



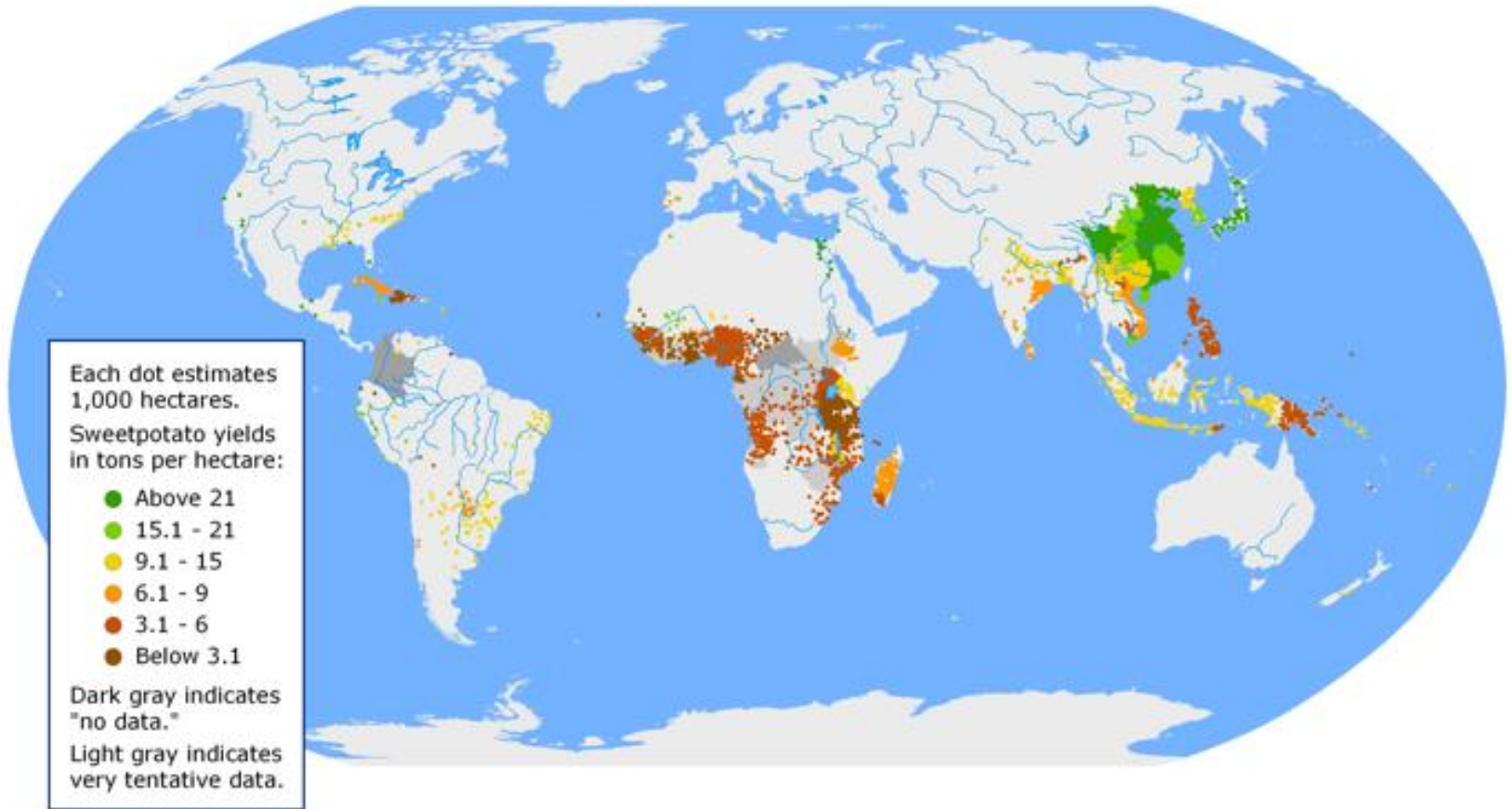
**A Vision for Next Generation
Sweetpotato Improvement in Africa:
Modern Breeding Tools, Increased Potential**

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NC State University
Bill and Melinda Gates Fdn.
Seattle, WA
June 3-5, 2013

Global Sweetpotato Production

(2000 – 2006)

Sweetpotato Production
Areas of Cultivation and Average Yields



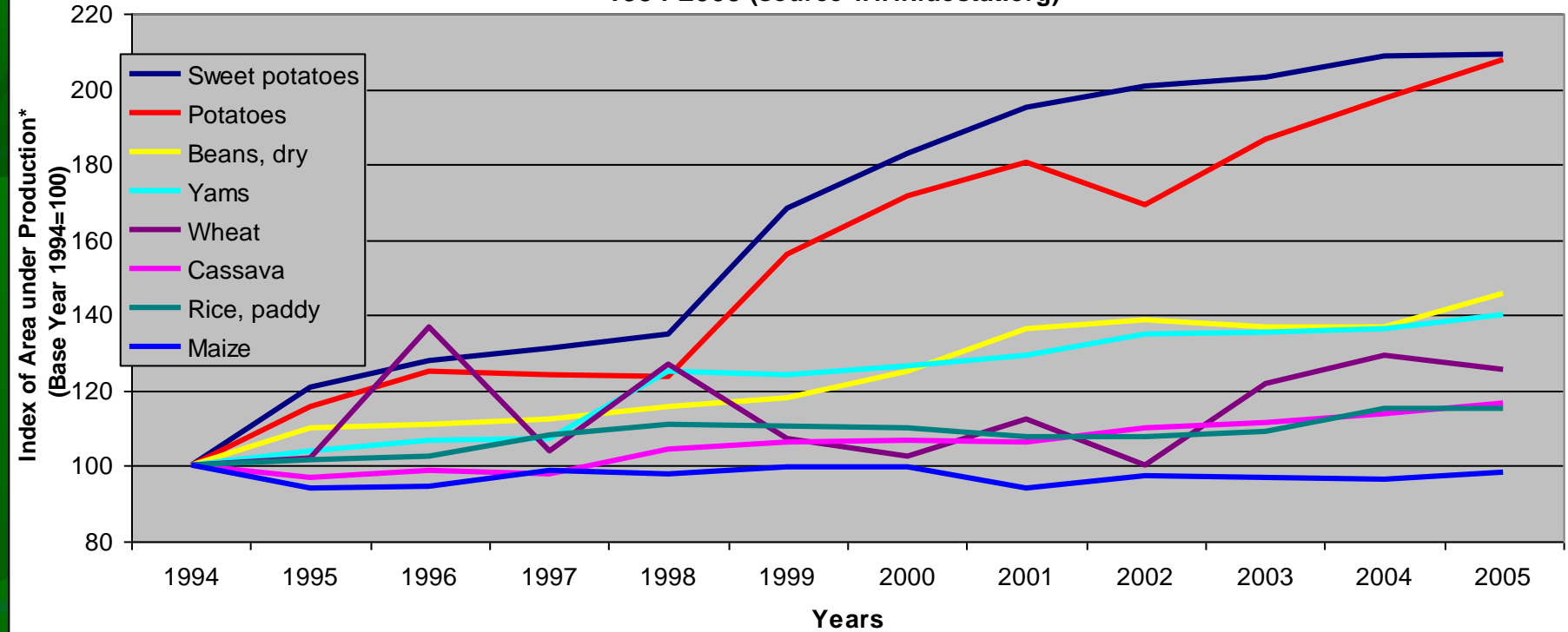


NCPUR06-020



Sweetpotato is expanding faster in area than any other major food crop in SSA

Figure 1. Major African Field Crops Area Growth
1994-2005 (source www.faostat.org)



*For sweetpotato, the area under production doubled (index rising from 100 to 200) between 1994 and 2003.

In 2005, 3.2 million hectares in sweetpotato

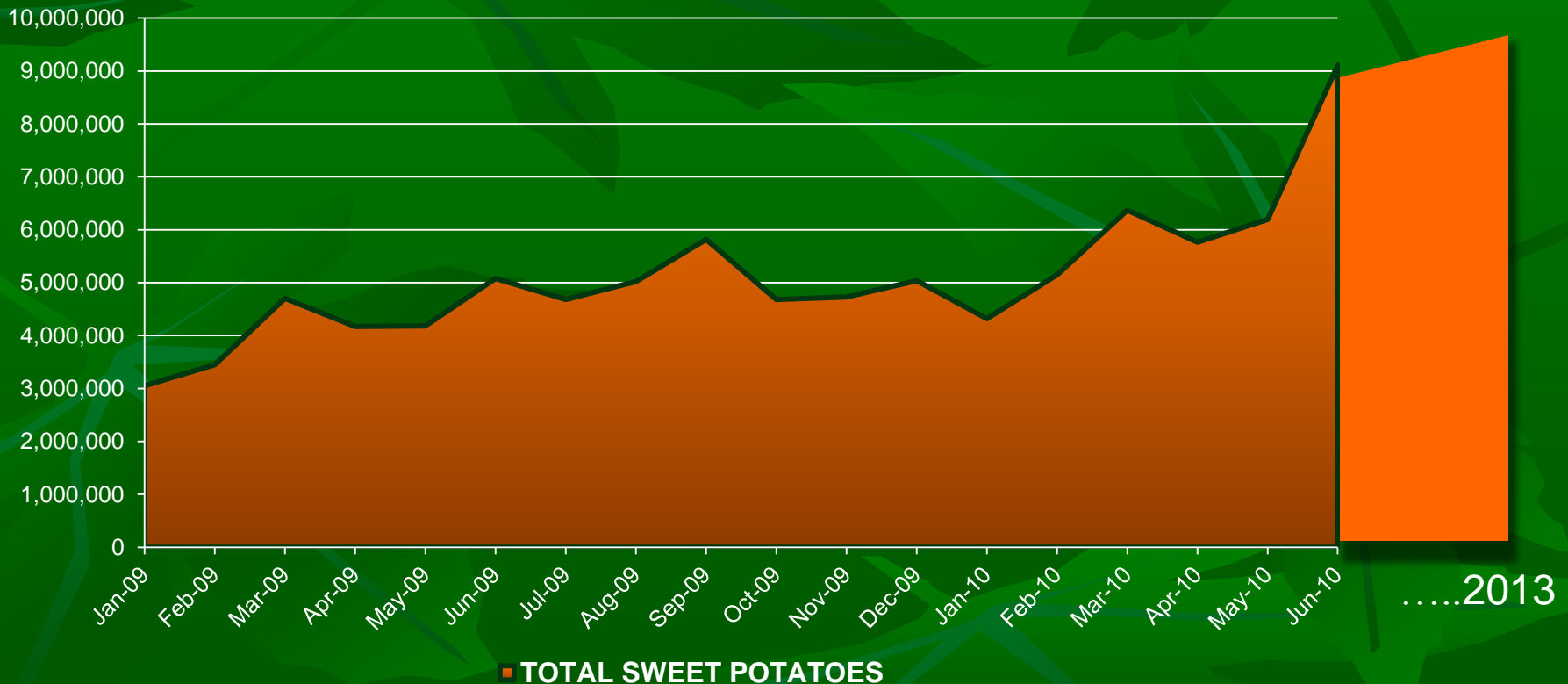
Yet.. this is only 1/8 of the area under maize

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)



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

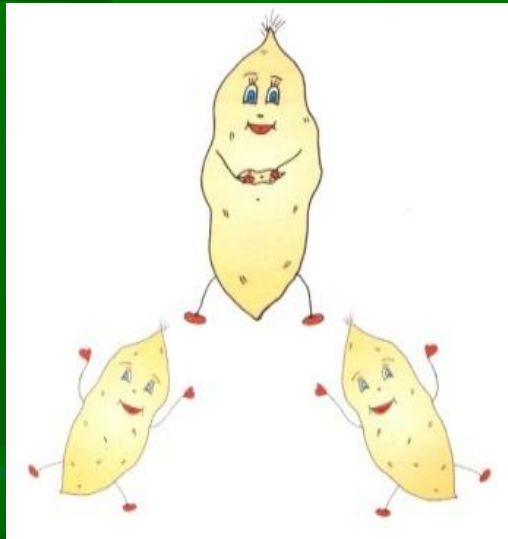


Focus 3 : Breeding & Varietal Development

Heterosis Exploitation

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 2nd hybrid populations now underway in Uganda, Mozambique, and Peru*
 - In Uganda, distinct populations formed using molecular markers

Focus 4 : Management & Sweetpotato Support Platforms

to organize the work around research for development 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 (2 minutes) assessment of major macro- and micronutrients

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



Variety Development – 2009-2013

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

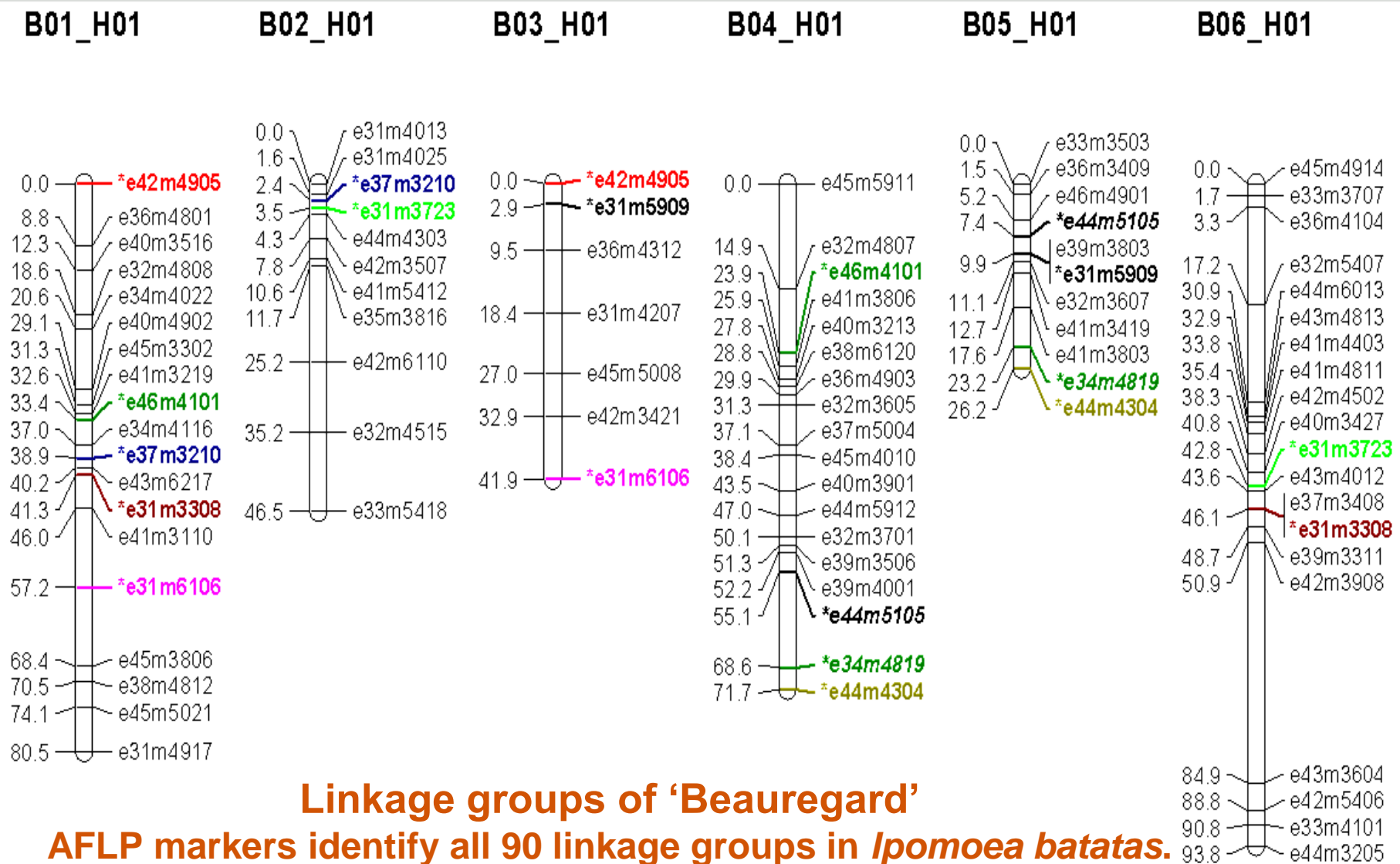
Current Status

- 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 sweetpotato are noticeably
lacking!!

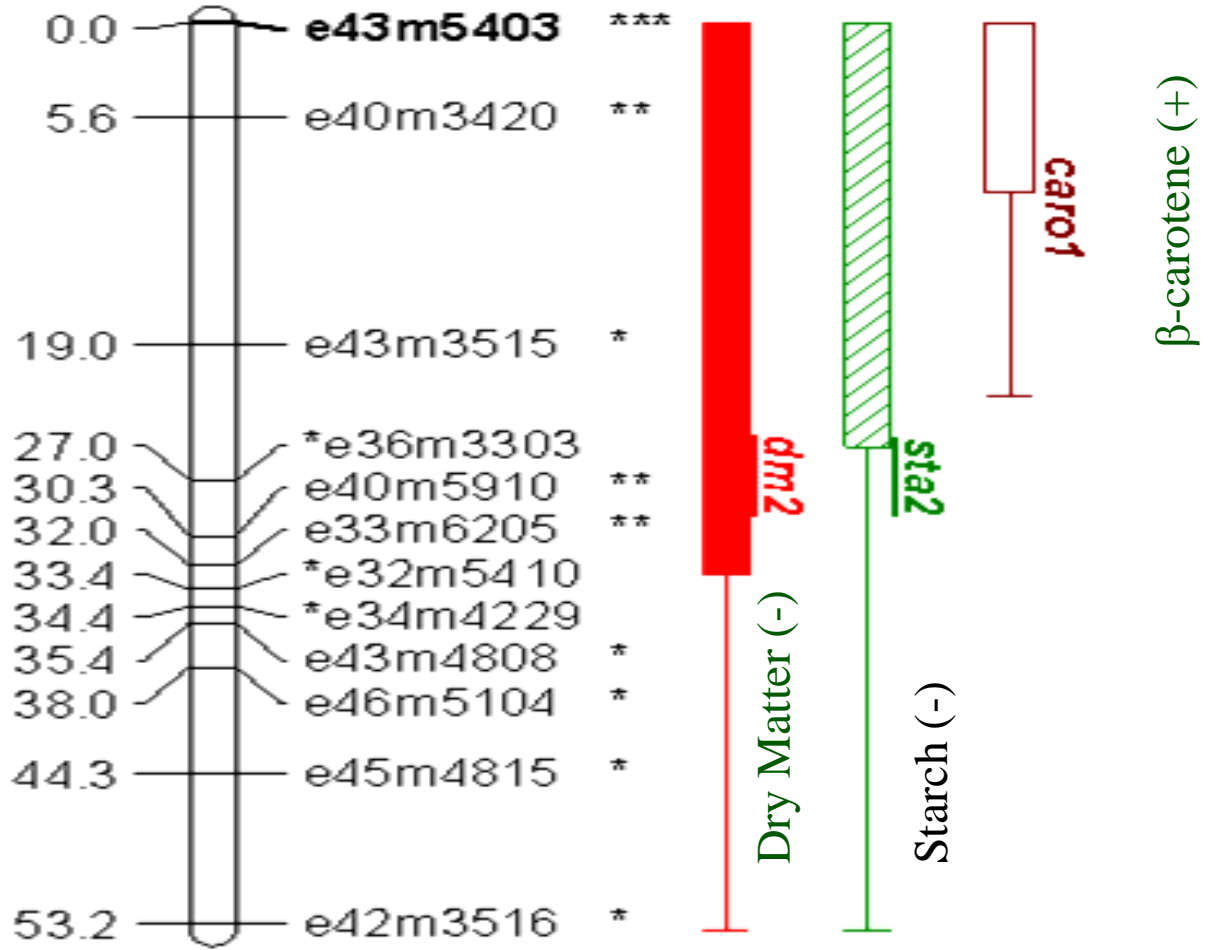
The 1st Complete Genetic Map of Sweetpotato – Developed at NCSU (Cervantes et al. 2008a,b, 2011)



Linkage groups of 'Beauregard'

AFLP markers identify all 90 linkage groups in *Ipomoea batatas*.

B23_H04



Some Examples of Genomic Resources for Sweetpotato

CIP

- Schafleitner R, Tincopa LR, Palomino O, Rossel G, Robles RF, et al. (2010) A sweetpotato gene index established by de novo assembly of pyrosequencing and Sanger sequences and mining for gene-based microsatellite markers. *BMC Genomics* 11: 604.

China

- Liu, Q. 2011. Sweet potato Omics and Biotechnology in China. *Plant Omics J* 4(6):295-301 (2011)
- Tao X, Gu Y-H, Wang H-Y, Zheng W, Li X, et al. (2012) Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [*Ipomoea batatas* (L.) Lam.]. *PLoS ONE* 7(4): e36234. doi:10.1371/journal.pone.0036234
- Wang ZY, Fang BP, Chen JY, Zhang XJ, Luo ZX, et al. (2010) De novo assembly and characterization of root transcriptome using Illumina paired-end sequencing and development of cSSR markers in sweetpotato (*Ipomoea batatas*). *BMC Genomics* 11: 726.

South Korea

- Park S-C, Kim Y-H, Ji CY, Park S, Jeong Jc, et al. (2012) Stable Internal Reference Genes for the Normalization of Real-Time PCR in Different Sweetpotato Cultivars Subjected to Abiotic Stress Conditions. *PLoS ONE* 7(12): e51502. doi:10.1371/journal.pone.0051502
- You MK, Hur CG, Ahn YS, Suh MC, Jeong BC, et al. (2003) Identification of genes possibly related to storage root induction in sweetpotato. *FEBS Lett* 536: 101–105.

USA

- McGregor CE Differential expression and detection of transcripts in sweetpotato (*Ipomoea batatas* (L.) Lam.) using cDNA microarrays: Louisiana State University. 143 p.

Sweetpotato Omics at CIP

(Jan Kreuze, et al.)

5th Korea-China-Japan Sweetpotato Workshop)

See : http://www.bjrccd.re.kr/board//bbs/board.php?bo_table=notice&wr_id=13

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 –

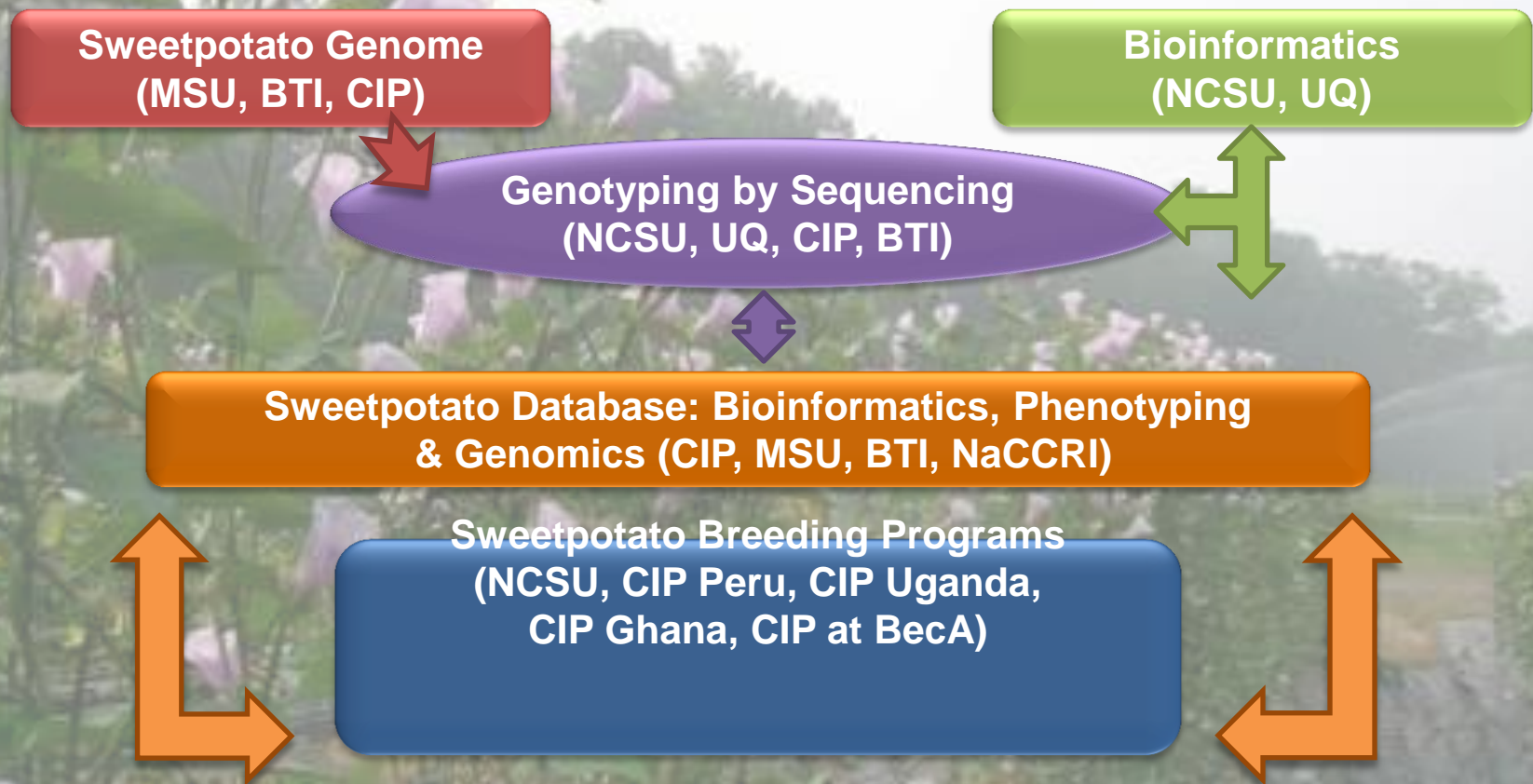
- Marker development – we are way behind the curve....
- A robust set of SNP markers
- 2x and 6x mapping, training and test populations
- 1x genetic resources

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



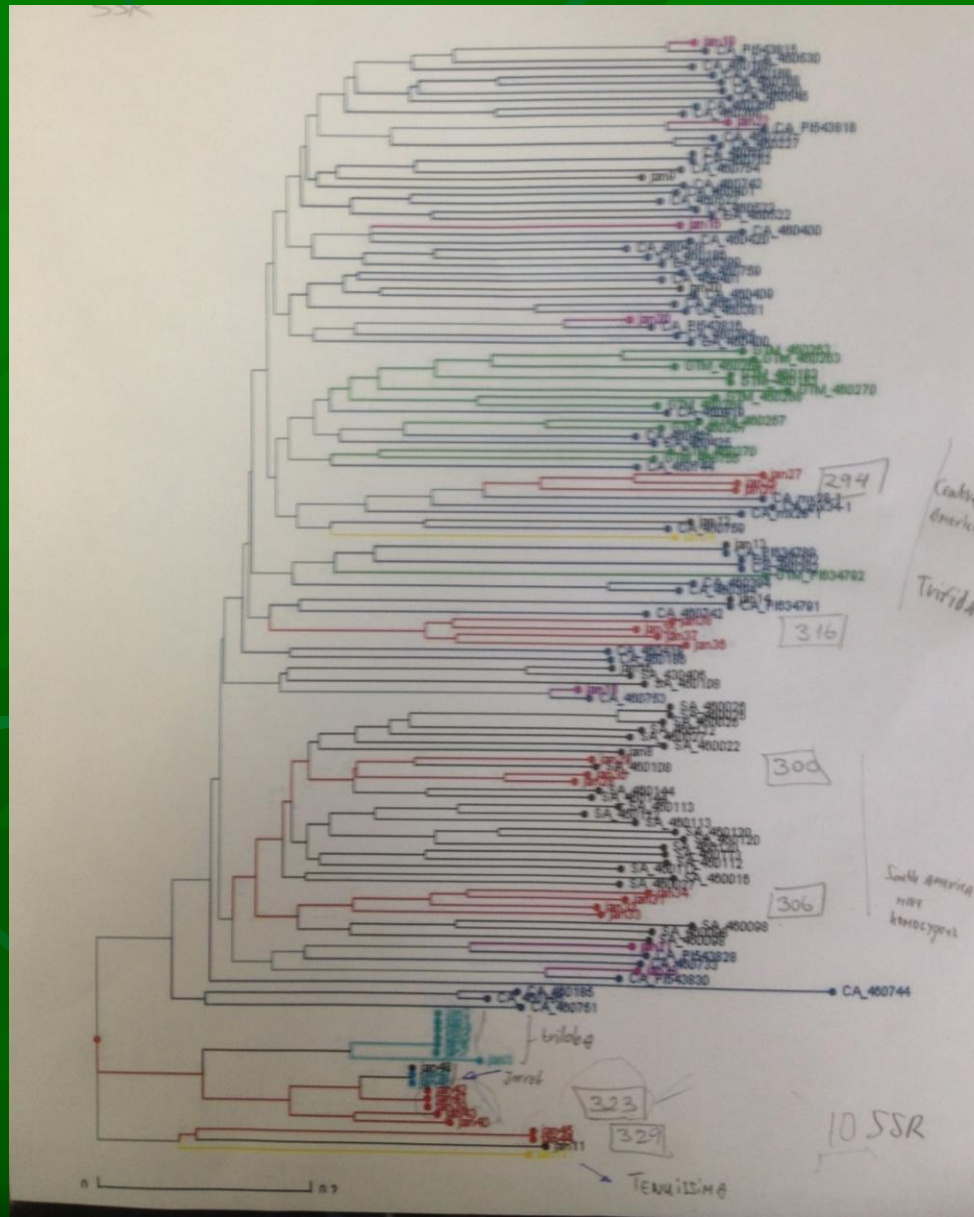
An ambitious project to sequence sweetpotato and develop modern breeding tools for a food crop that sustains million of people in SSA.

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; 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.

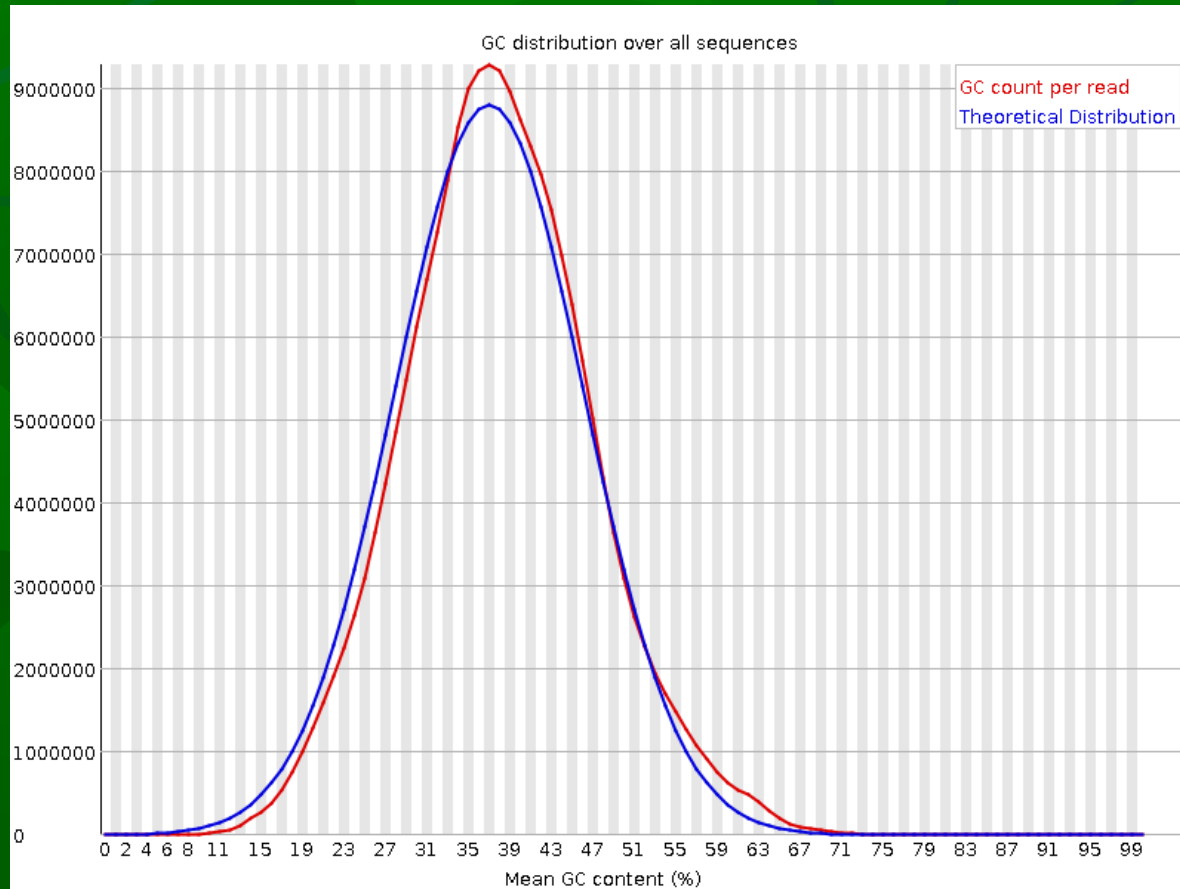
Phylogenetic Analyses of NCNSP *Ipomoea* spp. Lines (CIP,2013)



Assembly

- Scaffolds \geq 100 bp
 - Total: 385,197,028 bp
 - Total # : 533,395
 - N50 : 3,044 bp

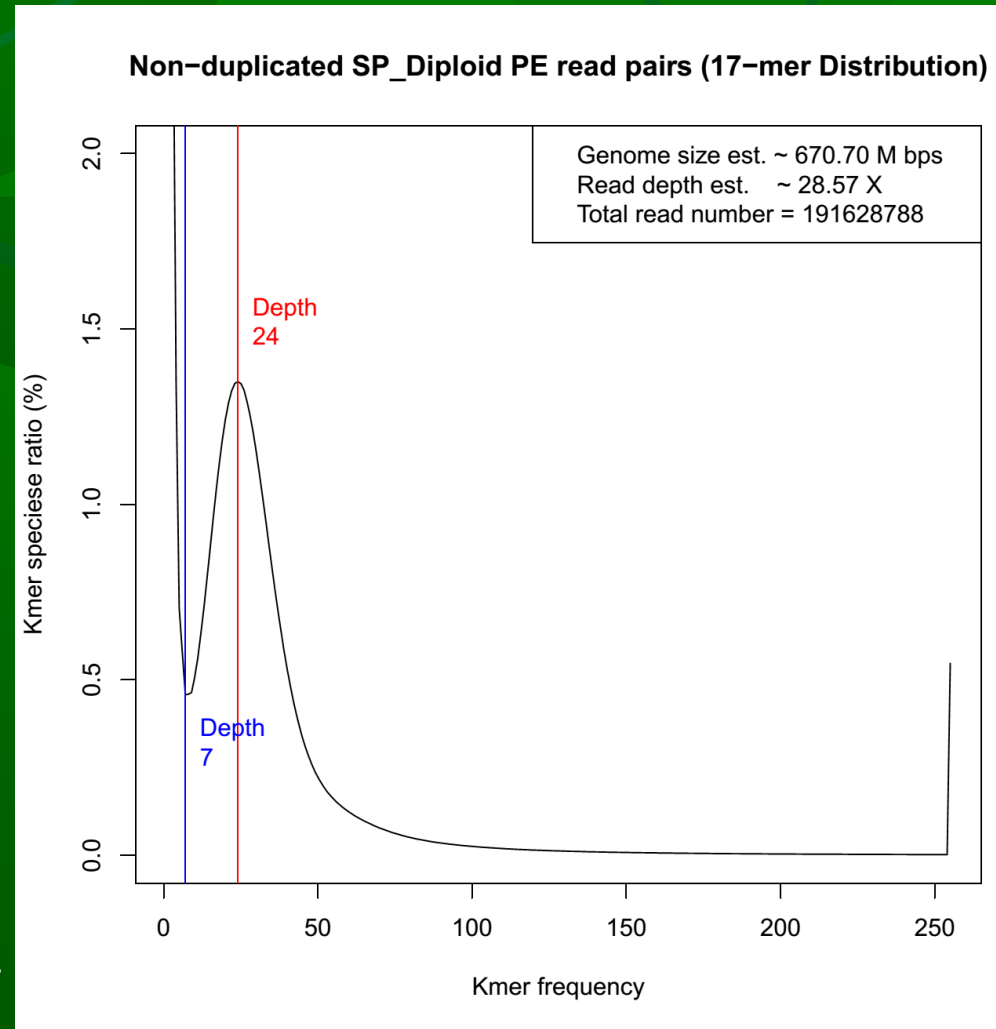
GC content distribution indicates no bacterial and virus contamination



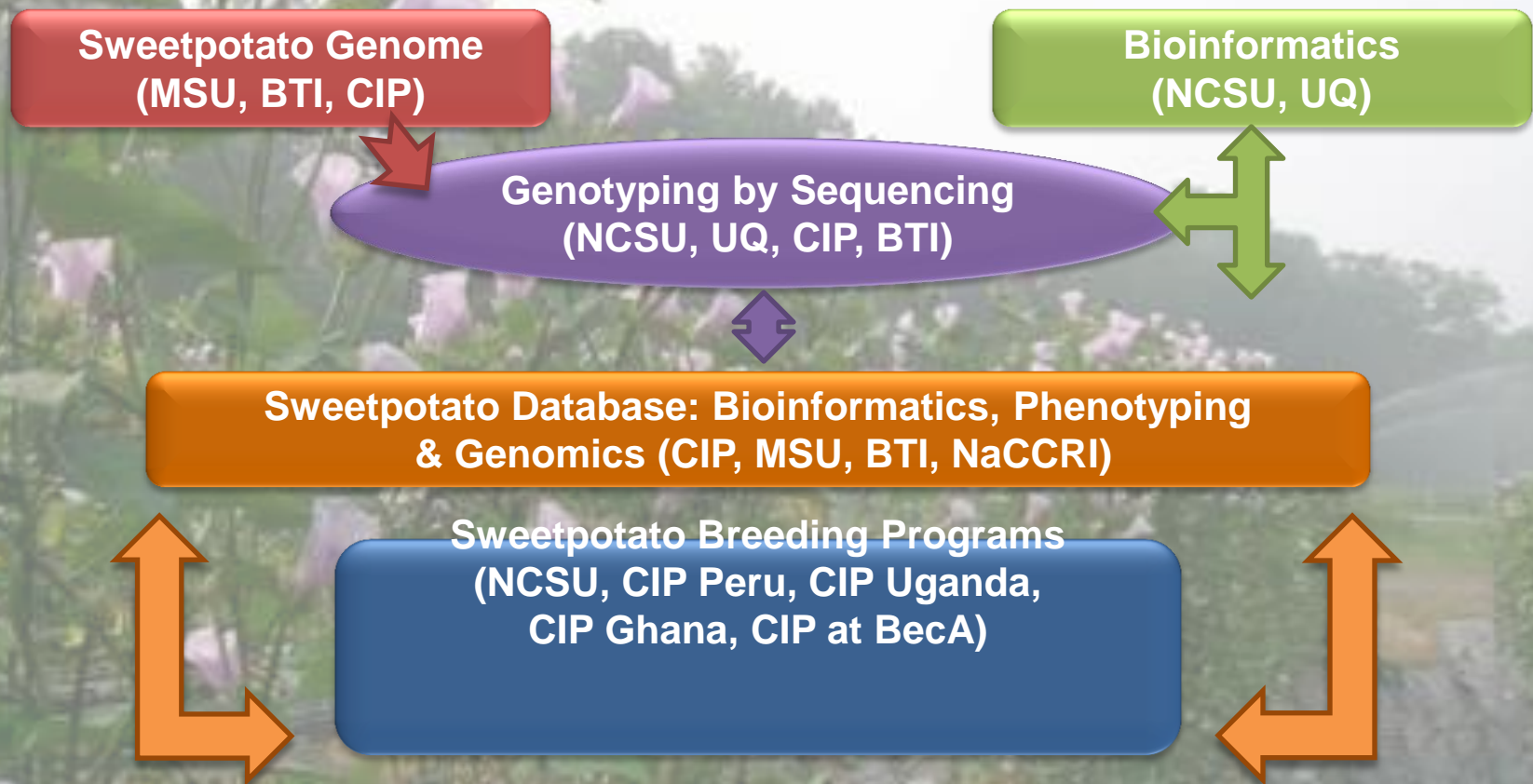
NCNSP023-3 *Ipomoea* sp. genome sequencing

One lane paired-end reads

- Raw
 - Read length : 100 bp
 - Pairs #: 201,589,735
- Remove duplications
 - Non-duplicated pairs : 9,5814,394
 - 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



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