

# The Genomic Tools for Sweetpotato Improvement (GT4SP) Project

A new four year investment to develop genomic and genetic resources for sweetpotato improvement has been launched with the goal of establishing a molecular marker-assisted breeding program in sweetpotato.



Fig. 1 The research team at the GT4SP Start-Up meeting in San Diego, USA

intensification, seed systems, nutritious value-added food products and dissemination efforts will enable the sweetpotato community to *achieve the potential*.

## What is the promise?

Sweetpotato is a widely recognized food security crop, grown predominantly in small plots by poor women farmers 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, and its value as a source of  $\beta$ -carotene, a vitamin A precursor, is well recognized.

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 \$21.25 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. The SASHA project is linked to the longer-term Sweetpotato for Profit and Health Initiative (SPHI) - also led by CIP - a 10-year effort designed to unleash the full potential of sweetpotato in SSA, with the overall goal of reaching 10 million households by the year 2020. These initial efforts have progressed very well in terms of *exploring the potential* in sweetpotato. Continued investments in sweetpotato breeding, smallholder agronomic

## What is the problem?

### Critical Production Constraints

HarvestPlus and CIP, with the support of the BMGF and others, has demonstrated the benefits of OFSP, and this remarkable diverse and resilient crop has significant great potential to improve the health status of women and children in Africa, while improving livelihoods and farm profits. However, the production of this crop has been low in SSA relative to its potential. Cultivar decline caused by virus, bacterial and fungus diseases and losses due to sweetpotato weevil and post harvest damage are major factors limiting sweetpotato production. Thus, it's essential to breed more disease and 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

Sweetpotato is a hexaploid crop with two non-homologous ancestral genomes hypothesized. Knowledge of genome sequences is indispensable for basic biological research and long-term crop improvement. However, the polyploidy and the high degree of heterozygosity of the sweetpotato genome make it infeasible for whole genome sequencing. As an alternative, we are in the process of generating high-quality genome sequences of diploid and highly homozygous accessions of *Ipomea trifida* and *I. triloba*, the two closest wild relatives and putative wild ancestors

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of the cultivated sweetpotato. The resulting two high-quality draft 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 Improvement (GT4SP) project, funded by BMGF in 2014, has established a multidisciplinary team 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 (Fig. 3).

Our specific project objectives include:

- (i) development of genomic and genetic resources for sweetpotato improvement, including complete genome sequencing of NCNSP-0323 and NCNSP0306, two diploid lines expected to be suitable for use as the cultivated sweetpotato, *I. batatas*, reference genomes;
- (ii) development of a genome sequence-based molecular marker platform, with supporting bioinformatics, quantitative genetic methods, and analytical environment to facilitate modern sweetpotato breeding;
- (iii) multi-location phenotyping and marker-trait/validation studies in Uganda and Ghana;
- (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 newly-developed resources to

the wider sweetpotato and scientific communities. Achievement of our project objectives will provide the core resources needed to bring sweetpotato breeding into the genomics era. Initially, this project will focus on developing the genomic breeding tools and intellectual and institutional capacity required to facilitate crop improvement, setting the stage for increased rates of genetic gain for key traits (e.g., yield, resistance to sweetpotato virus disease (SPVD), combined high storage root  $\beta$ -carotene and dry matter content), drought and heat tolerance and decreased time required to release improved varieties to farmers in SSA. Advanced breeding approaches such as genomic selection (GS) will be phased in as the genomic foundation for sweetpotato is built and as results from other crop improvement efforts in diploid crops (e.g., the NEXTGEN Cassava Breeding project and ongoing public sector experiments in other crops) are better understood.

### ✦ Our Team

Key partner organizations directly involved in SSA breeding activities are NCSU, CIP, NaCRRI, and CSIR-CRI. CIP has a history of presence in BMGF priority countries as well as with partner institutions engaged in sweetpotato improvement. NCSU and CIP have long exchanged germplasm, having collaborated on numerous occasions, especially with research on molecular marker technology. NaCRRI, NCSU and CIP have ties that predate the SASHA project started in 2009, whereas, connections with CRI are more recent but rapidly evolving towards strengthening the sweetpotato breeding program. At BecA and NaCRRI, sweetpotato biotechnology activities have been implemented since 2009. BTI is collaborating with CIP on a Grand Challenges Explorations, Round 8 (GCE8) grant to establish the African sweetpotato virome.

NCSU's sweetpotato breeding program and CIP have a history of commitment to development of Africa's sweetpotato breeding programs. NCSU will continue to work very closely with the sweetpotato breeding community to identify young breeders for advanced training to build long-term capacity in use of genomic breeding. During the project term, we will make efforts in training to ensure that new researchers and partners are fully capable of employing newly developed tools. CIP, a CGIAR member whose primary mandate is to conduct research mainly on potato and sweetpotato for improving the lives of the poor, is investing deeply in these efforts. This project will build capacity in the current breeding programs at CIP, NaCRRI, and CRI in Uganda and Ghana, respectively, so that efforts can continue and expand after the grant period.

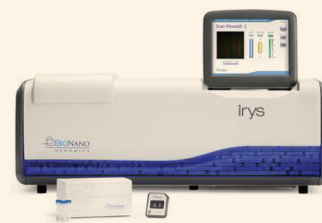


Fig. 2 BioNano technology will be used to build the genome map

### The GT4SP Team:

- North Carolina State University (NCSU), Raleigh, North Carolina (Lead Institution)
- International Potato Center (CIP): Lima, Peru; Kumasi, Ghana; Kampala, Uganda
- Biosciences for Eastern and Central Africa (BeCA)-ILRI Hub, Nairobi, Kenya
- Michigan State University (MSU), East Lansing, 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

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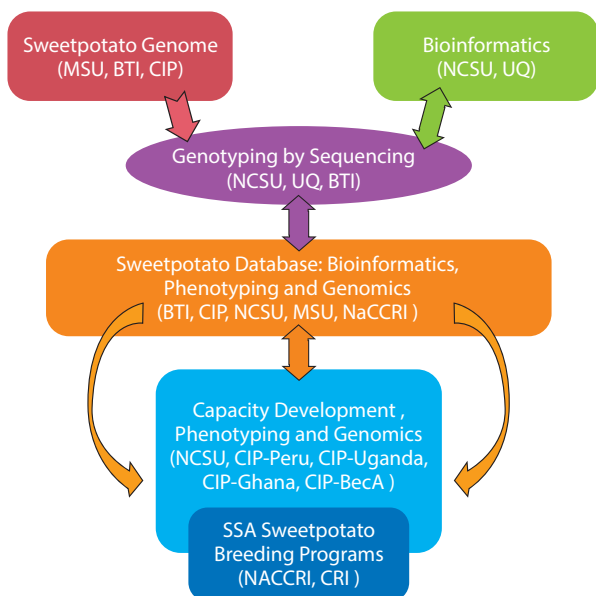


Fig. 3 The GT4SP Project, an ambitious project to sequence sweetpotato and develop modern breeding tools for a food crop that sustains millions of people in SSA