

The Genomic Tools for Sweetpotato Improvement (GT4SP) Project

The GT4SP project, launched in September 2014, is a four-year investment to develop genomic and genetic resources for sweetpotato improvement with the goal of establishing molecular marker-assisted breeding resources for the global sweetpotato breeding community. We have several “firsts” already in generating new genetic resources.



Fig. 1 GT4SP multidisciplinary team during the project’s third review meeting.

What is the problem

Sweetpotato is a widely-recognized food security crop across sub-Saharan Africa (SSA). Its critical food security characteristics stem from its ability to generate large amounts of food per unit area and time under less optimal conditions compared to other major staples, and the orange-fleshed types (OFSP) rank first among roots and tubers in SSA for nutritional quality.

The International Potato Center (CIP) and HarvestPlus, with the support of the Bill & Melinda Gates Foundation (BMGF) and others, have demonstrated the benefits of OFSP. However, productivity of sweetpotato remains low in SSA relative to its potential. Yield losses caused by viruses, bacteria and fungi, and losses due to sweetpotato weevil (Fig. 2) and post-harvest damage are among the major factors limiting sweetpotato production. It is essential to breed for more resilient, disease and pest resistant nutrient-dense sweetpotato cultivars. Sweetpotato breeding is currently limited by its hexaploid genetic complexity and the lack of genomic resources to support the current breeding efforts.

What are we doing about it?

The Genomic Tools for Sweetpotato Improvement (GT4SP) project, funded by the Bill & Melinda Gates Foundation in 2014 and led by North Carolina State University, has assembled a multidisciplinary team (Fig. 1) with expertise in applied breeding, crop production, molecular genetics and genomics, and bioinformatics and database management to address the critical elements required to establish a molecular marker-assisted breeding (MAB) program in sweetpotato.

Our specific project objectives include:

- 1) Establishment of a reference genome and a web-based genome browser for cultivated sweetpotato based on the genomic sequencing of two wild relatives of sweetpotato;
- 2) Development of a MAB platform, supporting bioinformatics, quantitative genetic methods, and analytical resources to facilitate modern sweetpotato breeding;
- 3) Multi-location phenotyping and marker-trait validation studies in Ghana, Peru, Uganda and the USA;
- 4) Traditional and web-based training and capacity development efforts to incorporate MAB tools into sweetpotato breeding programs in Africa; and
- 5) Effective project management and communication processes to ensure project success and dissemination of the newly developed resources to the wider scientific community.

What have we achieved so far?

The GT4SP project is on-track and we have generated significant new genetic resources for this important crop, many of which are firsts:



Key Partners

North Carolina State University (NC State) Raleigh, North Carolina (Lead Institution); CIP-Lima, Ghana, Kenya and Uganda; Biosciences for Eastern and Central Africa (BeCA), Nairobi, Kenya; Michigan State University (MSU) East Lansing, Michigan; Michigan Boyce Thompson Institute (BTI) at Cornell University, Ithaca, New York; University of Queensland (UQ), Brisbane, Australia; National Crops Resources Research Institute (NaCRRI), National Agricultural Research Organization (NARO), Namulonge, Uganda; Council for Scientific and Industrial Research, Crops Research Institute (CSIR-CRI), Kumasi, Ghana.



Fig. 2 A weevil damaged sweetpotato, one of the biotic challenges GT4SP is seeking a solution.

- We have finalized the genome assemblies of *I. trifida* and *I. triloba*. The most recent version (v3) of the *I. trifida* genome assembly has a total size of 462.0 MB (87.7% of the estimated genome size), while that of *I. triloba* has a total size of 457.8 MB (92.3% of the estimated genome size). Both genome assemblies have been released at <http://sweetpotato.plantbiology.msu.edu/>.
- We have annotated the two genome assemblies. The final annotation of *I. trifida* has 32,301 annotated high confidence gene models, whereas the *I. triloba* has 31,426 annotated high confidence gene models. All annotation data have been released at <http://sweetpotato.plantbiology.msu.edu/>.
- We have developed a high-throughput DNA sequence-based genotyping method and a high-quality single nucleotide polymorphism (SNP) data calling pipeline that enables genotyping of both diploid *I. trifida* and hexaploid sweetpotato.
- We have developed a high-density genetic map from the F1 population of *I. trifida*. The map contains 15 linkage groups with a total genetic length of 6,458 cM and 46,511 SNP markers. This map was used to anchor and order the assembled scaffolds of *I. trifida* and *I. triloba* above.
- We have developed expression atlases for both diploid (*I. trifida* and *I. triloba*) and hexaploid sweetpotato under different conditions such as abiotic stress (heat, salt and drought), viruses, storage root formation, among others, to enable study of allele specific expression and results aligned to the genome assemblies.
- The JBrowse released in April 2017 (<http://sweetpotato.plantbiology.msu.edu/>) contains the pseudomolecules, gene models (high confidence, working set, and representative gene models), RNAseq datasets (wiggle and X-Y plots), repetitive sequences, and variants detected from the diversity panel parents.
- We have developed several genetic studies populations (Fig. 3) and collected high-quality data for various traits of interest to be used in dissecting traits of interest.
- We have developed a sweetpotato database (SPBase) that is available for SSA breeders to use for data storage and management together with breeder



Fig. 3 One of the GT4SP populations in a field trial at NaCRRI, Uganda.

friendly analytical tools. We have also contributed to the development of a sweetpotato ontology for unified naming of traits to allow proper use of SPBase.

- We are in the process of developing genetic mapping and quantitative trait loci (QTL) mapping methods using high-quality genetic and phenotypic data that are specific to analysis of the complex hexaploid sweetpotato.

To translate this research into applied breeding programs in SSA, we have collaborated with the Sweetpotato Action for Security and Health in Africa (SASHA) project to hold joint, annual meetings of the SpeedBreeders and Genomics Community of Practice (CoP), and broadcast several webinars, with more to come. Consequently, the African sweetpotato community has started to use the reference genome to identify genes of interest.

We will continue to empower the sweetpotato community through other relevant trainings (Fig. 4). Our aim is to build a cohort of breeders that can apply next generation breeding methods for sweetpotato improvement.



Fig. 4 Sweetpotato breeders and students attending a GT4SP training session on the use of the reference genome in Kigali, Rwanda (credit C. Bukania)

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