We need to communicate the commonalties in our goal to solve similar challenges.	
To what extent are you going beyond science and into tools from behavioural science like change management, risk management to combat confirmation bias? Studies have shown that providing more information does not necessarily budge people from their positions, in fact it sometimes serves to entrench them further in their positions.	We actually spend most of the time during our engagements communicating the benefits rather the hard science.

Buckler Lab Roadmap | Ed Buckler

Year 1 accomplishments.

▪ Development of Practical Haplotype Graph software to enable inputting any genotyping system data and output a uniform set of genotypes

▪ Evaluation of rAmpSeq genotyping technology in maize & sorghum to inform design of cassava assays

▪ Comparison of DARTseq with GBS and development of pipeline to impute

▪ Developed a pipeline for assembly of genomes using Nanopore sequencing technology

Improvements in quality control and management

▪ Problems with imputation between pipelines investigated. Sample mix-up was detected. The team is working on the difference in calls in the different sequence genotyping platforms and some of the coordinate system issues.

▪ SNP calls between Whole Genome sequencing, GBS, and DArT do not agree. Data comparisons between GBS and DArT uncovered that a substantial population of samples were just not the same. 80% looked good but 20% of the lines looked like they had been swapped. "We are trying to figure out at what step it's happening and continue to test and evaluate and re-genotype to make sure this level of error doesn't recur", Edward reported. In terms of imputation, the accuracy is now pretty good for any genomic selection purpose.

Roadblocks encountered and solutions found.

Roadblocks	Solutions found
▪ Staffing challenges; loss of long standing member of the team and also family leave for molecular director, difficulty ▪ Visa applications to US very slow	Evan Long –1st year graduate student started. Nisha Singh postdoc (designed genotyping platforms for 3 species before) joined the team
rAmpSeq testing delayed	Imputation of GBS to DArT now works after some filtering

Goals for Year 2.

▪ Integrate genotyping with EiB Module 3 (some AmpSeq with potential pathway to rAmpSeq) to create a robust system
▪ Impute all GBS, DArT, WGS to Cassava Build 7
▪ Build PHG for all above data
▪ Work with Cassavabase on pedigree verification
▪ Initial sequencing and assembly of additional key cassava clones (Evaluate imputation of rare alleles) in order to populate PHG.

▪ Initial sequencing and assembly of Euphorbiaceae with the goal of quantifying deleterious mutations

Challenging the room.

▪ Deleterious mutations are a key problem in cassava, the vegetative propagation of the species over millennia has built up high levels of genetic load. We need to discuss the most efficient approaches for purging that load.

▪ Should breeding cycles specifically include a single selfing generation? Should deleterious mutation burden be added to the selection index? It is still unclear how to estimate that burden accurately enough but this could be solved next year.

▪ How do we get cooking quality high enough for various varieties, for all the environments? The team is considering emulating different breeding designs where there are breeding pools that are used for selection on environmental adaptation and for quality, then pull the hybrids out these two pools.

▪ Also on breeding cycles, self-selection on vigour followed by alternation with a cross then selection of a target trait might help fast track GS and purge load. Selecting on vigor means not relying on genomics models thus progressing really fast.

Questions.

Concern/Issue	Response
On plant vigor vs root yield as a means of selection at S1 level: combining selfing with GS is a good tool in selection for in built tolerance because you'll have data on homozygosity. You are not going to select the homozygous plant.	The main drawback to selfing all the way down is you get a big drop in S1 generation, from 100% to 50%. In subsequent generations drops of 50% to 25%; 25% to 12.5% and so on. This is time consuming and very difficult without giving you a big gain. We should consider maximizing photosynthetic apparatus to judge vigor.
There are cases where more heterozygosity than expected is observed. Almost all CMD2 released varieties in Nigeria are heterozygous. Protective inbreeding was done along with a lot of filtering to try and uncover the expected 50% reduction in heterozygosity with each generation. This was not uncovered. Is it possible that there is some structural heterozygosity or difficulty in getting homozygosity?	We've had marker genotyping technology issues that are showing up all the duplications and other noise making. It looks like there is more heterozygosity than there actually is. Also, mutation allows 1 or 2 copies of the gene to keep it going. We're making a few more assemblies to help us clean up the genome, and deal with true heterozygosity on the genotype side and then the question, "is there some strong selection of seeds with lots of abortions that allow more heterozygosity you would expect?" can be posed.
A couple of thoughts on pedigree verification and verifying genotypes: Have you considered building into Cassavabase logic that it is presented with a new genotype against pedigree and a vote of confidence to both data points? Build a confidence score for data points.	
What do you think about the glaziovii chunks in the genome in relation to selfing with heterozygosity?	Generally, I am a big fan of breaking up and recombining as fast as you can. In a lot of breeding we're limited by our ability to break and recombine these segments. I think we ought to simulate more.
What kind of road map / timelines do you have for sequencing a dozen species of euphorbiaceae?	It will depend on cost, and how well we deal with issues surrounding movement of germplasm between states, plan to source locally.
Regarding selfing for purging, when we have tried simulation, the results suggest it isn't efficient. Spend a year selfing and you don't come out ahead. Perhaps assaying the plant in the first 3 months then selecting on tolerance to inbreeding is less important than high yield, depends less on genetic correlation between tolerance to inbreeding and performance as an outcross if that correlation is not particularly high.	If we breed with 2 pools, we can push different deleterious material into different pools, maintain the same load on both sides. Hopefully that should help.
A lot of work has been done on flowering, a bottleneck not only for genomic selection but breeding in general. The next bottleneck to be looked at is recombination. Considering how much time is spent on crossing over and effects in cycle S4, and effect of environmental factors on recombination. We should invest more time and money to find ways to address this.	

Embrapa Roadmap | Eder de Oliveira
Year 1 Accomplishments.

In breeding and GS, DArTSeq markers were used to select clones for crosses and advancement in the breeding program at Embrapa. 98 Cycle 1 parents were selected for crosses to generate second cycle. 16% flowering currently recorded in the field. Crossing to start next month. 823 clones were selected for clonal evaluation trials, divided into 20 blocks, each with three checks and parents. Evaluation of the training population of 900 plants both for productivity and quality traits was concluded.

Trait linked markers to use for selection were also identified. In collaboration with Cornell, GWAS was used to find genetic regions associated with cyanide composition in cassava. A strong peak was found on chromosome 16 and a small peak on chromosome 14. A candidate gene with no synonymous mutation was also isolated. This SNP is linked to a protein associated with cyanide detoxification in other crops. "It seems like we have some biological evidence for the variation of the cyanide component in our germplasm. Our next step is allele mining of this trait and validation of this SNP in our germplasm for future use in sweet cassava," Oliveira noted.

Time was also spent on leaf bud propagation to increase multiplication efficiency—a strategy developed by the CIAT team. Some modifications and adaptations were made to the strategy to simplify it for future use at Cassavabase level. Using a chemical developed by Embrapa in partnership with Syngenta foundation, 20 plants can be produced from a single stem.

In phenotyping, the NIRS prediction tool is being used for dry matter content and starch. Higher prediction accuracy has been achieved for dry matter than starch. More data is being received and the team hopes to increase prediction accuracy going forward.

The team at Embrapa have also used un-manned aerial vehicles with multi-spectral cameras to analyse early traits like leaf vegetation index, disease damage, plant height, and ground coverage ability. These are not key traits for the breeding program but in Brazil, farmers are interested in ground coverage ability because it is a factor in the cost of production, especially in weed control.

Preliminary results from the work with the drones suggest a variation of heritability depending on when after planting the evaluation is done. However, good heritability in some traits can be estimated, but the values that have been used so far have been automatically generated thus the need for more time to customise this technology for the NextGen breeding program.

Regarding germplasm development, some genotyping for bacterial blight and anthracnose was done. 279 clones were evaluated and the top 26 selected. For drought tolerance, 120 clones were evaluated in semi-arid conditions and the top 23 clones selected.

For germplasm exchange, 98 clones were sent to Stephan Winter's lab and should be available for sharing with partners. Also, legal procedures for germplasm exchange were revised by the Brazilian Genetic Heritage Management Council (CGen). NextGen project was registered in CGen; a new form of Material Transfer Term available; and approximately 3000 seeds of 11 wild species will be shipped. Progress being made with the application to share this material with the project.

Oliveira further reported that, "In flowering experiments, we evaluated our germplasm to correlate flowering phenology with climatic factors, to characterize genotypes for crossing and genomic studies. our 2017 results have been revised and submitted for publication." The second year of evaluation started in September 2018.

Training in flowering induction was also undertaken. "Our doctoral student, Leonardo Souza, is going to defend his thesis on this

theme. He has also published a paper in Scientia Horticulturae.

Improvements in Quality control and management.

▪ Designed all trials on Cassavabase in order to integrate the field data collection into the database

▪ Plots well labelled using PhenoApps, especially Fieldbook and Coordinate. Design and labelling was done to make data collection (phenotypic and genotypic) easy

▪ Updated existing phenotypic data on Cassavabase and applied for NextGen trials

▪ 4) Team members trained on data collection (different steps of field trials). Trials and clones labelled before planting to avoid clones mixing

Goals for Year 2.

▪ Breeding and genomic selection
  • Crossing to generate GS-C2 population and nursery trial implemented
  • DArTseqLD(or alternative method) genotyping of GS-C2
  • Evaluation and selection of the GS-C1 CET, and GS-C1 PYT in the field
  • Validate markers for MAS implementation to cyanide component

▪ Phenotyping
  • NIRS prediction for DMC, cooking quality, starch and carotenoid content
  • UAV analysis for early cassava phenotyping (plant height, area covered by leaves, mite severity and the spread of canopy)
Germplasm development
  • Continuing the germplasm character-

ization for resistance to shoot disease and drought tolerance
▪ Germplasm exchange
  • In vitro propagation of the GS-C1 parents to ship them to Stephan Winter Lab
  • Germplasm exchange of wild species implemented
▪ Flowering studies
  • Continuing the germplasm characterization for flowering
  • Validate the photoperiod extension and PGR application in field crosses

Roadblocks encountered and solutions found

Roadblocks	Solutions found
Low annual rainfall (short period for planting)	Use irrigation system in the first 3 months after planting
Long process for germplasm exchange	
Initial issues to operate new equipment (Scio) and to access the data	Discussions with NextGen team (Mike's Gore team, Jenna) to have access to some SOP
Issues of hiring staff (field assistant)	

Challenging the room.

Based on the fact that NextGen is working on several traits and methodologies for increasing the ability to develop new varieties, are there other research areas, not covered by this presentation, in which Embrapa can strengthen its R&D collaboration with other breeding programs?

EPAC Challenge Talk | David Meyer

David applauded project accomplishments in Year 1, despite the challenges faced and said this was a sign that things are coming together. "It has also been remarkable that everyone is embracing the Cassava Inc. mentality and also that the farmer has been the focus of our talks. It is important that we keep in mind who we're doing all this for; not just genetic gains but adopted genetic gain," he added.

He was amazed to watch the convergence of effort in a team so big, and was excited and confident that this team will achieve its goals. He congratulated the team on this huge turning point in their journey. "Right as we're adopting the Cassava inc. mentality, EiB and BPAT reporting, the product profiles are coming along just at the perfect time and all the advice you have received from EPAC coalescing," David noted.

He further congratulated the breeding teams whose reports indicated where the material was in the pipeline stage gates and every program knew exactly where they were. He was happy the genotyping challenge has also been solved which is a huge accomplishment.

"Qchamps also did a tremendous amount of work and the attitude with which they were received was fantastic. The ownership of your work is just pleasing to see," he related. David was also pleased by how much science and applied science there is in the flowering studies—from proof of concept to implementation. Every tool comes through the five stages: discovery, proof of concept, implementation, validation, and stabilization. Stabilization is the key step, and that is starting to be evident. David commended the survey team for "turning chaos into knowledge." He was also full of praise for the eagerness and willingness in the workshops to explore new ways to do things with high throughput tools. "Where others would be talking about creating or discovering a tool, we are talking about implementation,"

he added. Further, EPAC is happy to see a lot of workshops between the research and discovery of the tool and those who will use them, whence "the magic happens."

Collaboration across locations, shared learning, strong engagement and impact by EiB, COPP members and all the partners was applauded. The tremendous job by the Cassavabase team in thinking about the issues brought up to them by the users and working to fix them was praised. "In metrics and tracking, the feeling in the room has been to embrace the data and find ways to understand what that means for our journey," he noted.

David was invigorated to see young scientists and students as well as all the new faces in this year's meeting as these are signs that the project is thinking about its sustainability.

"All the divisions, survey, breeding and research are all doing great work individually but it is obvious we're pulling in the same direction, which is powerful," he said.

He talked about the challenges set in 2018 and updated the meeting on the status of these challenges.

Steps taken to ensure sustainable cassava breeding in Africa was scored orange because although the project had a really good year, it is a step in the journey and a lot of work remains to be done.

What steps could we take as team to improve communication? We scored this yellow. The website, sharing ideas are going really well, but there is always room for improvement. As part of team, as you think about your role, think how it affects what people do two steps down the process and also how what people do two steps up the process affects you.

The disaster scenario: 'If CBSD struck west Africa and 40% of the farmers were affected, what do you wish you had done differently

now?' was also scored orange. Good progress was noted but it is so important that the focus on this issue is maintained.

The EPAC was generally very pleased with the response to the challenges and happy to say that the project is doing better than expected. "As I think about where we have got to and where we need to get over the next three years, I am convinced that the collective wisdom in this room will be equal to the challenges that lie ahead of us because I see and hear passion for our project," he concluded.

EPAC challenge discussion

Issue/Concern	Response
Regarding the last challenge to be mindful of overwhelming breeders with new initiatives, does anyone have any ideas about how we could structure it to make it easier for the breeders?	Everyone has to be their own advocate. The general tendency is to accept tasks but it is really important to say "I don't know how I can do that unless you take something else off my plate". We need to sit down together and prioritise. The other side of this is leaders here should encourage and facilitate these conversations.
On communication, it is impressive how much the team has used the Slack channel, leaders' meetings and workshops. It has really helped the success of the team that for example Fola has designed workshops to socialize Cassavabase in IITA and the COPP countries. Also the amount of communication when the genotyping challenge was addressed was commendable. Everyone on the project is encouraged to take more advantage of the communication channels available and also to think of ways to improve our external communications. It is also remarkable how much Barbara Zawedde has achieved. It also helps us to know that all these new initiatives share the same goal, they're essentially the same thing.	Communication is just as much about what you say to each other as it is about how you do it. It has to be in a safe, defensiveness-free environment. That is what helps learning and problem solving.
A good point was raised about prioritization although it is hard to get a good sense of how much money or time is spent in each breeding program on what. How can we go about sharing that sort of information within the program?	The EPAC team spoke about the product portfolio and strategic resource allocation and how to measure and adjust.
A big proportion of the resources have been spent in Africa and in breeding. Also a comment on the first challenge; when we think about product profiles and portfolio management, specifically those concerned with food quality and all the tools we use like Scio and the portable NIRS, at what stage gates should we deploy what tool? What traits should we be breeding for? We need to define timelines to answer these questions.	

We (Syngenta) have the best quality lab in North America, so that our competitors contract us to build their labs. That is how good our technicians and engineers are. The one drawback to all this is in advancement meetings, the quality group has veto power—something breeders are not happy about. There are other groups that also have veto power. For hybrid wheat the seed production research group has veto power because no matter how good a hybrid is, if they can't produce it, they can't sell it. This is just to highlight that the process George Kotch is starting has a lot of meaning for Cassava Inc. and for our professional development. I (Carlos Iglesias) spoke recently at the Africa Yam conference on the importance of intra-functional collaboration for variety development. Long gone is the time when a single person could deliver a variety successfully. I titled the talk "It takes a village," because it does take a village.

As we continue to work on defining the best tools to make decisions, it is no excuse for not knowing what the rules of the game are today. The rules may change as we get more information and tools, but there should be a defined set of procedures for the basis on which decisions can be made today.
Who should have veto power in a system with cross functional teams making decisions?

In the wheat business, which is very similar to cassava, the way we make money is by releasing better varieties every so often. Farmers buy the seeds based on these improvements, so breeders bring to the advancement process what they think will make it to market. Described briefly, the selection process: from thousands of genotypes we select the best 100 for protein using NIRS, use a micro-mill to select the best 50 for flour yield, from those we chose the best 10 using mixo-graph and brabinder's characterisation for starch along with micromill. Finally, we do a full bake. We do not incorporate thousands of loaves, we don't even design tools to try and mimic that, we just whittle it down through these stages until we have a manageable amount for a full bake.

Perhaps we should explore alternative ways to concentrating veto power by defining breeding criteria in terms that are personality neutral, say for Gari a minimum standard for dry matter, a minimum standard of beta carotene or in the case of fresh roots, less than 20 mins boiling time. There are parameters we can use to define these characteristics than can be easily agreed upon.	Unfortunately, there isn't an ideotype in cassava. It is a fine balancing act to replace the best product in the market with the best product we have. Often in cassava, yield and quality aren't positively correlated.
Thinking about how good it would be to release as soon as possible but there is potentially going to be a trade-off between how soon we can release and how good our first product is. We have some better clones coming through but if our cross functional team think they aren't good enough to make a splash in the market, what happens? Any thoughts?	• It depends on the brand you choose as a program. You can put everything you have on the market or put out quality. In the end you will be defined by your brand. There are many brands that dump on the market and lose credibility and market share over time.

• It also comes down to managing expectations. If you believe that your first launch is not going to be the greatest thing out there but better than what is out or a step in that direction, then communicate it that way. It is important that your first launch isn't a failure.

• It's not so much what you release but also about how you release. Cross your t's and dot your i's to make sure you are not surprised by any late developments when it is in farmer's fields.

• The launch is a point in time, the most important thing is the pipeline you have. You need to ensure that as your product profile moves through the stages, the second generation is better than the first, third better the second and so on.

• In Tanzania, we have two big markets; fresh use and flour for local bread. They have different quality traits. We also found that there are two new markets; in starch manufacturing and brewery. We as breeders need to understand that beyond food security there are emerging markets in industrial use and to bear that in mind in our prioritisation. |

Product profiles and project pipeline is a journey. Unfortunately, there isn't a single product profile that can match all the uses. So we need a product portfolio for the different uses then match that to the end user's need.

▪ 15 years ago when breeders started to form companies, the issues were exactly the same; there wasn't enough money and clarity. What happened then was instead of starting with molecular breeding across the board, a very strategic decision was made; only five programs implemented molecular breeding because by and large the issues are not about the markers or the bioinformatics, they're about day to day operational issues. The experience in corn was very pragmatic. The breeders with an entrepreneurial perspective were happy to fail cheaply and quickly, and once enough learning from their mistakes was accumulated, that wisdom was shared with the other breeding programs. And the same thing happened with developing technologies. There are commonalities here with the flowering technology in cassava. They define a few programs that will deal with the issues in the prototype and once the issues are resolved then we can release right across the board. It may not the only way forward but it is worth it considering depending on the expertise and commitment of the programs which are willing to be guinea pigs to test out the prototypes.

▪ The above model works; work out issues with your early adopters, work through issues, then go slightly bigger. Hopefully at this meeting next year, when someone is presenting about a new technology, they'll be a breeder next to him talking about how it is being used in the field.

Addressing the challenge about how to extend the work the quality champions (QChamps) have been doing, we have the expertise, the knowledge and the motivation to do these things. What would be the next steps to get SOPs? A lot of development is happening in parallel; each breeding program doing things with the structures they have established for themselves to tackle issues specific to their area of operation. Those people are in this room. They need to take time and brainstorm about what they want to achieve next year. How can we make that happen?	▪ Joseph (Onyeka) shared that his farm manager assigns a plot every year based on the rotation. Sometimes it is not what he needs but he has to make the best of it. It takes communication with that structure—farm managers and technicians in the field—to make sure that the plots a breeder receives have not been herbicide tested or fertility tested the year before. ▪ First everyone has to define the problems they are having, list those that you can do something about, things that you do not have decision making power about but you can influence and the things you have no control or influence over. EiB is a collective voice back to the CG centres telling them what you need. But the first thing is to collect those ideas.
A lot of breeding effort has gone into Nigeria through IITA and NRCRI, and we have a lot of released varieties. So to add value to what is existing will take a lot of effort. High level interactions with those in the ministry indicate to us that the Government of Nigeria is very eager to know how we're doing breeding for CBSD. The challenge this year is to get clarity in defining our product profiles in terms of prioritisation. In breeding for CBSD vs pressing need, how do justify allocating a large chunk of resources to breeding for a problem that may never occur?	▪ The future is not planned in the future. It is planned today. ▪ The one way of guaranteeing that you'll need these varieties is by not having any. ▪ In your product profiles, some must have CBSD resistance, and then allocate resources accordingly. Although the risk of not having them is too great. ▪ Across the different programs there will be different priorities. Those in contact with CBSD need to urgently push resources and develop tools and those can be shared and integrated right across the board. There has to be a joint strategy and that's what we need to discuss.
It is a privilege to work with smart resourceful people, sharing ideas about how to improve processes and prioritise work which is very important in the breeding profession. I feel that National breeding divisions in Africa aren't as established as in private companies and breeders are spread thin as a result. So please come and visit us and work with us.	

EPAC challenge talk | Carlos Iglesias.

"How do we get clarity in defining product profiles in terms of prioritisation?" Carlos inquired.

Portfolio management is the next step after defining. "I am lucky to worked most of my life with crops that are bred not only for yield but also quality and learnt that improvements in genetic gain without quality means that they won't be adopted," he added. It is key to define phenotyping tools in what is measured and at what stage. It hurts when a breeder is asked to stop their work but that is a reality to be dealt with. It is important that there is coordination and agreement about how quality is dealt with within NextGen.

A lot of progress has been made by the Qchamps, and the same concept should be extended to other areas of NextGen work—testing, trialing, quality of field plots and quality of phenotyping. It may be a bit more difficult in the field but it will improve the quality of our work.

On maintaining the sustainability of what has been achieved so far at the end of Phase 2, Carlos advised the team to start thinking about the different stages to make sure that what is being managed now gets to completion. Managing breeding programs is a balancing act between enthusiasm about the new things and delivering on what is being done. "We need to make sure that the programs have assimilated the learning and tools from Phase 2 and that there's real impact at program and farmer level," he emphasized.

"We also need to make sure that we have fixed goals for Year 2, have milestones set out that are measurable so that next year we can tell whether we exceeded them or came up short," he added.

Phase 2 ends in 3 years. Theoretically the project should have launched NextGen Cassava varieties by then. In the spirit of Cassava Inc., the project team needs to start thinking about what has to be in place and have some defined actions for next year's meeting. A lot that has to be in place. It is imperative to come up with a technical launch plan. This is usually prepared four years in advance because there is need to ensure that there's sufficient seed, sufficient marketing attached etc.

"We also need to think about time challenges. Cassava breeders are often overwhelmed not only by the demands within the program but also by the partners we team up with. So let's be mindful that our breeders spend more time in the field doing breeding work. It will pay a high dividend to the program," Carlos advised.

He reassured the meeting that the EPAC team feels truly part of NextGen, and that the EPAC gets a high pay-out from these meetings in terms of the learning they get and they are very thankful for that.

QChamps Update | Marnin Wolfe, Cornell University

Trial by trial analysis of data quality parameters

Germplasm exchange:

▪ Share the Hawaii seedlings with NRCRI, NaCRRI, Colombia, Vietnam and Thailand

▪ Send elite clones to COPP members (following proper phytosanitary procedures)

Population improvement (West Africa)

▪ IITA will genotype using QC and CMD-linked SNPs

▪ GSC4B – presently in CET. Will genotype using DArTseq (including Genetic Gain and All Parents from C1, C2, C3). Harvest in June 2019, genomic prediction. Select parents to plant into crossing block. Crosses Sept – Dec 2019 for new cycle.

▪ What to do with the 2019 seedling nursery – MAS, perhaps phenotypic selection

Population improvement (East Africa)

▪ Seeds from CBSD resistant parents

▪ Seeds from 2018 crossing block to be planted in SN (involves 5 clones that are virus resistant) in April. To be grown through a full cycle.

▪ Genotyping: CET and PYT from Ed's population. Not genotyped due to missing phenotyping data. Smith to partake in harvesting and evaluation in April 2019. To genotype with DArTseq. Increase QC levels associated with plots. Validate CMD2 gene in the population. Include Chambezi populations for the MAS and QC fingerprint SNPs.

Variety release pipeline:

▪ NCRP
  ◦ Lab analysis
  ◦ Proximate for on-farm trial (moisture, protein, fat, ash)
  ◦ DM, amylose/amylopectin ration, fiber, CNP
  ◦ Process roots for sensory parameters
  ◦ 2-3 locations (Mokwa, Umudike and Ikenne), 2 reps

▪ Planting materials multiplication:
  • SAH and stem multiplication – ongoing
  • Consider the numbers per genotype to multiply

▪ On-farm trials
  • Follow standard procedure for on-farm trial establishment
  • Approx. 50 farmers (ensure sufficient planting materials)
  • Select candidates using the NCRP data plus all historical data

▪ ***Other items***
  • Training workshops – planned alongside COPP after second half of 2019.

Research Division Group

▪ Accounting for plot yield and other parameter variability
  • Sprouting, early vigor (usually one

month but can record the same at three months after planting), stem weight (done one trial).

- Consider doing an experiment to assess stem portion in vigor and clone performance.

▪ GxE

- Consider genomic prediction models that take GxE into account
- Consider splitting breeding program resources across mega-environments
- Move some trials far north (e.g. Kaduna, Kano and Zaria) to ensure we breed for climate adaptation

▪ Economic weights

- Include PLTYP in SI

Cassavabase group

▪ Field design

- Field GPS coordinate – there is a need to buy field RTK GPS station.
- Metadata template generated. Should be made mandatory.
- Images – can be uploaded in bulk.
- More support for East Africa for Cassavabase user support.

Survey division

▪ TRICOT study planning

- What products?
- Gari and fufu pipeline
- Select about 30 clones, 5 x 6 plot size or larger?
- Three regions
- 250 farmers, each 3 varieties (750 data points, 8 reps/region)
- Distribution of planting materials
  ◦ ADPs?,
  ◦ IITA staff (Bela et al.) in conjunction with local ADPs/lead farmers
  ◦ Ensure land is ready for planting be-

fore stem cutting
- Data collection
  ◦ Outsource to ADP, lead farmers, on site visits
  ◦ Recorded at 3 months interval (1, 3, 6, 9, 12..)
- Process ethical approval
  ◦ Industrial?

Research Division

▪ Flowering Objective

- Establish a separate experiment on this objective? Probably in Ibadan.
- Control/treatment design
  ◦ Red LED set up
  ◦ Pruning at the time of forking
  ◦ Hormones (BA and STS)
  ◦ All combined into joint package

▪ Flowering traits to measure

- Height at first branching events
- Number of branching events at harvest
- Number of fruits produced per branching level (more demanding than previous two)
- Hernan: Consider pruning + other treatments to enhance flowering in late flowering plants.
- Weather data loggers:
  ◦ Prof Setter to advise on which ones to procure, include for hubs ($300).
  ◦ Include rain-gauge + light (solar radiation) + temperature logger

World Café of collaborators

Field Phenotyping of Cassava for CASS and NextGen

Key suggestions from the discussions:

▪ Extension of quantifying plant traits from drones in larger field trials was seen valuable.

▪ Extend drone observations with RGB to multispectral. Enables more traits measurements.

- Data are flowing into Cassavabase in which the spatial correction maybe integrated.
- Use of drones for communication footage is possible (when Anna is at IITA).

Root quality phenotyping – Busie Maziya-Dixon | IITA

Key excerpts from Busie's presentation:

Why take note of the quality of cassava:
- To monitor changes in

the physical and chemical anti nutritional and functional characteristics as the breeders are developing the varieties.
- To apply our understanding of this quality trait, to eventually target the varieties on a

different end uses which could be human, feed and industrial use.
- Formulate noble food products so that we diversify the use of cassava.

The type of quality characteristics to look for in Root Quality phenotyping;
- Physical chemical characteristics
- Organoleptic and sensory attributes. (done in the cooking not in the root process)
- Nutritional value in terms of better carotene.
- Functional properties in terms of how the flour or the starch will be behave when during cooking and stirring.
- Safety in terms of CNP content
- Stability of the product during storage of the root.

Conventional methods;
They are laborious: you really need to take time. Slow; time consuming, destructive and expensive so there is need for rapid assessment of this trait because samples are given and results are needed immediately. The agents need to come up with methods to deliver results on time. High through put automated laboratory equipment becomes a necessity not a luxury any more.

Instruments used in the laboratory:
- NIR spectroscopy:
This is used to determine the Chemical composition used for yam, but soon will be also used for cassava. It allows the breeders to work on 200 samples a day for three parameters at the same time.

- High perceptual imaging:
It takes a picture, then it tells us the distribution of those components within the root. It eliminates the step of chopping the sample. Based on the plants availability, how much you have in the lab, you can go one step higher, where you look at the texture and

appearance of the processed root; you go to the digital eye. We also looked at how the genotype will behave during processing (carotenoids) if the cassava is grown in the same field some genotypes will retain more nutrients than others.

Preference of processors;

What the processor looks for in the root: (Fufu)

- Low water content
- Easy to peel
- Adequate soiling power
- High starch
- Good color (white)
- Low CNP
- High yield

What the Consumer looks for in the root:

- Good color (white)
- Soaked and non sticky
- Tasteless
- Soft and nonstick
- Odorless fufu (no smell)

In conclusion, sampling is very limiting when phenotyping for quality. One has to wash the root before peeling it and chopping. Since one has to work on approximately 200 samples, this is impossible.
At what stage of breeding do we screen for root product quality and how much are we willing to invest in root quality phenotyping? A query about the quality of water used during the processing of cassava was raised. It was noted that the quality of the water used needed to be taken note of.
The issue of the color of the gari to be preferred left more questions than answers. The question of white over yellow flour/gari color in different parts of Nigeria due to different tastes of consumers raised many questions that needed pondering.
The team agreed that there was an improvement in the technical equipment that is used in the breeding process which has made their job faster and better.

Communication-Chris Knight and Samantha Hautea

Chris and Samantha represented the NextGen communications team. Their job is to let the world know what cassava breeders are all about. They handle the NextGen website news and activities in order for the world to be informed about the good work cassava breeders and NextGen are doing.
Chris asked the meeting to share media (photos and videos) of their work so that they can work together and get their stories to the rest of the world through the website.

Closing Remarks

EPAC represented by David Meyer: He hoped that seven years after 2019 people would look back and ask: "How did they do it? That was such a good program, how did they do it?"

Jim Lorenzen on behalf of the donors: He encouraged the delegates and assured them that the work they do is very important. Jim noted that many people depend on them and that they are many teams that formed one strong team with great science. He assured the delegates that donors were fully behind them and thanked them for the hard work.

Chiedozie Egesi representing NextGen management: He reminded the delegates that they had to work towards their targets. He thanked all the delegates for participating in the conference and for sharing knowledge. Chiedozie also thanked all the partners—Cornell, Makerere University, BTI, TARI, NaCRRI, IITA, NRCRI, CIAT, Embrapa—for the good work so far, and BMGF for funding NextGen.