A Vision for Next Generation Sweetpotato Improvement in Africa:
Modern Breeding Tools, Increased Potential

Craig Yencho
NC State University
Bill and Melinda Gates Fdn.
Seattle, WA
June 3-5, 2013
Global Sweetpotato Production

Source: International Potato Center: World Sweetpotato Atlas
https://research.cip.cgiar.org/confluence/display/WSA/Global+Sweetpotato+Cultivation
Sweetpotato is expanding faster in area than any other major food crop in SSA

In 2005, 3.2 million hectares in sweetpotato

Yet.. this is only 1/8 of the area under maize
Growth of Sweetpotato Fries
Jan.’09 – June ‘10

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

Estimated Foodservice Volume
The SASHA Project –
Major Progress in 5 Key Areas

1. Population Development & Varietal Selection
2. Weevil Resistant Sweetpotato using Transgenics
3. Seed Systems
4. Delivery Systems (proof-of-concept)
5. Management and Sweetpotato Support Platforms
Focus 1: Breeding & Varietal Development

New Populations

seeks to generate a radically expanded range of sweetpotato varieties that combine different quality characteristics with significant improvements in yielding ability

1) 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 (130 parents)
- Southern Africa: drought resistance, orange-fleshed (56 parents)
- West Africa: non-sweet sweetpotato, orange & white-fleshed (59 parents)

Partners: National sweetpotato programs in Uganda, Ghana, Mozambique
Focus 2: Breeding & Varietal Development
New Breeding Methods

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
3) Additional new breeding methods tackled:

- Demonstrated that “hybrid vigor” or 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\textsuperscript{nd} hybrid populations now underway in Uganda, Mozambique, and Peru

In Uganda, distinct populations formed using molecular markers
Focus 4: Management & Sweetpotato Support Platforms

- 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

to organize the work around research for development platforms that integrate and support the work of institutional partners in each sub-region
Each Platform with Quality Lab and Clean-up Capacity

Near Infrared Spectrometer enables rapid (2 minutes) assessment of major macro- and micronutrients

Screen houses essential for maintaining stocks of disease free vines as primary foundation material
## Variety Development – 2009-1013

<table>
<thead>
<tr>
<th>Country</th>
<th>No of parents in crossing block</th>
<th>Clones in advanced yield trial 2012/2013</th>
<th>No. of on-farm trials 2012/2013</th>
<th>No. of varieties released</th>
<th>No. of clones in pipeline for release</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2009 to 2013</td>
<td>other</td>
</tr>
<tr>
<td>Malawi</td>
<td>36</td>
<td>15</td>
<td>56</td>
<td>5</td>
<td>2</td>
</tr>
<tr>
<td>Mozambique</td>
<td>52</td>
<td>108</td>
<td>64</td>
<td>15</td>
<td>0</td>
</tr>
<tr>
<td>Zambia</td>
<td>42</td>
<td>25</td>
<td>45</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>S. Africa</td>
<td>13</td>
<td>23</td>
<td>3</td>
<td>8</td>
<td>5</td>
</tr>
<tr>
<td>Ethiopia</td>
<td>24</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Rwanda</td>
<td>30</td>
<td>55</td>
<td>29</td>
<td>2</td>
<td>6</td>
</tr>
<tr>
<td>Uganda</td>
<td>28</td>
<td>12</td>
<td>75</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Tanzania</td>
<td>16</td>
<td>40</td>
<td>46</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Kenya</td>
<td>23</td>
<td>12</td>
<td>0</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>Ghana</td>
<td>48</td>
<td>14</td>
<td>12</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>Nigeria</td>
<td>15</td>
<td>18</td>
<td>48</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td><strong>56 varieties released by national programs between 2009 and 2013</strong></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Current Status

- The importance and potential of SP is becoming widely recognized across the globe.
- Many public and private organizations recognize this 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.
Current Status

However….genomic resources for sweet potato are noticeably lacking!!
The 1st Complete Genetic Map of Sweetpotato – Developed at NCSU (Cervantes et al. 2008a,b, 2011)

Linkage groups of ‘Beauregard’
AFLP markers identify all 90 linkage groups in *Ipomoea batatas*.
Dry Matter (-)

Starch (-)

β-carotene (+)
Some Examples of Genomic Resources for Sweetpotato

CIP


China


South Korea


USA

Sweetpotato Omics at CIP
(Jan Kreuze, et al.)
5th Korea-China-Japan Sweetpotato Workshop

Development of genetic and genomic resources for Sweetpotato
A “Vision” for SP Breeding in SSA

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 with applied breeding efforts.
A “Vision” for SP Breeding in SSA

Breeding pipeline investments should include:

- **Human Resources** –
  - 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 will be key
  - Multi-institutional training and capacity development

- **Genomic Resources** –
  - Marker development – we are way behind the curve….
  - A robust set of SNP markers
  - 2x and 6x mapping, training and test populations
  - 1x genetic resources
A “Vision” for SP Breeding in SSA

Breeding pipeline investments should include:

- High-throughput Phenotyping
  - Virus resistance
  - Drought tolerance
  - Nutritional traits
  - SPW

- Bioinformatics and Analytical Resources
- Data Analysis and Selection Platforms
- Use of cultivated and wild spp. for improvement?
- Developed country sequencing linked with developing country phenotyping and breeding activities
Pending Project – BMGF Genomic Tools for Sweetpotato Improvement Project

Sweetpotato Genome (MSU, BTI, CIP)

Bioinformatics (NCSU, UQ)

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

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

Sweetpotato Breeding Programs (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; Crops Research Institute, Ghana
Outcomes

- An effective 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, molecular geneticists and bioinformatics scientists capable of using the new tools to drive improvement.
- Linkage of genomic-based breeding to address the demand of new varieties and “products” will yield maximum long-term ROI on current SP investments in SSA.
Phylogenetic Analyses of NCNSP Ipomoea spp. Lines (CIP, 2013)
• Scaffolds $\geq 100$ bp
  • Total: 385,197,028 bp
  • Total #: 533,395
  • N50: 3,044 bp

GC content distribution indicates no bacterial and virus contamination
One lane paired-end reads

- Raw
  - Read length: 100 bp
  - Pairs #: 201,589,735

- Remove duplications
  - Non-duplicated pairs: 9,581,439
  - Duplication %: 52.47

- Clean by quality (Q20)
  - Good pairs #: 80,982,947
  - Good pairs bases: 15.26 Gbp
  - Mean read length: 94.22 bp
  - Single reads #: 6,751,168 / 3,268,734

**NCNSP023-3 Ipomoea sp. genome sequencing**

*Non-duplicated SP_Diploid PE read pairs (17-mer Distribution)*

- Genome size est. ~ 670.7 M bps
- Read depth est. ~ 28.57 X
- Total read number = 191628788

*Kmer specie ratio (%)*

- Depth 24
- Depth 7
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; Crops Research Institute, Ghana