GT4SP Quarterly Project Report
Investigator: International Potato Center (CIP)

Objective 1. Development of the core genomic and genetic resources for sweetpotato improvement

Objective 1.B. Transcriptome profiling
During the reporting period, CIP was involved in data analysis and manuscript development for the abiotic stress RNAseq experiments, together with Michigan State University (MSU). This work is still ongoing.

Objective 1.C. Development of diploid mapping populations for high-density single nucleotide (SNP) genome sequence anchoring and quantitative trait loci (QTL) mapping
There is no activity to report for this objective during this reporting period.

Objective 2. Establishment of a genotyping-by-sequencing (GBS)-based SNP genotyping, bioinformatics, and analytical environment for hexaploid sweetpotato

Objective 2.A. GBS-based genotyping platform development at North Carolina State University (NCSU)
There are no activities to report on developing GBS platform with NCSU during this reporting period.

Objective 2.B. Software for calling genotypes and phased haplotypes from raw 6x GBS data, coupled with software to construct 6x linkage maps from genotypes called from GBS data
There are no activities to report on testing new software from NCSU and Univ. of Queensland during this reporting period.

Objective 2.D. Databases for genotypic, phenotypic, and QTL information compatible with the CGIAR Generation Challenge Program Integrated Breeding Platform
Following the departure of R. Simon at the end of June 2017, CIP assembled a team to complete committed deliverables regarding databases. Ivan Perez, Omar Benites, and Raul Eyzaguirre are responsible for the different activities and have all been invited to attend the project database meeting at NCSU in November. When putting the new team together, a list of activities was listed and agreed between CIP and NCSU (the lead institution). The project lead, Prof. Craig Yencho, was also invited to Lima in August to meet with the new team. Good progress has been made by the team within this reporting period.

- *Setting up Boyce Thompson Institute (BTI) shiny server and R studio to host the* Highly Interactive Data Analysis Platform (*HIDAP) online.* The new team has already tested the running of HIDAP on Rstudio/Shiny server, and will be moving this to the BTI server in October. The team is already in touch with the BTI group over access to the server. Any technicalities encountered during this process will be discussed during the database meeting in NCSU in November. This activity is currently at 50% implementation. The

previous testing of HIDAP online by R. Simon was pulled down to avoid the misconception that there were two versions of HIDAP. During the visit by the project lead, the team explained the workings of HIDAP as to include other modules which may already be implemented in SPBase (e.g., trial management) because institutionally it also served potato experiments. It was agreed in this meeting to have only modules related to data exploration and analytics on SPBase.

- *Development of R BrAPI within HIDAP*. The team has tested data exchange between SPBase and HIDAP. This is progressing well—at about 70% implementation—although the group has encountered a few technical problems that may be related to BrAPI. These will be discussed in the DB meeting

- *Test and validate HIDAP connection to SPBase*. This is related to the activity above and is at about 70% implementation.

- *Reproducible reports available on SPBase*. These have been tested to be running already on HIDAP online with SPBase data. This activity is at about 80% implementation.

- *Development of the exploratory data analysis module in HIDAP*. This activity is almost done, but the group would like to hear feedback from the meeting in November as to whether they should include anything else. The team thinks this activity is at 90% implementation.

- *Exploratory data analysis module available in SPBase*. This is already implemented in HIDAP online; however, a few plots are not implemented yet. The team is working on this. The activity is thought to be at 50% implementation.

Generally, the new team has put their best foot forward and are excited to participate in sharing experiences and getting feedback from the joint meeting at NCSU in November.

Objective 3. Population development, multilocation phenotyping, and marker-assisted breeding studies

Objective 3.A. Selective or target phenotyping and QTL analysis of two diploid *I. trifida* populations

Phenotyping of the M9 x M19 population is already complete. QTL analysis and manuscript development are ongoing between CIP and NCSU; all data are analyzed. D. Gemenet will be finalizing the manuscript framework, together with B. Olukolu, during her visit to NCSU in early October. The draft manuscript should be ready by the end of the year.

Objective 3.B. Genotyping, multilocation phenotyping, and QTL analyses of previously developed 6x New Kawogo x Beauregard and Beauregard x Tanzania (BT) mapping populations

Phenotyping of the BT population in Peru is complete. Preliminary data analysis for phenotypic data is done. Multilocation data have been provided to NCSU to develop QTL mapping software. QTL analysis will follow once these methods are complete. D. Gemenet will visit the software development group at NCSU in early October and will discuss progress so far.

In Ghana, the last field experiment for the BT population was planted in Nyankpala in September 2017. This experiment will be evaluated under drought and control conditions.

Preparations are also underway to establish the root screening experiment under screenhouse conditions in Fumesua. First-season data are being analyzed.

In Uganda, the last experiments of the BT populations have also been planted. First-season data are being analyzed. All phenotypic data will be used for QTL mapping once the software is complete.

Objective 3.C. Genomic selection studies and new population development for genomic selection (GS) and marker-assisted genetic gain studies

Objective 3.C.1. Preliminary genomic selection studies
DNA extraction of the 3,000 genotypes of the P2 and P4 populations are complete. However, genotyping will not be done unless additional resources are identified to carry out GS work in Peru.

Objective 3.C.2. Population development for implementation of marker-assissted breeding (MAB) and genomic selection (GS) in sweetpotato breeding programs in sub-Saharan Africa (SSA)
Almost the entire Mwanga diversity panel (MDP) population has now been shipped to Uganda from Biosciences eastern and central Africa (BecA). Efforts are now directed to confirming the shipments and the screenhouse multiplications. D. Gemenet will be travelling to SSA in November to work with the team there to ensure that the population is well tracked in readiness for field experiments next year. M. Kitavi will start shipments to Ghana in the next reporting period.

Objective 4. Traditional and web-based training and capacity development efforts to incorporate MAB tools in sweetpotato breeding programs in Africa

Objective 4.A. Engage key SSA stakeholders by organizing regional, in-country, and web-based workshops on the potential of genomics-based breeding methods in sweetpotato
1. Long-term training (minimum 6 months with possible extension to a 1-year maximum):
- Benjamin Kivuva (senior breeder, Kenya Agricultural and Livestock Research Organisation [KALRO]–Kenya)
  o Project title: "Characterizing the diversity of the 100 SSA best bet sweetpotatoes"
  o Took a training leave to work on other duties as required by his institution.
- Gaspard Nihorimbere (researcher/Institut des Siences Agronomique du Burundi [ISABU]—wheat and sweetpotato)
  o Project tittle: "Diversity population and variations of sweetpotato varieties in Burundi"
  o Progress; currently doing simple sequence repeat (SSR) genotyping and re-extracting DNA for the same and waiting for illumina reagents to do DArTseq.
- Joanne Adero (research associate, National Crops Resources Research Institute [NaCRRI]–Uganda) reported on 1 July 2017
  o Project tittle: "Molecular variability of sweetpotato viruses in Uganda"

- o Progress: Given the African biosciences challenge fund (ABCF) entry presentation, sample recollection for RNA extraction, first set of RNA samples (24) extracted, and doing preliminary preps for library preparation.
- Eunice Wainaina (Ministry of Agriculture, Livestock and Fisheries–Kenya) reported on 10 July 2017
  - o Project tittle: "Development of beta carotene SSRs for marker assisted breeding"
  - o Progress: Webinar training by Dr. Robin Buell (MSU) on mining of markers from the reference genome and primer designing. She is almost done with primer design and will place an order and validate them. She has also planted the 100 genotypes at the Kenya plant health inspectorate Service, and the roots will be used for beta-carotene gene correlation.
- Bararyenya Astere (ISABU, Burundi) reported at end of September
  - o Project tittle: "Genome wide association studies (GWAS) and QTL analysis for continuous storage root formation and bulking traits in sweetpotato."
2. Short trainings
- The third community pf practice-led (sweetpotato improvement) proposal writing workshop at BecA (11–15 September 2017): Ernest Baafi (Crops Research Institute–Ghana), Benjamin Kivuva (KALRO–Kenya), Joanne Adero (NaCRRI–Uganda), Barayenya Astere (ISABU–Burundi), Gaspard Nihorimbere (ISABU–Burundi), and Mercy Kitavi (CIP) wrote a draft proposal in response to the African Union's 2017 call on food and nutrition security that targets African institutions. The proposed action is seeking to develop end user-preferred varieties through the genomics-assisted breeding. The proposal should be completed by the end of this month and presented to BecA for review and guidance.
3. Webinars
- Robin Buell gave a web training to two sweetpotato ABCF candidates and others ABCFs at BecA working on diverse crops, soybean, and maize. The webinar was streamed from MSU to the BecA-ILRI hub on 21, 22, and 25 August from 3:00 p.m. to 5:00 p.m. (EDT), and was interactive with Q&A. PowerPoint presentations were made available to the participants and capacity-building scientists, and will be posted on http://www.sweetpotatoknowledge.org/ https://sweetpotatogenomics.cals.ncsu.edu/
4. Regional breeders support
- DNA for 89 genotypes of the 100 best-bet sweetpotato varieties in SSA has been extracted and talks with the African orphan crop consortium (AOCC) initiated to make plans for resequencing them.

Objective 5. Project management and communication processes to ensure project success
During the reporting period, a financial report for Y3 was made and presented to the project lead. We also contributed to the annual report for Y3. The project lead was also invited to Lima to discuss strategies for moving forward, given the many changes that had occurred within CIP.