

Genomic Tools for Sweetpotato Improvement Project (GT4SP)



Fig 1. GT4SP team visiting one of the GT4SP trials in Uganda

What was the problem?

Sweetpotato is grown mainly in small plots by women and is often characterized as a poor person's food crop. Orange-fleshed sweetpotato delivering nutritional benefits to pregnant women and under five children has been introduced in sub-Saharan Africa (SSA) by the Sweetpotato Action for Security and Health in Africa (SASHA) project. One of the principal challenges faced by breeding sweetpotato breeders, is the obligate out-crossing and polyploidy nature of the crop – sweetpotato actually has 6 copies of its genome present in its nucleus - making the prediction and stacking of useful traits exceptionally difficult. Currently, there is an explosion of interest in sweetpotato and polyploid genomics. However, the critical issue of how to interpret the molecular data remains problematic, starting with the assignment of marker dosage, a.k.a. "genotype calling" and the development of new quantitative genetic algorithms to predict phenotypic performance in different environments. In addition, data collection from breeding trials has used paper-based excel forms followed by double data entry into a relational database. Although well established, this method is time-consuming and error-prone. Therefore, new data collection tools and processing methods have to be developed to facilitate crop improvement.

What objectives did we set?

The GT4SP project established a multidisciplinary team of breeders, molecular geneticists, quantitative geneticists, bioinformatics specialists and database management/internet technology experts to achieve these goals:

- We developed genomic and genetic resources for sweetpotato improvement, including genome sequencing and annotation of two diploid relatives, to be used as reference genomes for cultivated sweetpotato.
- We developed a sequence-based single nucleotide polymorphism (SNP) genotyping platform, with supporting bioinformatics and analytical tools to facilitate marker-assisted breeding. We additionally developed a database for data storage, analysis and sharing.
- We carried out multi-location phenotyping of populations and marker-trait association, quantitative trait loci (QTL), and causal gene validation studies, as well as genomic selection trials.
- We enhanced capacity for genomic-assisted breeding in African sweetpotato research programs through workshops, webinars, short and long-term training opportunities.



GENOMIC TOOLS
FOR SWEETPOTATO
IMPROVEMENT



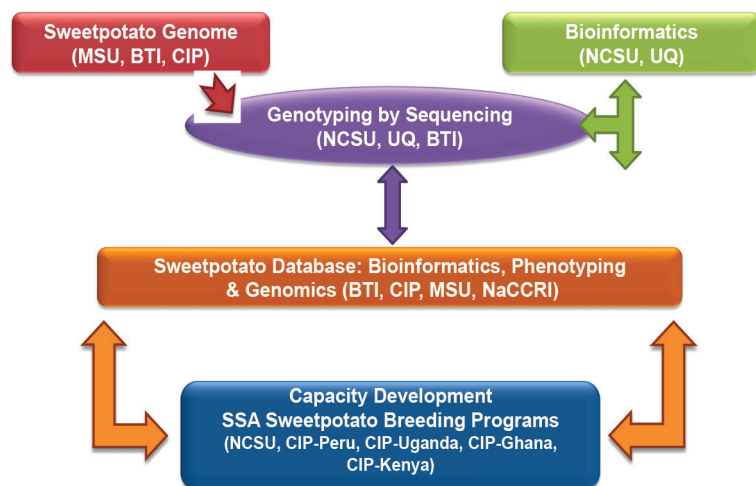
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1. Develop genomic and genetic resources for sweetpotato improvement, including genome sequencing and annotation of two diploid lines (*Ipomoea trifida* and *I. triloba*), for use as reference genomes for cultivated sweetpotato, *I. batatas*;
2. Deploy a sequence-based SNP genotyping platform, with supporting bioinformatics and an analytical tools/interface environment, to facilitate sweetpotato breeding;
3. Carry-out multi-location phenotyping and marker-trait association, QTL and causal gene validation studies, and genomic selection trials, for population improvement research in Ghana, Uganda, Peru and the USA;
4. Conduct traditional and web-based training capacity development efforts to incorporate genomics assisted breeding tools in sweetpotato breeding programs in Africa; and
5. Embrace good project management and communication processes to ensure project success and dissemination of newly-developed resources to the wider scientific communities.

Where and with whom did we work?

Our work was carried out by a multidisciplinary team from four continents and six countries including USA, Australia, Peru, Kenya, Uganda, Ghana. Led by North Carolina State University (NCSU), the team included scientists from the International Potato Center (CIP) in Peru (CIP-Peru), Kenya (CIP-Beca), Uganda (CIP-Uganda) and Ghana (CIP-Ghana); the Boyce Thompson Institute (BTI), Michigan State University (MSU), University of Queensland (UQ), and the National Crops Resources Research Institute (NaCRRI)-Uganda, with clearly defined roles as shown in the figure at the top of the next page..

The Genomic Tools for Sweetpotato Improvement Project GT4SP



9. We supervised three PhD students - two at NC State and one at WACCI - and supported another from Makerere University contributing to the development of next-generation breeders.
10. We supported six sweetpotato breeders from SSA to participate in the African Biosciences Challenge Fund and hosted them for short-term and long-term periods at the Bioscience east and central Africa (BecA) hub in Kenya, to introduce them to genomics-assisted breeding.
11. Last, we joined hands and became part of a very vibrant sweetpotato SpeedBreeders and genomics community of practice supported by the SASHA and GT4SP projects.

Were there any key challenges or lessons learned?

Many of the achievements listed above represent sweetpotato firsts. While we have learned much during the GT4SP project, there is still much to do if we are to realize the goal of genomic-assisted breeding in sweetpotato. While we believe the GT4SP project has succeeded in developing the core genetic and genomic resources required to conduct next generation breeding, we have yet to fully implement these tools in our breeding programs to further demonstrate their potential. The reality is that this technology is still quite new to sweetpotato and working in the data-intensive world of genomics will require significant coordination and, in some cases, totally new skill sets for our breeders. Thus, the learning process is complex, time-consuming and expensive. But we share a common vision and our team members are eager to work together to bring sweetpotato breeding to a higher level.

What's next?

We are convinced that sweetpotatoes can contribute significantly to the alleviation of poverty and hunger in rural poor households in SSA, and that plant breeding has a significant role for sweetpotato improvement. Not only can sweetpotato address the needs of only of the poorest of the poor—it can contribute to economic empowerment in small- to medium-sized and even larger farms through the development of improved varieties and seed systems and the increased production and sale of sweetpotatoes, either as typical food items in the marketplace, or via the development of a wide range of value-added products using sweetpotatoes as a key ingredient. New cultivars will undoubtedly play an important role in this upward trending crop that continues to increase in popularity and importance around the globe. We are currently working on a follow-on project in collaboration with the BMGF and USAID, and we are always interested in working with new partners in the future.

What did we achieve?

1. We published two high quality diploid reference genomes <https://www.nature.com/articles/s41467-018-06983-8>, that are annotated and available to the sweetpotato breeding community at <http://sweetpotato.plantbiology.msu.edu/>.
2. We optimized a sequence-based SNP genotyping platform for sweetpotato that enables high quality genotype calls for hexaploid sweetpotato, as described in <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6111789/pdf/fpls-09-01166.pdf>.
3. We developed an integrated database for sweetpotato breeding that is available for research teams upon registration and incorporates analytical programs to enhance faster analyses and decision making by breeders <https://sweetpotatobase.org/>.
4. We developed new linkage mapping methods that have increased our understanding of the inheritance of parental alleles in progeny using high density multi-locus data <https://www.biorxiv.org/content/10.1101/689638v1.full>.
5. We developed new methods for analyzing the genomic regions responsible for traits of interest in our breeding programs <https://www.biorxiv.org/content/10.1101/622951v1>.
6. We have generated and analyzed transcriptome sequencing data that allows us to identify candidate genes for important abiotic and biotic stresses <https://onlinelibrary.wiley.com/doi/full/10.1002/pld3.92>.
7. Applying the new genomic tools and combining different data sets, we have started to dissect the genetic basis of important traits in sweetpotato breeding for SSA.
8. We generated ≥ 30 genomic, transcriptomic and phenomic data sets that are still being analyzed to answer some of the most important questions towards genomics-assisted breeding in sweetpotato.

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Partners

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