The Genomic Tools for Sweetpotato Improvement Project - GT4SP

Funded by:

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SPHI Annual Technical Meeting
Villa Portofino Hotel, Kigali, Rwanda
Global Sweetpotato Production

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

- SWEET POTATOES - PRODUCTION ($1000)
- SWEET POTATOES - ACRES HARVESTED
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)
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, orange-fleshed
- 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 2nd 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\textsuperscript{st}!
  – 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
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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 millions 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**
‘New Kawogo’ (NK) x ‘Beauregard’ (B) mapping population at NaCRRI (A), NgeZARDI (B), NaSARRI (C), and overall mean across sites and seasons (D)

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.
Stay tuned
...and engaged!