

The Genomic Tools for Sweetpotato (GT4SP) Improvement 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.

What is the promise?

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 time compared to other major staples.

Sweetpotato is a very hardy crop that can be planted in low fertility, drought-prone soils, producing relatively good yields with low inputs and labor costs. In orange-fleshed types, it ranks first among roots and tubers in SSA in nutritional quality.

During the last decade, the crop's potential in the underdeveloped world has become widely recognized. However, sweetpotato improvement has lagged far behind that of all other major food crops because of its complex genetics and limited production in developed countries. In 2009, the Bill & Melinda Gates Foundation (BMGF) invested in the Sweetpotato Action for Security and Health in Africa (SASHA) project. This grant, led by the International Potato Center (CIP), established three sweetpotato improvement support platforms and a network of ten sweetpotato breeding programs across SSA. This breeding effort has progressed very well in terms of exploring the potential in sweetpotato. Continued investments in sweetpotato breeding, smallholder agronomic intensification, seed systems, nutritious value-added food products and dissemination efforts will enable the sweetpotato community to achieve the potential.

What is the problem?

Critical Production Constraints

HarvestPlus and CIP, with the support of the BMGF and others, has demonstrated the benefits of OFSP. However, the production of this crop has been low in SSA relative to its potential. Cultivar decline caused by viruses, bacterial and fungus diseases and losses due to sweetpotato weevil and post-harvest damage are major factors limiting sweetpotato production. It is essential to breed more disease and



Fig 1. The Genomic Tools for Sweetpotato Team

insect resistant and more nutrient-rich sweetpotato cultivars. However, sweetpotato breeding is currently limited by its genetic complexity and the lack of genomic resources.

Critical Scientific Constraints

Cultivated sweetpotato is a hexaploid crop with two ancestral genomes. Knowledge of genome sequences is indispensable for basic biological research and long-term crop improvement. However, the complexity of the sweetpotato genome makes it difficult to understand. As an alternative, we are in the process of generating high-quality genome sequences of diploid accessions of *Ipomea trifida* and *I. triloba*, the two closest wild relatives and wild ancestors of the cultivated sweetpotato. These high-quality genomes will serve as references for cultivated sweetpotato and as the foundation for next generation breeding technologies for sweetpotato improvement.

What are we going to do to make it happen?

The Genomic Tools for Sweetpotato (GT4SP) Improvement Project, funded by BMGF in 2014, has assembled a multidisciplinary team (Figs 1 and 2) with expertise in applied breeding, crop production, molecular genetics and genomics, and bioinformatics and database management to address the critical elements required to

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Partners:

North Carolina State University (NCSU) 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.

establish a molecular marker-assisted breeding (MAB) program in sweetpotato.

Our specific project objectives include:

(i) establishment of a reference genome and a web-based genome browser for cultivated sweetpotato based on the genomic sequencing of two wild relative of sweetpotato;

(ii) development of a MAB platform, with supporting bioinformatics, quantitative genetic methods, and analytical resources to facilitate modern sweetpotato breeding;

(iii) multi-location phenotyping and marker-trait validation studies in Ghana, Peru, Uganda and USA;

(iv) traditional and web-based training and capacity development efforts to incorporate MAB tools in sweetpotato breeding programs in Africa; and

(v) effective project management and communication processes to ensure project success and dissemination of the newly-developed resources to the wider sweetpotato and scientific communities.

NC State University's sweetpotato breeding program and CIP have a history of commitment to the development of Africa's sweetpotato breeding programs. In fact, CIP sweetpotato breeders, Drs. Maria Andrade and Robert Mwanga, two of the four recipients of the 2016 World Food Prize for their sweetpotato biofortification efforts, attained their training in sweetpotato breeding at NC State University. NC State will continue to identify young breeders for advanced training to build long-term capacity in use of genomic breeding and fully capable of employing newly developed tools. CIP, a CGIAR member whose primary mandate is to conduct research mainly on potato and

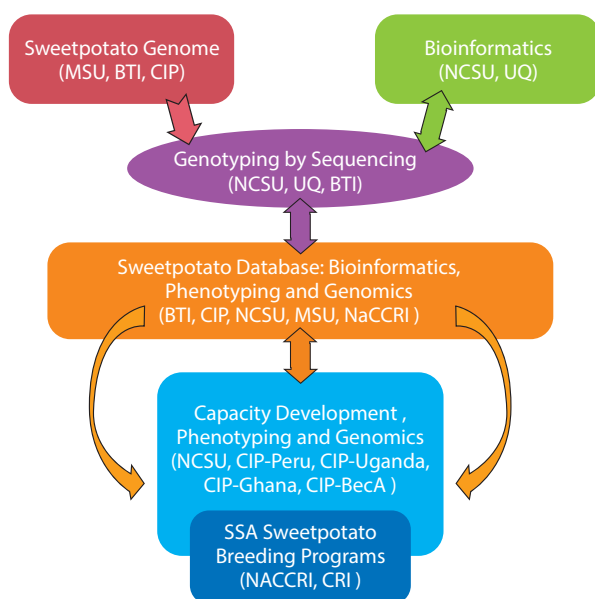


Fig 2. The GT4SP Project, an ambitious project to sequence sweetpotato and develop modern breeding tools for a food crop that sustains millions of people in SSA

sweetpotato for improving the lives of the poor, is investing deeply in these efforts.

What have we achieved so far?

The GT4SP project is on track and we are developing significant new genomic resources, many of which are important firsts. We now have reference genomes for *I. trifida* and *I. triloba*. These genomes are an important first step toward the realization of MAB in sweetpotato and will enable us to identify candidate genes associated with important biotic resistance traits like resistance to SPVD, and nutritional traits like beta-carotene, starch and sugar content.

The Sweetpotato Genomics Resource genome browser, another first, is now publicly available. With gene annotation being layered on the browser through concurrent DNA and RNA sequencing studies of sweetpotato conducted by GT4SP investigators and our collaborators, this browser is continually being improved. We expect to see the global sweetpotato community starting to use this important resource.

In the field, our applied breeding teams have already developed five genetic sweetpotato mapping populations for our MAB research. Several have already been planted and harvested at each of our sites as part of our multi-location trialing scheme. We are also well on our way to the establishment of a new sequence-based MAB platform for sweetpotato and our population genotyping efforts are well underway.

To translate this research into applied breeding programs in SSA we have already held two collaborative meetings with the SASHA project breeders and broadcast several webinars, with more to come. At the second, SASHA-GT4SP SSA sweetpotato breeder's meeting held in Nairobi, Kenya June 6-10, 2016, the GT4SP project hosted a 2-day sweetpotato genetics and genomics workshop with 31 participants (27 sweetpotato breeders and 4 PhD students) with the SASHA sweetpotato breeder's meeting. The workshop covered the following topics: 1) a keynote address on genomics-assisted sweetpotato improvement; 2) lectures on genetic diversity studies and analysis of sweetpotato diversity using DNA markers, marker-assisted selection and its potential use for sweetpotato improvement, and high-throughput phenotyping; and 3) a day of "hands-on" practical laboratory training on extraction of high quality DNA at the BecA-ILRI facility (Fig 3).

These outputs represent significant milestones for the global sweetpotato research community in our quest to develop next generation breeding methods for SSA breeders working to improve this important crop.



Fig 3. Practical laboratory training on extraction of high quality DNA at the BecA-ILRI facility. (credit C. Bukania)

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