The Genomic Tools for Sweetpotato Improvement Project – GT4SP

Bill & Melinda Gates Foundation
Seattle, WA

Beginning the Discussion

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North Carolina State University
Raleigh, NC USA

SASHA/GT4SP Annual Sweetpotato Breeders Meeting
Colline Hotel, Mukono, Uganda
June 2-5, 2015
L96-117 x NC415 –
Think about the opportunities in this cross...

Functional Food Products
- Anthocyanins
- β-Carotene
- Phenolics
- Lower-glycemic index

New flavors
Exciting colors
Different sugar, starch and texture profiles
Lower acrylamide levels?

The challenge is...
How do we decide what to develop and what tools do we use to get there?!
HELLO! COVINGTON

Ending America’s dependence on foreign vodka.

THE BEST YAM VODKA ON EARTH®

GOLD MEDAL WINNER — 2013 SAN FRANCISCO WORLD SPIRITS COMPETITION!

COVINGTON SPIRITS LLC SNOW HILL, NC – COVINGTONVODKA.COM
NC Sweet Potato Exports

Exports now account for between 10% and 20% of production
Growth of Sweetpotato Fries
Jan.’09 – June ‘10

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

Estimated Foodservice Volume

TOTAL SWEET POTATOES
## More types of SP varieties = more traits to evaluate

<table>
<thead>
<tr>
<th>1997 (total traits evaluated = 28)</th>
<th>2014 (total traits evaluated &gt; 50)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield (Total, No. 1, canner’s, jumbos, culls)</td>
<td>Yield (Total, No. 1’s, petites, canners, jumbos, culls)</td>
</tr>
<tr>
<td>Maturity (E, M, L)</td>
<td>Maturity (E, M, L)</td>
</tr>
<tr>
<td>Storage root shape and appearance (6 traits)</td>
<td>Storage root shape and appearance (6 traits)</td>
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<tr>
<td>Skin color and texture</td>
<td>Skin color and texture</td>
</tr>
<tr>
<td>Flesh color – O, W</td>
<td>Flesh Color – O, W, Y, P</td>
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<tr>
<td>Dry Matter Content</td>
<td>Dry Matter Content - Starch, amylose:amylopectin</td>
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<tr>
<td>Skinning</td>
<td>Skinning</td>
</tr>
<tr>
<td>Taste – Baking test (6 traits)</td>
<td>Taste – Baking test (6 traits), plus glucose, sucrose, fructose, maltose, total sugars</td>
</tr>
<tr>
<td>Storage</td>
<td>Storage – Internal beak-down, browning potential</td>
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<tr>
<td>Disease resistance – FW, SSR, RKN</td>
<td>Disease resistance – FW, SSR, RKN, FLD Screen, SPFMV</td>
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<tr>
<td>Sprouting behavior</td>
<td>Chip and fry tests (2-3x/yr)</td>
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<tr>
<td></td>
<td>Anthocyanin profiling</td>
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<td></td>
<td>Sprouting behavior</td>
</tr>
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<td></td>
<td>Cut root piece potential</td>
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US Sweetpotato Growth
1994 - 2014
Global Sweetpotato Production

Source: International Potato Center: World Sweetpotato Atlas
https://research.cip.cgiar.org/confluence/display/WSA/Global+Sweetpotato+Cultivation
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
   ▪ In Uganda, distinct populations formed using molecular markers
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 is becoming 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” and Sweetpotato for Profit and Health Initiative (SPHI) 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!!
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
  – 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** –
  – Improved web-based bioinformatic resources
  – New 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
McKnight Foundation
Collaborative Crop Research Program, Est. 1993

Helping smallholder farmers feed their world.
McKnight Foundation
Collaborative Crops Research Program

- Promote crop research partnerships between developing and developed countries
  - Developing country partners lead
  - Long-term projects - 8-10 years
  - Promotes capacity building and increased scientific infrastructure

  - Development of high yielding, high dry matter, orange-fleshed cultivars with increased resistance to viruses and insects.
  - Lead PIs, Drs. Robert Mwanga, Gorrettie Ssemakula, NARO
  - Drs. Craig Yencho, NCSU and Phil Stevenson, NRI
Development of High Yielding Multiple Resistant Sweetpotato Germplasm
Sweetpotato production constraints in Uganda
NC State Sub-contract
Sweetpotato Genetic Mapping

Dr. Jim Cervantes, Dr. Benard Yada
Dr. Gorrettie Ssemakula, Dr. Robert Mwanga,
Ken Pecota, Craig Yencho

NC State University
Think and Do
ncsu.edu
First Genetic Linkage Map Of Sweetpotato AFLP Linkage Map Of Of Sweetpotato
Linkage groups of ‘Beauregard’
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)

**Frequency Distribution of Mean Sweetpotato Weevil Severity**

**Transgressive segregants = 25**
Distribution of mean storage root hydroxycinnamic acid ester content in the progeny and parents of the ‘New Kawogo’ (NK) x ‘Beauregard’ (B) across sites

- Broad sense heritability $H^2 = 0.49 \pm 0.0471$
- Weak correlation of HCA with field SPW ($r=0.103$, $P=0.015$)
Association of SSR marker loci with the best linear unbiased predictions of overall mean across-sites and seasons sweetpotato weevil severity of genotypes

<table>
<thead>
<tr>
<th>Marker</th>
<th>Total variance (%)</th>
<th>Most significant allele</th>
<th>R²</th>
<th>ProbF</th>
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<tbody>
<tr>
<td>IBS11</td>
<td>22.3</td>
<td>IBS11NKB253</td>
<td>0.0443</td>
<td>0.032</td>
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<tr>
<td>IbE5</td>
<td></td>
<td>IbE5B218</td>
<td>0.0311</td>
<td>0.033</td>
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<tr>
<td>IbL16</td>
<td></td>
<td>IbL16NK183</td>
<td>0.0446</td>
<td>0.028</td>
</tr>
<tr>
<td>IbO5</td>
<td></td>
<td>IbO5NKB181</td>
<td>0.0233</td>
<td>0.038</td>
</tr>
<tr>
<td>J116A</td>
<td></td>
<td>J116ANKB210</td>
<td>0.0806</td>
<td>0.000</td>
</tr>
</tbody>
</table>
A Vision for Sweetpotato Improvement in Africa:

Modern Breeding Tools
Increased Potential, Improved Genetic Gain, Reduced Hunger and Poverty

Craig Yencho
NC State University
Bill and Melinda Gates Fdn.
Seattle, WA
June 3-5, 2013
The Genomic Tools for Sweetpotato Improvement Project – GT4SP

Sweetpotato Genome (MSU, BTI, CIP)

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

Bioinformatics (NCSU, UQ, CIP)

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;
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.
GTSPi Start-up Meeting,
San Diego, CA Jan. 7-9, 2015
Stay tuned
...and engaged!