Best Sweetpotato Scientific Paper of 2018 - Jan W. Low Award

10th Annual Sweetpotato for Profit and Health Initiative Technical Meeting
SPHI Meeting, 24th August 2019, Ubumwe Grande Hotel - Kigali

Mercy Kitavi
More than 140 million children at greater risk of illness, hearing loss, blindness and even death globally and depend on vitamin A supplements (UNICEF) (UN news 2019)
How will we grow an adequate quantity - and quality - of food to feed and nourish a rapidly growing, urbanizing world in the face of increasing water insecurity?
Sweetpotato breeding Challenges

SPVD-affected plant (left) showing small, pale green misshapen leaves with a normal plant (right) (R. Gibson).

Pests; the evil weevil

Agronomic improvement of sweetpotato has lagged behind other major food crops due to a lack of genomic and genetic resources
Climate Change Is Here - and It Looks Like Starvation

Rain-fed agriculture accounts for about 60% of global and 90% for Sub-Saharan African (SSA) staple food production. (World Relief)

As famine and drought spread through Somaliland, a villager carries bags of rice, sugar, dates and palm oil back to his house after collecting food from a charity, May 2017. (Joe Giddens / PA Wire)

Stranded locals look on during floods after Cyclone Idai, in Buzi district, outside Beira, Mozambique, March 21, 2019. (Reuters / Siphiwe Sibeko)
The next generation era!

- Genomics research is generating new tools, such as functional molecular markers and informatics, as well as new knowledge about statistics and inheritance phenomena that could increase the efficiency and precision of crop improvement.

- In particular, the elucidation of the fundamental mechanisms of heterosis and epigenetics, and their manipulation, has great potential.

- Eventually, knowledge of the relative values of alleles at all loci segregating in a population could allow the breeder to design a genotype in silico and to practice whole genome selection.

- As the costs for the implementation of genomics-assisted crop improvement come down, particularly for inbreeding and/or minor crops; marker-assisted breeding and selection is gradually evolving into 'genomics-assisted breeding' for crop improvement.
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, NaCRRRI)

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

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

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

  http://sweetpotato.plantbiology.msu.edu/

- Sweetpotato database (SPBase) for data storage and management together with breeder friendly analytical tools

- High-throughput DNA sequence-based genotyping method. *trifida* and hexaploid sweetpotato

- Capacity building to translate this research into applied breeding programs in SSA

- Genetic mapping and quantitative trait loci (QTL) mapping methods specific to analysis of the complex hexaploid sweetpotato
“Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement”


NATURE COMMUNICATIONS | (2018) 9:4580 | DOI: 10.1038/s41467-018-06983-8 | www.nature.com/naturecommunications
Introduction

- Sweetpotato [Ipomoea batatas (L.) Lam.] is a globally important staple food crop, especially for sub-Saharan Africa

- Inherent challenges in breeding
  - heterozygous,
  - clonally propagated
  - Polyploid (n=6, a set has 15, therefore 90 chromosomes)

- Agronomic improvement of sweetpotato has lagged behind other major food crops due to a lack of genomic and genetic resources

- The paper reports the genome sequences of two diploid relatives, I. trifida and I. triloba, and show that these high-quality genome assemblies are robust references for hexaploid sweetpotato
Scientist take any part of the sweetpotato plant and treat them with chemicals that break them open, releasing the DNA. The DNA is the purified Whole Genome Sequencing (WGS)

WGS is a laboratory procedure that determines the order of the bases in the genome of an organism in one process. WGS provides a very precise DNA fingerprint that can help understand genes and enzymes for all biological functions, molecular pathways and cellular components.
Morphology of Ipomoea batatas, I. trifida, and I. triloba. a, b Flowers (a) and roots (b) of I. batatas “Taizhong6”, I. trifida NCNSP0306, and I. triloba NCNSP0323
Reference Genome is a good representative of the hexaploid sweetpotato

**a**, Percentages of hexaploid ‘Tanzania’ reads aligned to the *I. trifida* and *I. triloba* genome assemblies

**b**, Percentages of reads aligning better to the *I. trifida* genome than the *I. triloba* genome

**c**, Comparison of the hexaploid sweetpotato molecules with the two diploid assemblies trifida (left)/triloba (right) (innermost circle displays homologies)
Comparative genomics and lineage-specific family expansion

I. batatas “Beauregard” and the predicted proteomes from I. trifida, I. triloba, and seven other representative plant species, including I. nil (Japanese morning glory), Solanum lycopersicum (tomato), Solanum tuberosum (potato), Vitis vinifera (grapevine), Arabidopsis thaliana (model eudicot), Oryza sativa (rice), and Amborella trichopoda (basal angiosperm)

a, 79.3% of total input sequences clustered into 19,901 orthologous groups, of which 3269 were present only in the four Ipomoea species, and 1680 specific to the Batatas complex (I. batatas, I. trifida, and I. triloba) and absent in I. nil

b, Distribution of $K_s$ of orthologous or paralogous genes within and between genomes of I. trifida (Itf), I. triloba (Itb), I. nil (Inl), tomato (Sly) and potato (Stu). Estimated times of speciation

c, Percentage of multiplicated genomic regions in I. trifida, I. triloba, I. nil, and tomato (triplicated blocks (23.5%, 34.8%, and 28.0% in I. trifida, I. triloba, and I. nil, respectively), and in tomato genome (6.0%) WGT events were calculated using a mutation rate of $7 \times 10^{-9}$ substitutions per site per year. Mya, million years ago
Origins and evolution of the Batatas complex

six distinct lineages recovered, early divergence of ancestral lineages for *I. splendor-sylva* and the remainder of the Batatas complex.
Key take home messages

- Hexaploid sweetpotato genome contains sequences that are uniquely shared with either of these two diploid species.

- Collectively, our results suggest that the two diploid genome assemblies can serve as robust reference sequences for hexaploid sweetpotato as suggested by the high percentages (>90%) of hexaploid reads aligned to either I. trifida or I. triloba.

- The I. trifida genome is a slightly better reference, while the I. triloba genome shares unique features with the hexaploid genome and can serve as a complement to the I. trifida genome.

- There is lineage-specific adaptation events in these root and tuber crops. In particular, two I. batatas sporamin genes, orthologous to the I. trifida genes itf10g10920 and itf01g01870 that are within the Ipomoea lineage-specific expansion, were upregulated during storage root development in “Beauregard.”

  - Sporamin, a Kunitz-type trypsin inhibitor (KTI), is a major storage protein in sweetpotato storage roots, and is analogous to patatin in potato which plays an important role in storage, defense, and development.
Genomics-Enabled Next-Generation Breeding Approaches for Food security, Nutrition and Climate resilient
Enabling scientists unravel the complex genetics of hexaploid sweetpotato

Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping

Marcelo Mollinari, Bode A. Olukolu, Guilherme da S. Pereira, Awais Khan, Dorcus Gemenet, Craig Yencho Zhao-Bang Zeng (doi: https://doi.org/10.1101/689638)

Creation of linkage groups

Identify allele present at each locus for each individual and the mutation occurring
QTL Mapping for β-Carotene & Starch

Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population

Developing diagnostic markers for important agronomic traits

Storage root formation and bulking in sweetpotato

1) Estimate the genetic variability CSRFB sweetpotato cultivars in Uganda
2) Discover genetic markers and associated putative functional genes for CSRFAB traits to speed its improvement in sweetpotato
   • genes related to growth and regulation of growth hormones, leaf senescence and root development
3) Determine the general and specific combining ability of parents, heritability and the components of heterosis of CSRFAB in sweetpotato
Potential increase using CSRFAB is a major step towards solving the problem in food insecurity around the sweetpotato farmers in the region and beyond.

Crossing CSRFAB and DCSRFAB genotypes resulted in heterosis increment in hybrid population leading to transgressive segregation which is a key for the development of superior hybrid varieties.

The genetic gain achieved for yield indicates the progress plant breeders can make in F1 by crossing CSRFAB and DCSRFAB sweetpotato parental genotypes. Such huge genetic gain for a single generation highlights the importance of CSRFAB traits for improving sweetpotato yields.

Achieved genetic gains for Heterosis exploitation

Genome-Wide Association Study Identified Candidate Genes Controlling Continuous Storage Root Formation and Bulking in Hexaploid Sweetpotato

Astère Bararyenya¹,², Bode Olukolu³, Phinehas Tukamuhabwa¹, Robert O.M. Mwanga⁴, Wolfgang J. Grüneberg⁵, Wellington Ekaya⁶, Jan Low⁷, Mildred Ochwo-Ssemakula¹, Thomas L Odong¹, Herbert Talwana¹, Arfang Badji¹, Martina Kyalo⁶, Yao Nasser⁶, Dorcus Gemenet⁷, Mercy Kitavi⁷

Submitted to BMC Plant Biology PBIO-D-19-00916
"Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively-associated β-carotene and starch content in hexaploid sweetpotato [Ipomoea batatas (L.) Lam.]”

Dorcus C Gemenet¹,²,a, Guilherme da Silva Pereira²,a, Bert De Bœck³, Joshua C Wood⁴, Marcelo Mollinari², Bode A Olukolu²,¹¹, Federico Diaz³, Veronica Mosquera³, Reuben T Ssali³, Maria David³, Mercy N Kitavi³, Gabriela Burgos³, Thomas Zum Felde³, Marc Ghislain¹, Edward Carey⁶, Jolien Swanckaert⁶, Lachlan JM Coin⁷, Zhangjun Fei⁸, John P Hamilton⁴, Benard Yada⁹, G Craig Yencho², Zhao-Bang Zeng², Robert OM Mwanga⁵, C Robin Buell⁴, Awais Khan³,¹⁰, Wolfgang J Gruneberg³

Accepted yesterday - TAAG-D-19-00373

Close linkage between SuSY (sucrose synthase which determines starch content) and PSY (main rate determining enzyme of the carotenoid pathway)
Improve breeding efficiency

When a phenotype is not the genotype: Implications of phenotype misclassification and pedigree errors in genomics-assisted breeding of sweetpotato [*Ipomoea batatas* (L.) Lam.]

DorcuC. Gemenet¹*, Bert De Boeck², Guilherme Da Silva Pereira³, Mercy N. Kitavi¹, Reuben T. Ssali⁴, Obaiya Utoblo⁴, Jolien Swanckaert⁵, Edward Carey⁴, Wolfgang Gruneberg², Benard Yada⁶, Craig Yencho³, Robert O. M. Mwanga⁵

Submitted to Frontiers in Plant Science-Plant breeding

**Quality control of genotypes**: Tracking the purity of genotypes at different breeding stages
Understanding breeding populations and development of QC SNP set for forward breeding and genomic selection
Using genomics to understand taxonomy and distribution of pathogen populations

MiSeq confirms the Promiscuity of sweetpotato viruses in Uganda

Adero J., Yada B., Yencho C, Nasser Y., Machuka E., Mwanga R., Low J., Kitavi M. (Manuscript in preparation)

<table>
<thead>
<tr>
<th>Pathogen Type</th>
<th>Pathogen Name</th>
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<tbody>
<tr>
<td>Crown gall</td>
<td>Agrobacterium tumefaciens</td>
</tr>
<tr>
<td>Hairy roots</td>
<td>Agrobacterium rhizogenes</td>
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Sweetpotato chlorotic fleck virus

- Sweet potato virus C: 29%
- Sweet potato badnavirus A: 26%
- Sweet potato badnavirus B: 24%

Joanne Adero
Transcriptome studies; heatmap of up and down regulated genes during heat stress in sweetpotato
Knowing the differentially expressed genes is important for breeding abiotic and abiotic stresses.

Differentially Expressed Genes (DEGs) during heat stress and their possible role in augmenting stress tolerance in Sweetpotato

Mercy Kitavi, Robin Buell, Dorcus Gemenet, John Hamilton, Joshua Wood
(work done during the Borlaug fellowship at MSU - Manuscript in preparation)

- response to heat
- response to high light intensity
- protein folding
- response to hydrogen peroxide
- Jasponic and salicylic acid pathways
Why genomics enabled breeding?

**Natural Populations**

- **Selected individuals**
- **Progeny testing**
- **Elite individuals**
- **Breeding population**

**Introduction of new genetic variation**

\[ y_t = \frac{ir \sigma_A}{y} \]

- **Time/Resource consuming**
- **Crossing**
- **Testing**
- **Selection**

**Improved varieties**

**Several generations**
Acknowledgements

The African Biosciences Challenge Fund (ABCF)
Asanteni Sana!

Haiku
Genes, genetics, genomes
What a golden sweetpotato
Food, feed, health and wealth