

## The Genomic Tools for Sweetpotato Improvement Project - GT4SP

### Funded by:

BILL& MELINDA GATES foundation

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## **Global Sweetpotato Production**

(2000 - 2006)

#### Sweetpotato Production

Areas of Cultivation and Average Yields



Source: International Potato Center: World Sweetpotato Atlas https://research.cip.cgiar.org/confluence/display/WSA/Global+Sweetpotato+Cultivation





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## Growth of Sweetpotato Fries Jan.'09 – June '10

### **Impressive, but this represents < 2% of total fry market**

**Estimated Foodservice Volume** 





## US Sweetpotato Growth 1994 - 2014





#### African Sweetpotato Production Trends 1993-2013



Source: FAOSTAT3.FAO.ORG (March 2015)

The SASHA Project – Sweetpotato Action for Security and Health, 2009-2014 Lead Institute: International Potato Center

### Major Progress in 4 Key Areas

- 1. Population Development & Varietal Selection
- 2. Seed Systems
- 3. Delivery Systems (proof-of-concept)
- 4. Management and Sweetpotato Support Platforms



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## Focus 1 : Breeding & Varietal Development New Populations

GOAL 1: Generate a radically expanded range of sweetpotato varieties that combine different quality characteristics with significant improvements in yielding ability

- Generate populations to meet dominant needs of users
- All sites: High dry matter
- East & Central Africa: virus-resistance, orange-fleshed, dual purpose for animal feed
- Southern Africa: drought resistance, orangefleshed
- West Africa: non-sweet sweetpotato, orange & white-fleshed



## Focus 2 : Breeding & Varietal Development New Breeding Methods

GOAL 2: Redesign sweetpotato breeding systems in Africa to produce varieties in fewer years (3-4) than currently (7-8 years) - "accelerated breeding"

- More sites at the earliest stages of breeding to substitute for fewer sites over more seasons
- At least one site being the "tough" selection conditions; for instance, consistently drought stressed
- In February 2011, released 15 new, more drought tolerant OFSP in Mozambique
- Also released varieties using accelerated breeding in Malawi and Rwanda



## Focus 3 : Breeding & Varietal Development

#### GOAL 3: Exploitation of Heterosis -

#### Demonstration that heterosis exists for root and foliage weight... but not for quality traits?



- A) Working with two heterotic genepools, on average for first
  - hybrid population:
    - 22.9% root yield jump (dry matter basis)
  - 7.8% more biomass production.
- B) Potential of further yield jumps by selecting the best "hybrid

family parents"

- up to 100% more root yield (dry matter basis)
- up to 85% more biomass production.
  - These 2<sup>nd</sup> hybrid populations now underway in Uganda, Mozambique, and Peru

### Focus 4 : Management & Sweetpotato Support Platforms

GOAL 4 : Research organized around breeding platforms that integrate and support the work of institutional partners in each sub-region



- Provide technical backstopping
  - Special emphasis on Alliance for a Green Revolution (AGRA) supported national breeding programs and PhD training programs (ACCI & WACCI)
- Assure clean germplasm exchange
- Assure gender-sensitive design and implementation
- Assure comparable data collection between countries engaged in the breeding and germplasm exchange
- Facilitate information exchange

## Each Platform with Quality Lab and Clean-up Capacity



Near Infrared Spectrometer enables rapid assessment of major macro- and micronutrients

Screen houses essential for maintaining stocks of disease free vines as primary foundation material





# **Current Status of Sweetpotato**

- The importance and potential of SP has become widely recognized across the globe.
- Many public and private organizations recognize the superior nutritional value in SP compared to many other staple crops and investments are increasing.
- SASHA "1" has been very successful new breeding programs (4-6), new varieties (18+), 3 region SSP's established, NIRS technology introduced, seed systems, virus studies, value-added POC's, etc.
- SASHA "2", SPHI, etc. recently launched.
  - See http://sweetpotatoknowledge.org/



# In short.....A lot of people are more interested in sweetpotato than ever before!!!

However....genomic resources for sweetpotato are noticeably lacking!!



Sweetpotato Genomics Convening A "Vision" for SP Improvement in SSA BMGF, Seattle, WA June 3-5, 2013

With the help of the SASHA project, sweetpotato is poised for significant growth in SSA.

However, to fully realize SP's true long-term potential, we need to invest in modern breeding tools, and integrate them into applied breeding efforts connected to improved seed systems and market-based value-chains.



# A "Vision" for MAB Breeding in SSA

#### **Breeding pipeline investments should include:**

- Genomic Resources
  - A reference genome the 1<sup>st</sup>!
  - Marker development we are way behind the curve....
  - A robust set of SNP markers and a low-cost genotyping platform
  - Advanced laboratory sequencing linked with developing country phenotyping and breeding activities
  - 2x and 6x mapping, training and test populations

#### • Bioinformatics, analytics and database resources –

- Stand-alone and web-based bioinformatics resources
- Sweetpotato database, data collection and phenotyping options
- New analysis resources
- Human Resources and Capacity Development
  - Continue to assemble and develop a dynamic team of breeders and allied disciplines
  - Training in the use of traditional and genomic breeding methods
  - Effective communication and collaboration
  - Multi-institutional training and capacity development

### The Genomic Tools for Sweetpotato Improvement Project – GT4SP

Sweetpotato Genome (MSU, BTI, CIP) Bioinformatics (NCSU, UQ, CIP)

Genotyping by Sequencing (NCSU, UQ, CIP, BTI)

Sweetpotato Database: Bioinformatics, Phenotyping & Genomics (CIP, MSU, BTI, NaCCRI)

Sweetpotato Breeding & Capacity Development (NCSU, CIP Peru, CIP Uganda, CIP Ghana, CIP at BecA)

An ambitious project to sequence sweetpotato and develop modern breeding tools for a food crop that sustains million of people in SSA.

Collaborators: Boyce Thompson Institute at Cornell, Michigan State University, University of Queensland, Australia; The International Potato Center, Peru; BioSciences East and Central Africa, Kenya; National Crops Resources Research Institute, Uganda;

# GTSPI Start-up Meeting, San Diego, CA Jan. 7-9, 2015



### Sweetpotato genome sequencing

**Strategy:** Sequencing the closely related wild ancestors that are diploid and homozygous

• Examples: potato, wheat, cotton, strawberry





# Development of High Yielding Multiple Resistant Sweetpotato Germplasm



## Impact of sweetpotato weevils (SPW) in SSA





- Yield losses of 67-100%
- Oviposition and feeding
- Pathogenic microbial accumulation
- Sesquiterpenes
- Impeded translocation of phytochemicals
- Difficult to manage



#### **Frequency Distribution of Mean Sweetpotato Weevil Severity**

'New Kawogo' (NK) x 'Beauregard' (B) mapping population at NaCRRI (A), NgeZARDI (B), NaSARRI (C), and overall mean across sites and seasons (D)

80 6 4 2 2 Number of clones NK NK Β В Α Mean severity Β Mean severity Number of clones Number of clones Number of clones NK Number of clones Number of clones Number of clones NK Β Β Mean severity Mean severity D С

**Transgressive segregants = 25** 



# Outcomes

- An MAB breeding pipeline that utilizes up- and down-stream breeding methods
- Genomic selection technologies integrated with the SASHA accelerated breeding program
- A new generation of sweetpotato breeders, and a new cadre of molecular geneticists and bioinformatics scientists interested in using the new tools to study sweetpotato.
- Linkage of genomic-based breeding to address the demand of new varieties and "products" will yield maximum long-term ROI on current SP crop improvement investments in SSA.
- Note: We can't expect "omics" to solve all our breeding problems. Conventional breeding will still be the workhorse, but it will offer new solutions for difficult traits.

