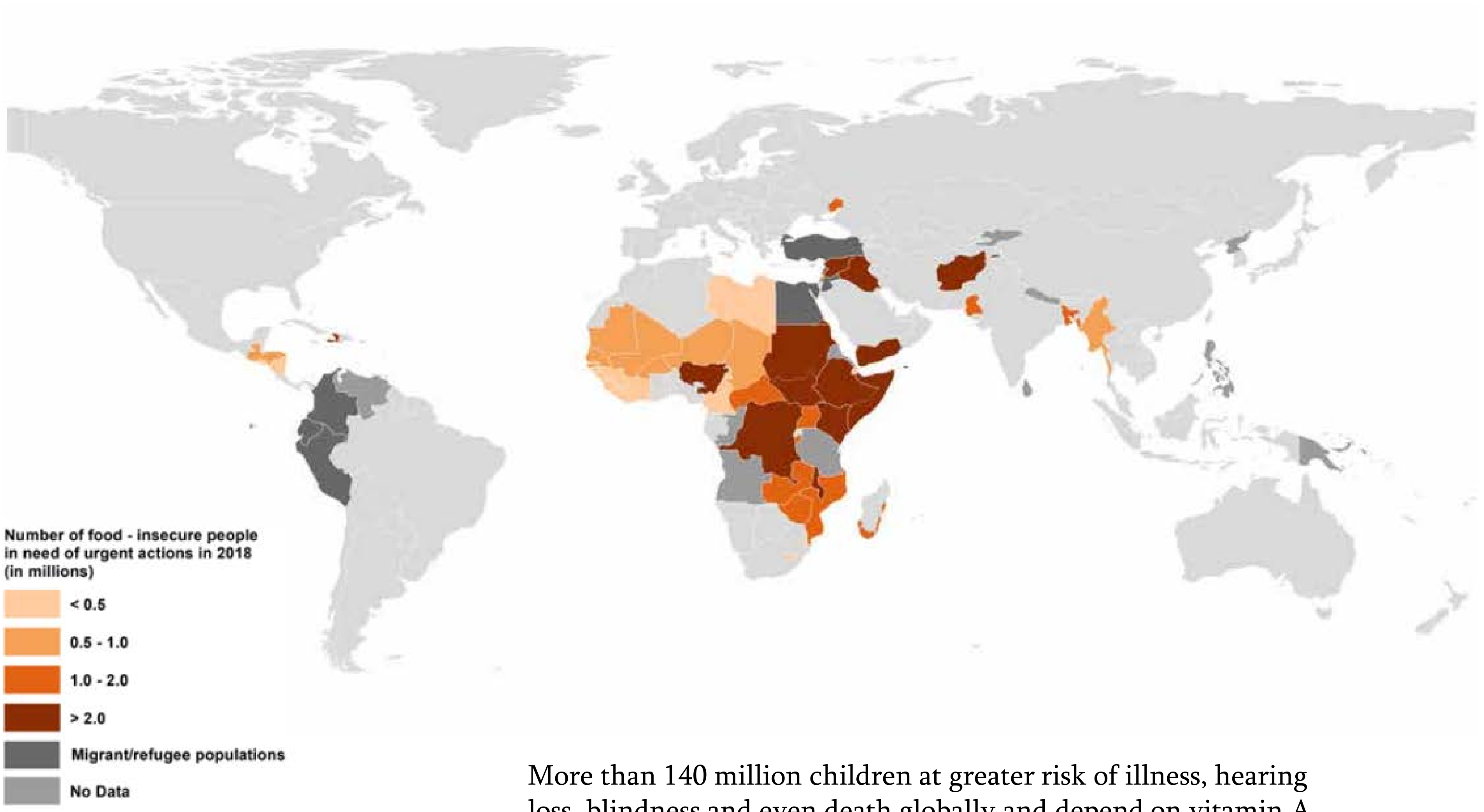
Best Sweetpotato Scientific Paper of 2018 - Jan W. Low Award

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

Mercy Kitavi

Global food status 2019

FSIN
Food Security Information Network



Source: FSIN GRFC March 2019

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)

2019 Facts

Rural populations account for 45.3% of the world's total population, but 70% of the world's extremely poor. The global poverty rate in rural areas is currently 17%, more than double the urban poverty rate of 7%

2019 Global Food Policy Report

2019 Global Food Policy Report

INTERNATIONAL
FOOD POLICY
RESEARCH
INSTITUTE
IFPRI

Crises in Rural Areas Threatens Progress in Hunger, Poverty Reduction; Urgent Need for Rural Revitalization, Strong Policies and Accountability

GLOBAL FOOD SECURITY SYMPOSIUM 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?

THE CHICAGO
COUNCIL
ON
GLOBAL
AFFAIRS

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)

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

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)*

The next generation era!

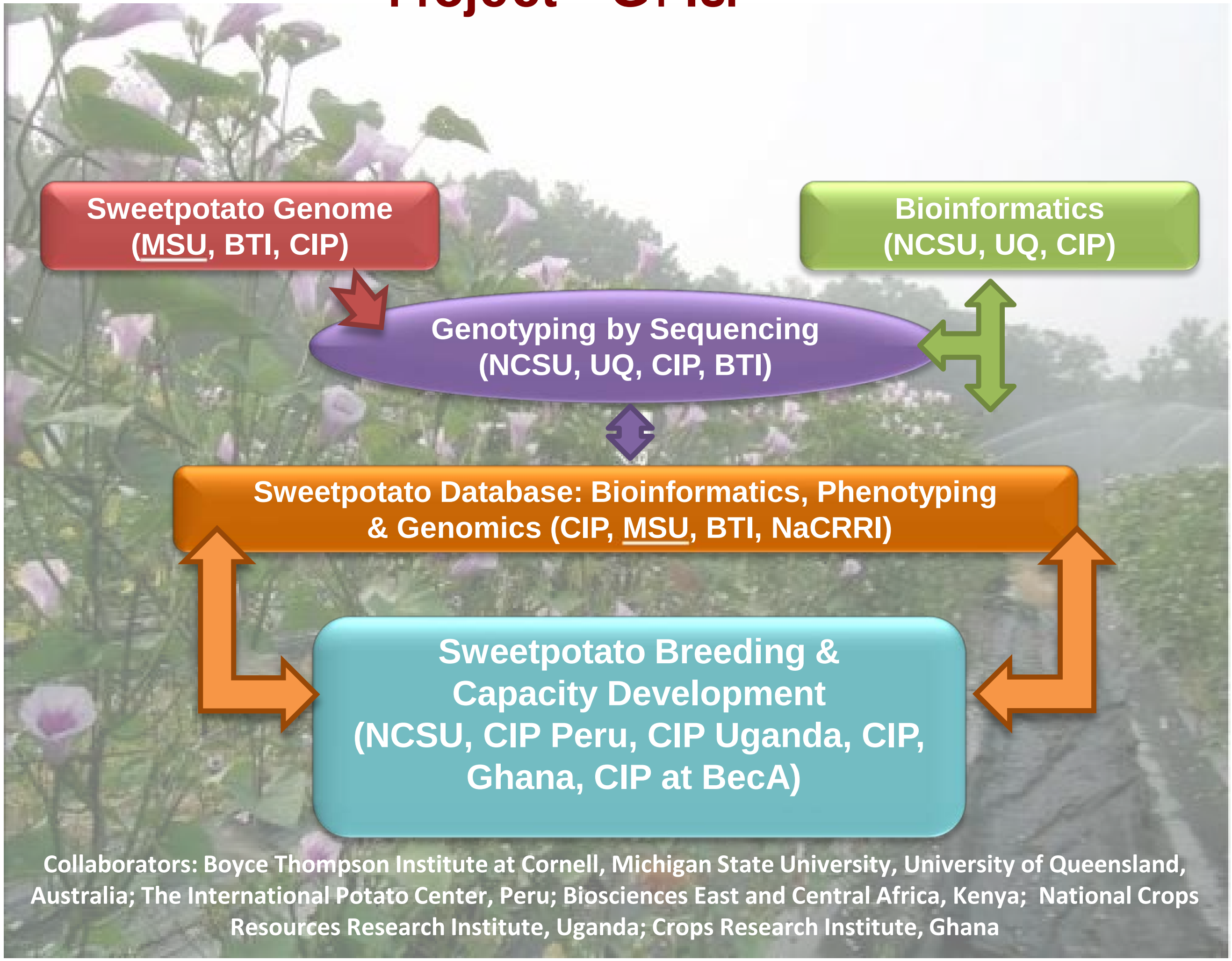
- Genomics research is generating new tools, such as functional molecular markers and informatics, as well as new knowledge about statistics and inheritance phenomena that could increase the efficiency and precision of crop improvement.

- 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, NaCRRI)

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 million of people in SSA

- Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement – Wu et al 2018 *Nature Communications* **volume 9**, Article number: 4580 (2018)

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”

Shan Wu , Kin H. Lau , Qinghe Cao, John P. Hamilton , Honghe Sun, Chenxi Zhou ,Lauren Eserman, Dorcus C. Gemenet, Bode A. Olukolu, Haiyan Wang, Emily Crisovan, Grant T. Godden, Chen Jiao, Xin Wang, Mercy Kitavi, Norma Manrique-Carpintero, Brieanne Vaillancourt, Krystle Wiegert-Rininger, Xinsun Yang, Kan Bao, Jennifer Schaff, Jan Kreuze, Wolfgang Gruneberg, Awais Khan, Marc Ghislain, Daifu Ma, Jiming Jiang, Robert O.M. Mwanga, Jim Leebens-Mack, Lachlan J.M. Coin, G. Craig Yencho, C. Robin Buell & Zhangjun Fei

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

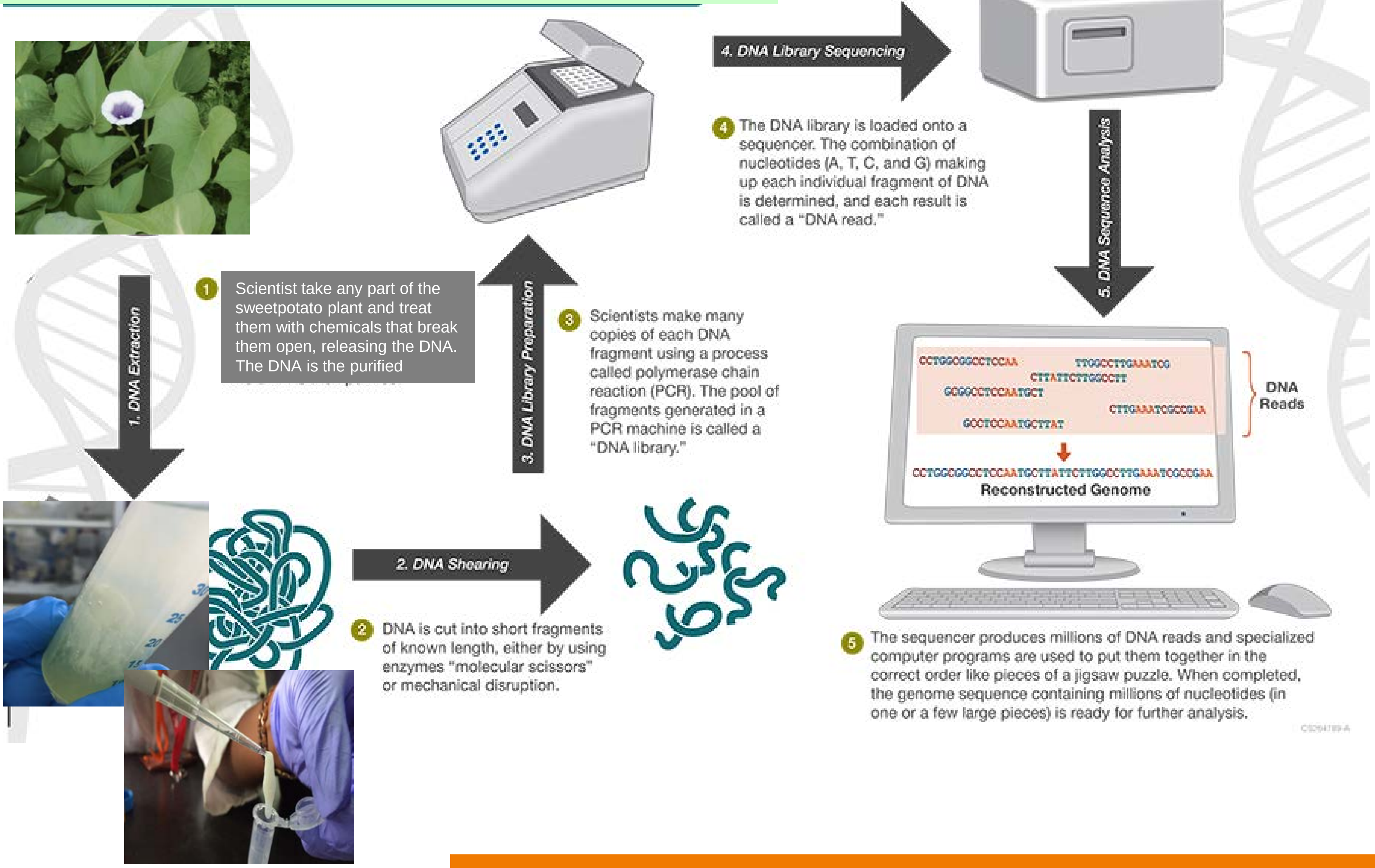
- Inherent challenges in breeding
  - heterozygous,
  - clonally propagated
  - Polyploid (n=6, a set has 15, therefore 90 chromosomes)

- 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

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



① 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

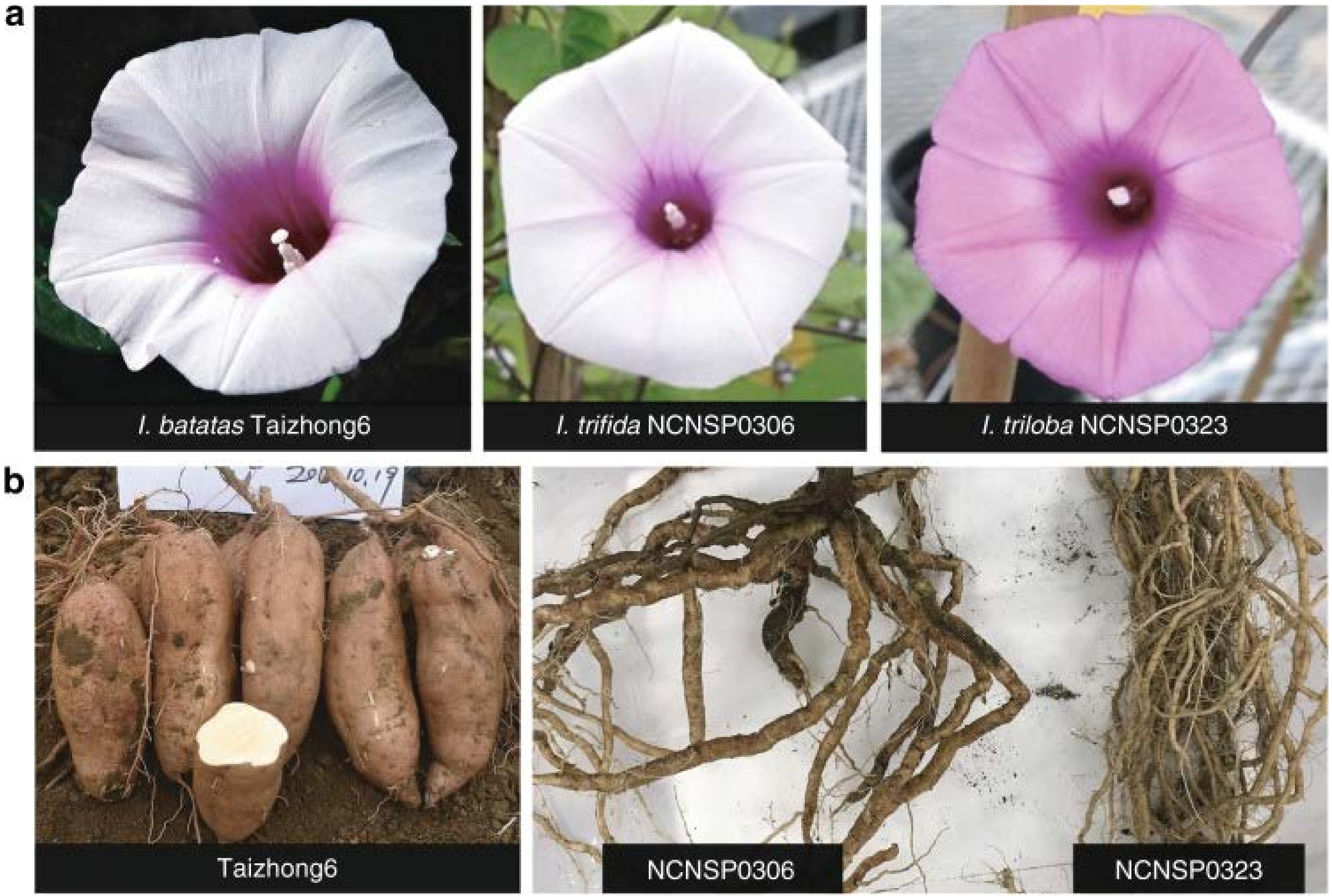
② DNA is cut into short fragments of known length, either by using enzymes "molecular scissors" or mechanical disruption.

③ Scientists make many copies of each DNA fragment using a process called polymerase chain reaction (PCR). The pool of fragments generated in a PCR machine is called a "DNA library."

④ The DNA library is loaded onto a sequencer. The combination of nucleotides (A, T, C, and G) making up each individual fragment of DNA is determined, and each result is called a "DNA read."

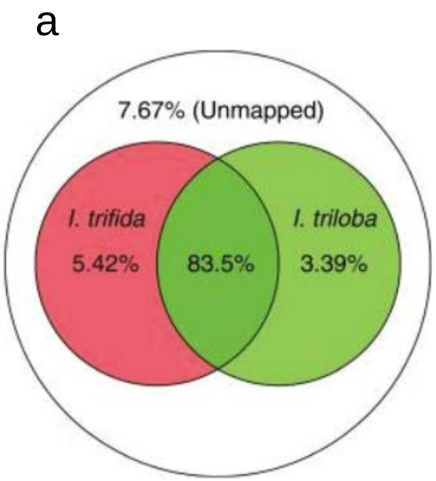
⑤ The sequencer produces millions of DNA reads and specialized computer programs are used to put them together in the correct order like pieces of a jigsaw puzzle. When completed, the genome sequence containing millions of nucleotides (in one or a few large pieces) is ready for further analysis.

Study Materials

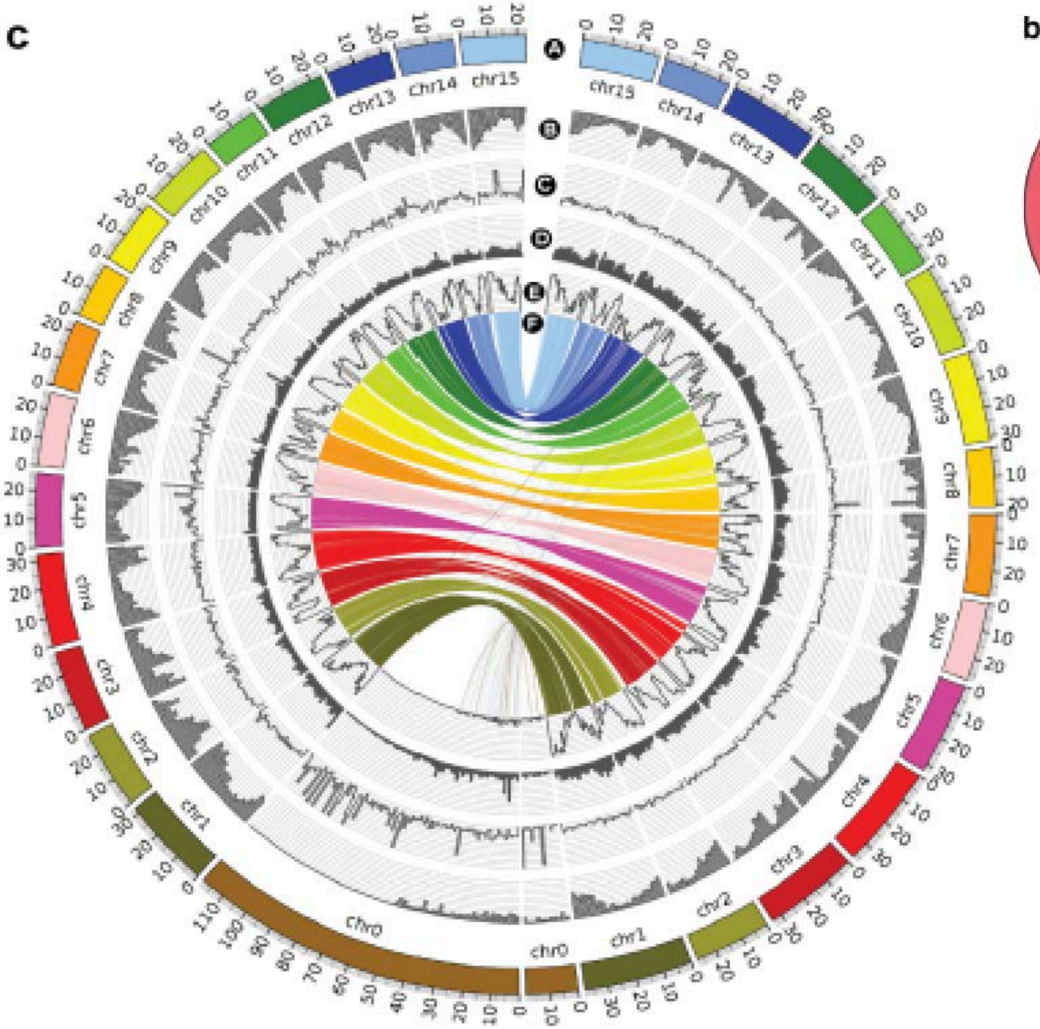


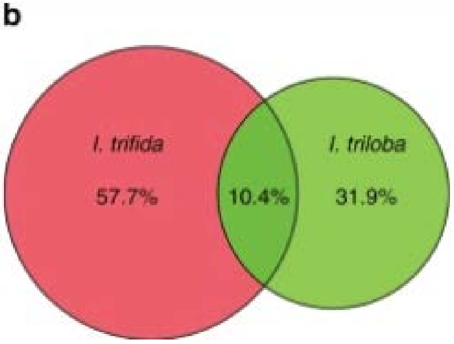
Morphology of Ipomoea batatas, I. trifida, and I. triloba. a, b Flowers (a) and roots (b) of I. batatas “Taizhong6”, I. trifida NCNSP0306, and I. triloba NCNSP0323

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

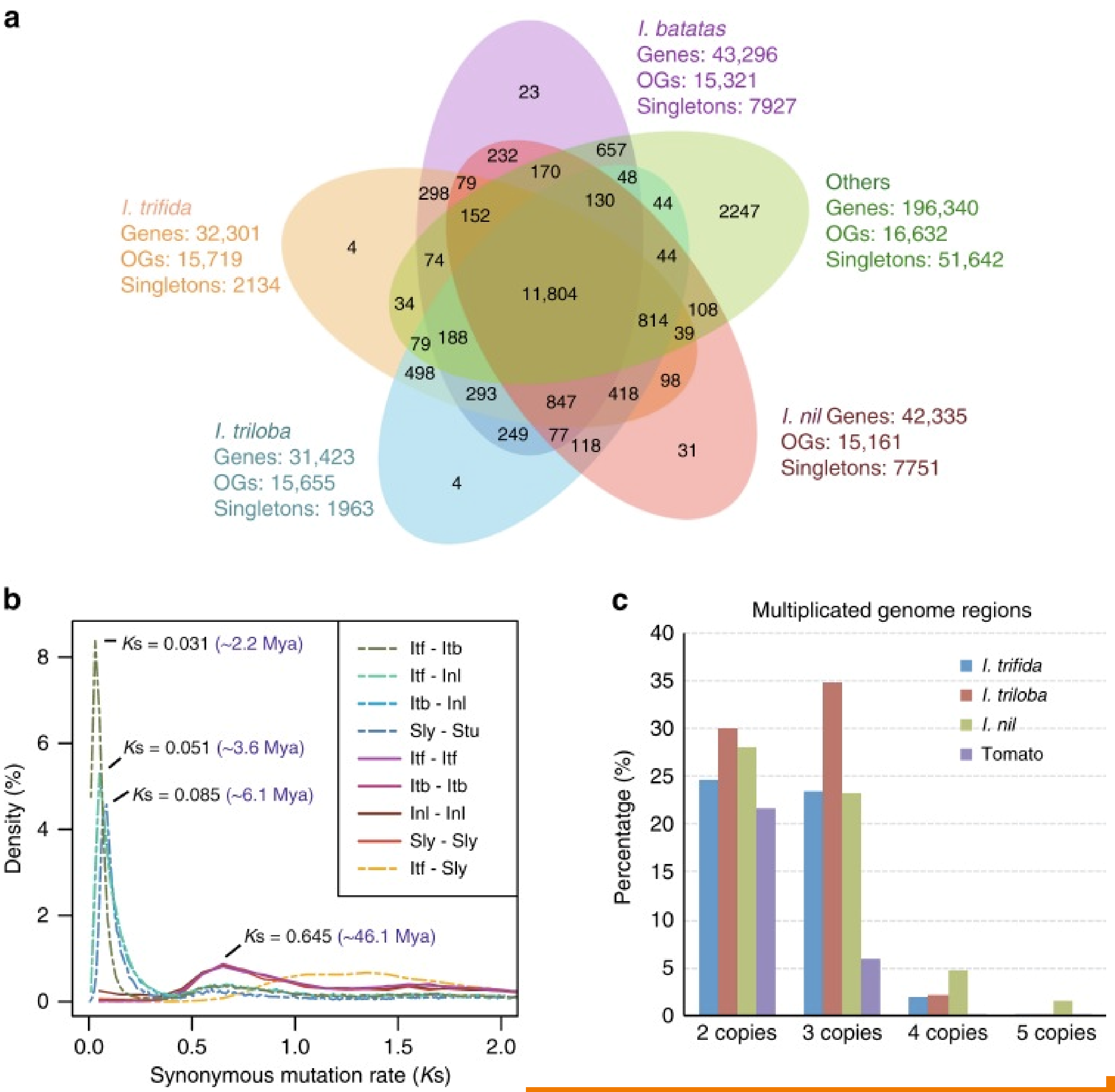




b, Percentages of reads aligning better to the *I. trifida* genome than the *I. triloba* genome

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)

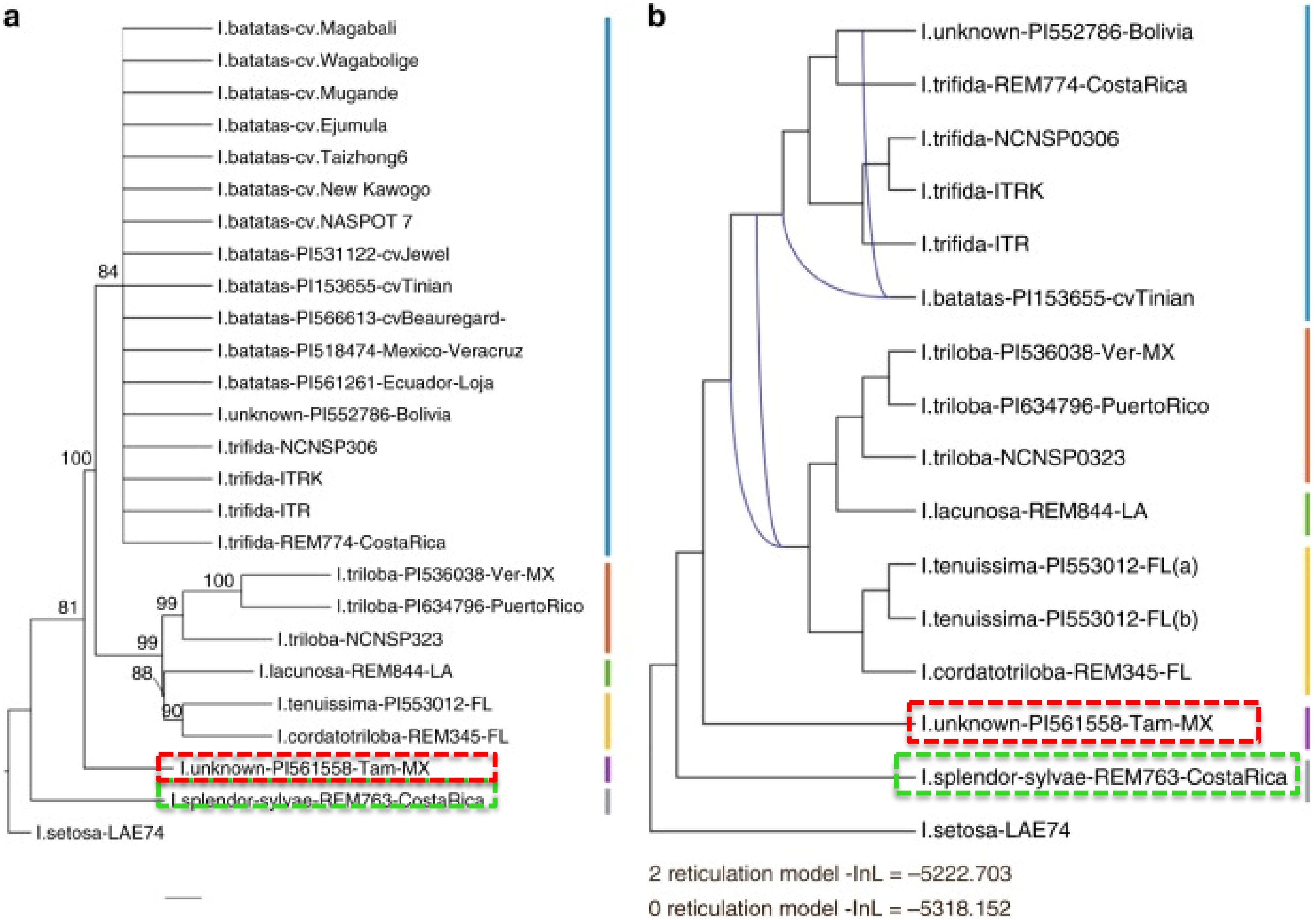
a, 79.3% of total input sequences clustered into 19,901 orthologous groups, of which 3269 were present only in the four Ipomoea species, and 1680 specific to the Batatas complex (I. batatas, I. trifida, and I. triloba) and absent in I. nil

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 7×10^{-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-sylvae* 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

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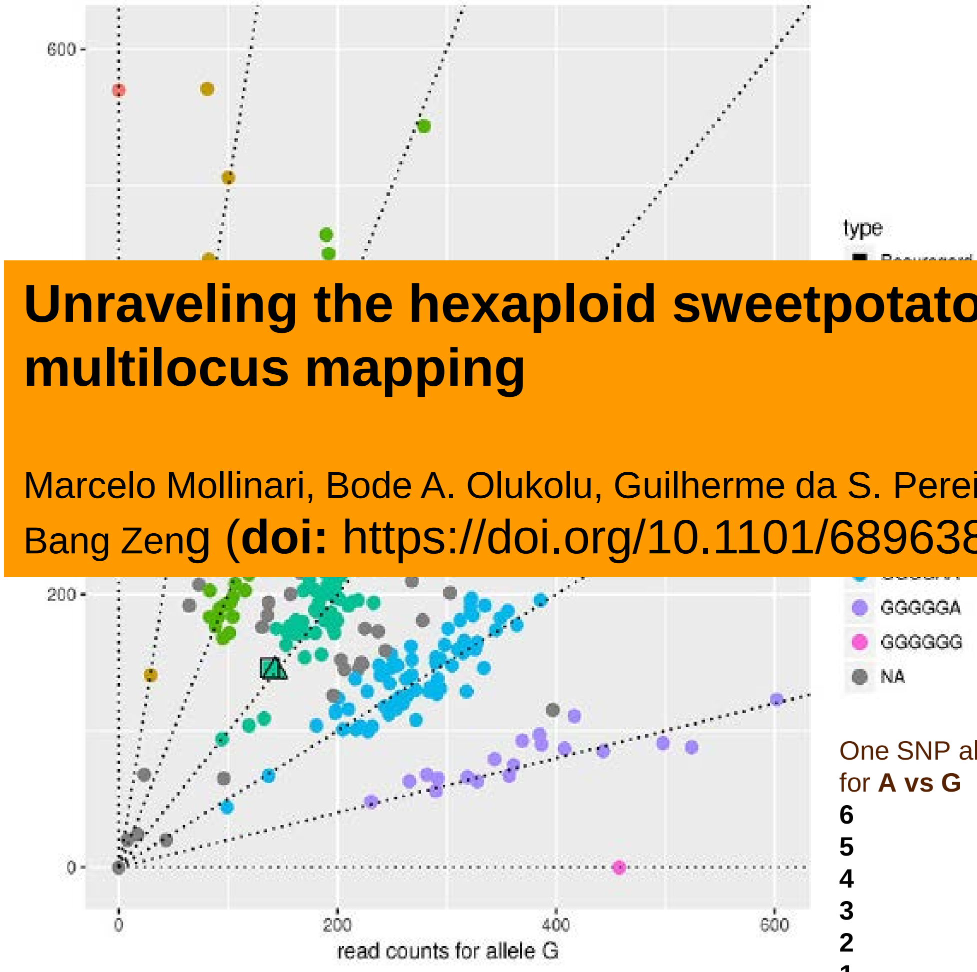
Genomics-Enabled Next-Generation Breeding Approaches for Food security, Nutrition and Climate resilient

SPHI
Sweetpotato for Profit and Health Initiative

Enabling scientists unravel the complex genetics of hexaploid sweetpotato



Unraveling the hexaploid sweetpotato inheritance using ultra-dense multilocus mapping

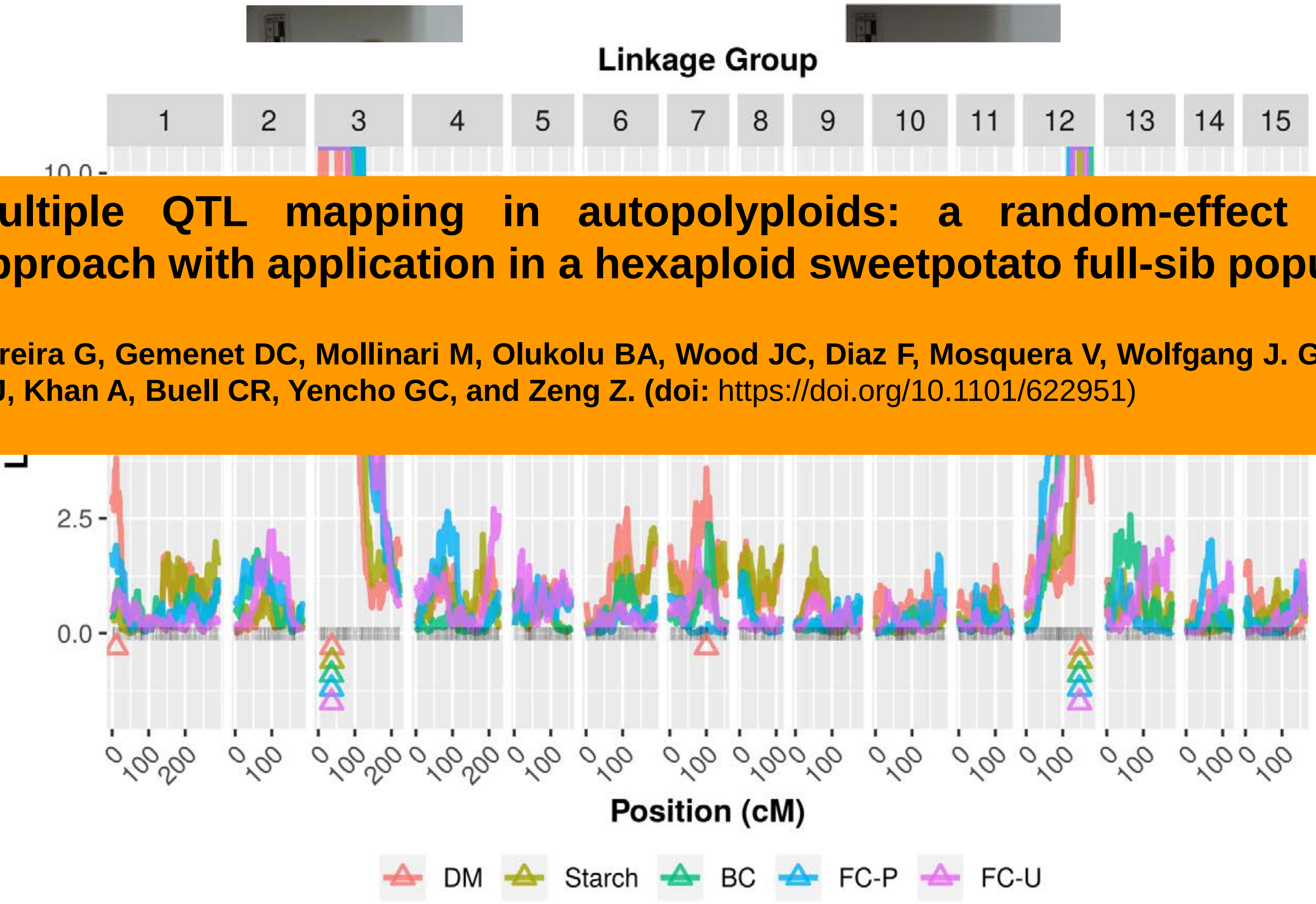
Marcelo Mollinari, Bode A. Olukolu, Guilherme da S. Pereira, Awais Khan, Dorcus Gemenet, Craig Yencho Zhao-Bang Zeng (**doi:** https://doi.org/10.1101/689638)

Creation of linkage groups

One SNP allele dosage
for **A vs G**
6
5
4
3
2
1
0

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

Pereira G, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Diaz F, Mosquera V, Wolfgang J. Gruneberg WJ, Khan A, Buell CR, Yencho GC, and Zeng Z. (doi: https://doi.org/10.1101/622951)

Developing diagnostic markers for important agronomic traits

Storage root formation and bulking in sweetpotato

Continous

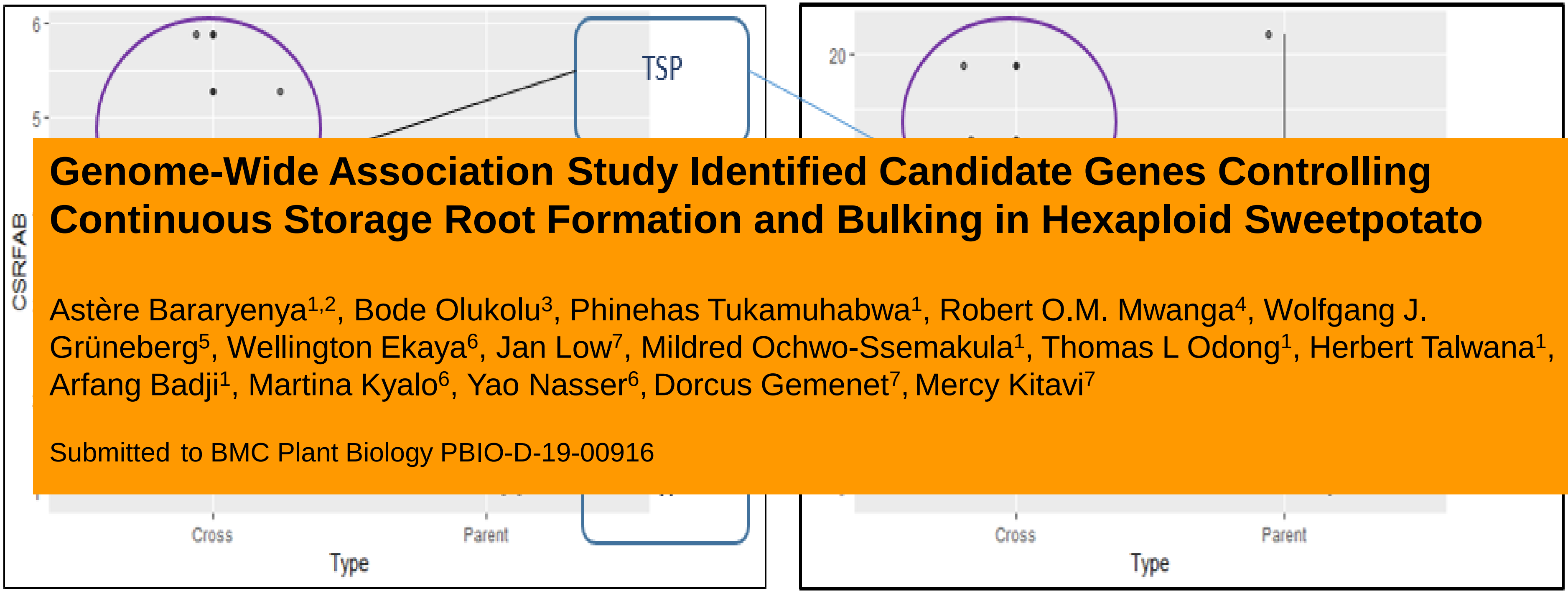
Discontinous

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

Achieved genetic gains for Heterosis exploitation



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

Astère Bararyenya[1,2], Bode Olukolu[3], Phinehas Tukamuhabwa[1], Robert O.M. Mwanga[4], Wolfgang J. Grüneberg[5], Wellington Ekaya[6], Jan Low[7], Mildred Ochwo-Ssemakula[1], Thomas L Odong[1], Herbert Talwana[1], Arfang Badji[1], Martina Kyalo[6], Yao Nasser[6], Dorcus Gemenet[7], Mercy Kitavi[7]

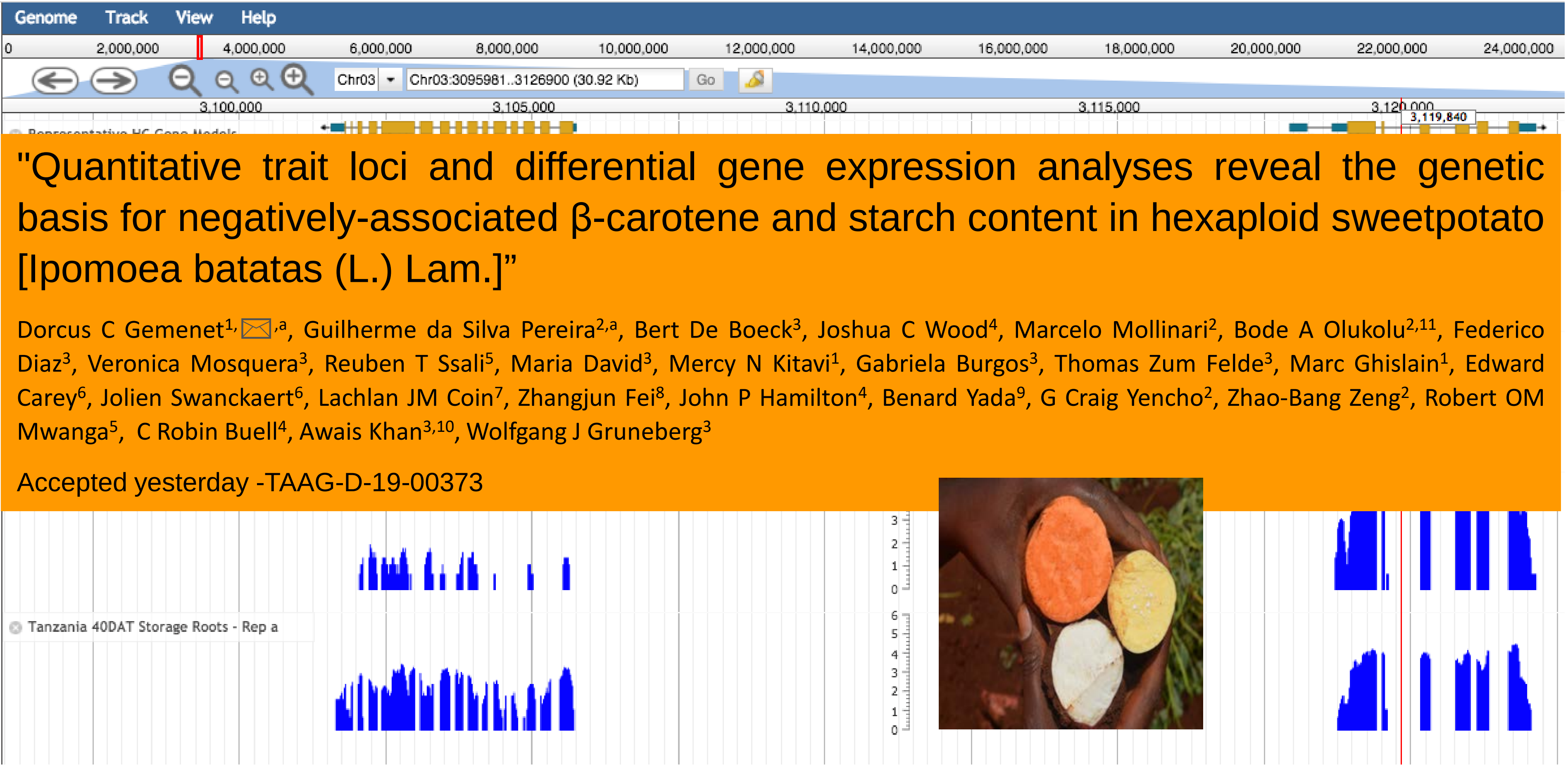
Submitted to BMC Plant Biology PBIO-D-19-00916

- Potential increase using CSRFAB is a 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

Understanding Trait Architecture



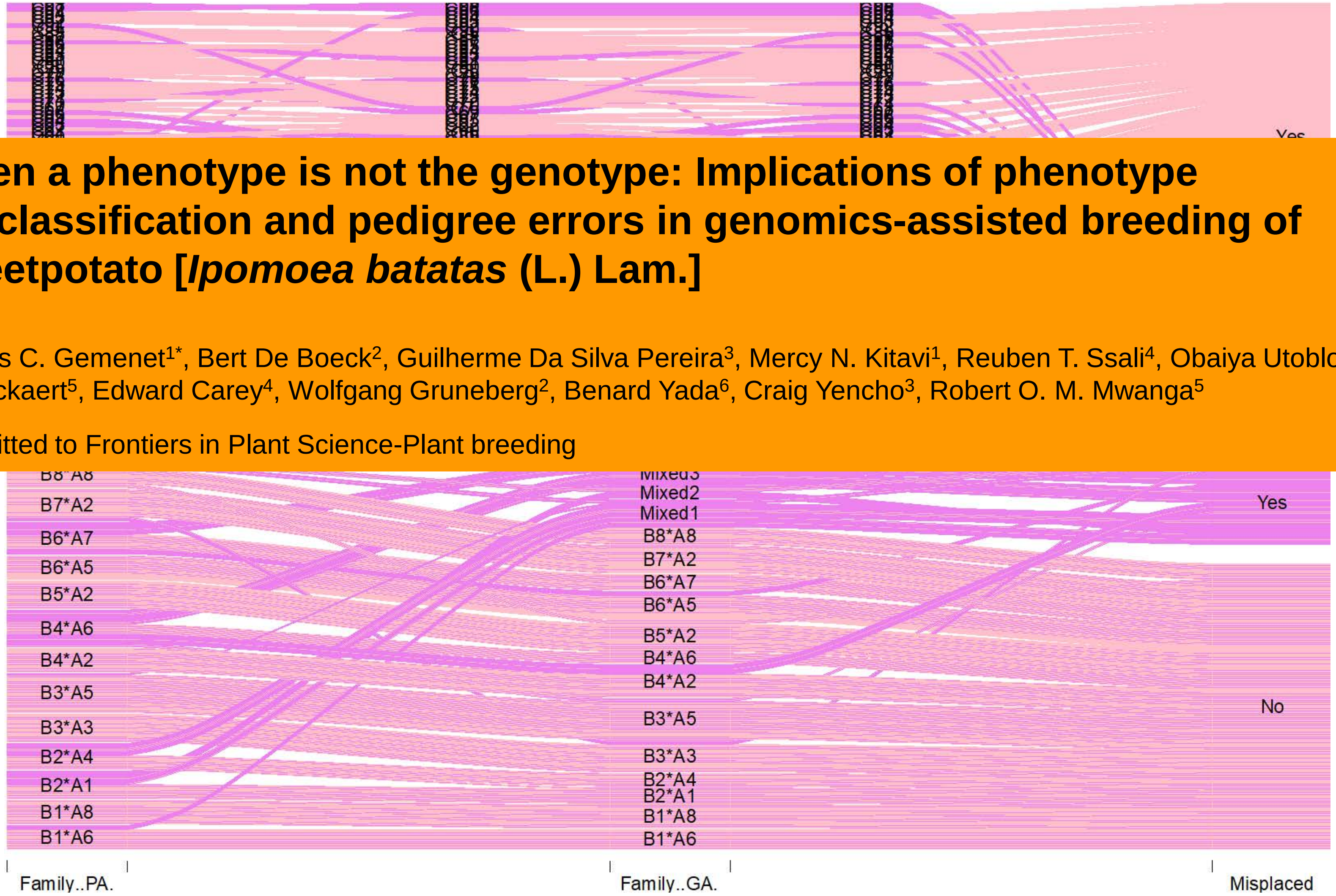
"Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively-associated β-carotene and starch content in hexaploid sweetpotato [Ipomoea batatas (L.) Lam.]"

Dorcus C Gemenet[1,✉,a], Guilherme da Silva Pereira[2,a], Bert De Boeck[3], Joshua C Wood[4], Marcelo Mollinari[2], Bode A Olukolu[2,11], Federico Diaz[3], Veronica Mosquera[3], Reuben T Ssali[5], Maria David[3], Mercy N Kitavi[1], Gabriela Burgos[3], Thomas Zum Felde[3], Marc Ghislain[1], Edward Carey[6], Jolien Swanckaert[6], Lachlan JM Coin[7], Zhangjun Fei[8], John P Hamilton[4], Benard Yada[9], G Craig Yencho[2], Zhao-Bang Zeng[2], Robert OM Mwanga[5], C Robin Buell[4], Awais Khan[3,10], Wolfgang J Gruneberg[3]

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



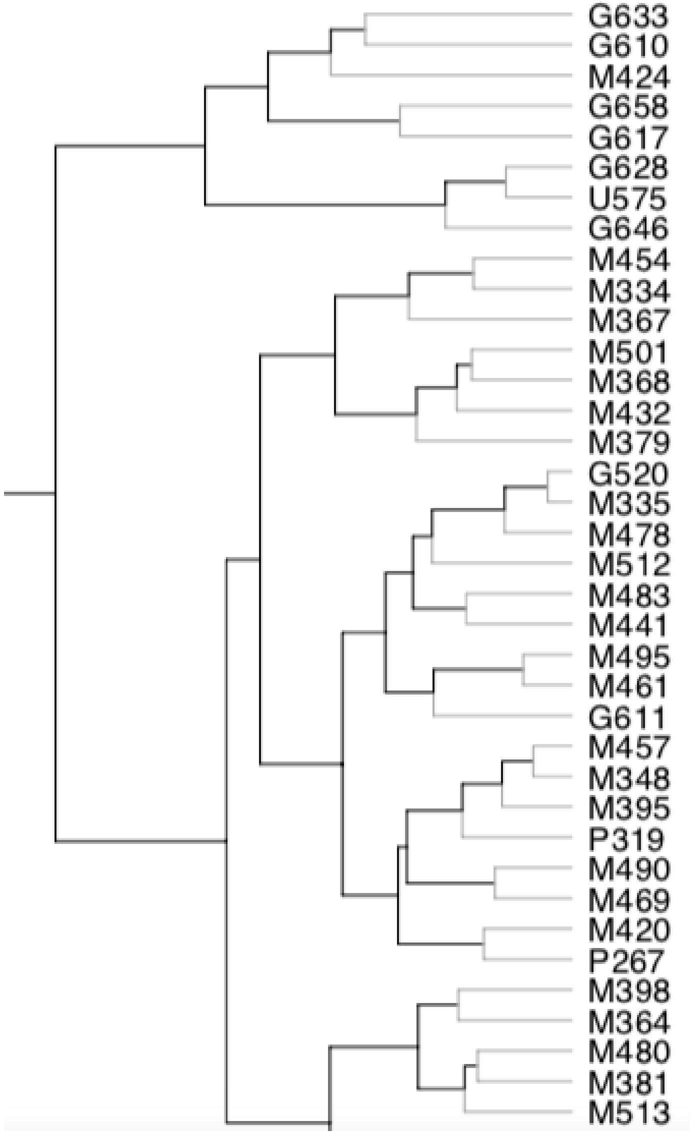
When a phenotype is not the genotype: Implications of phenotype misclassification and pedigree errors in genomics-assisted breeding of sweetpotato [*Ipomoea batatas* (L.) Lam.]

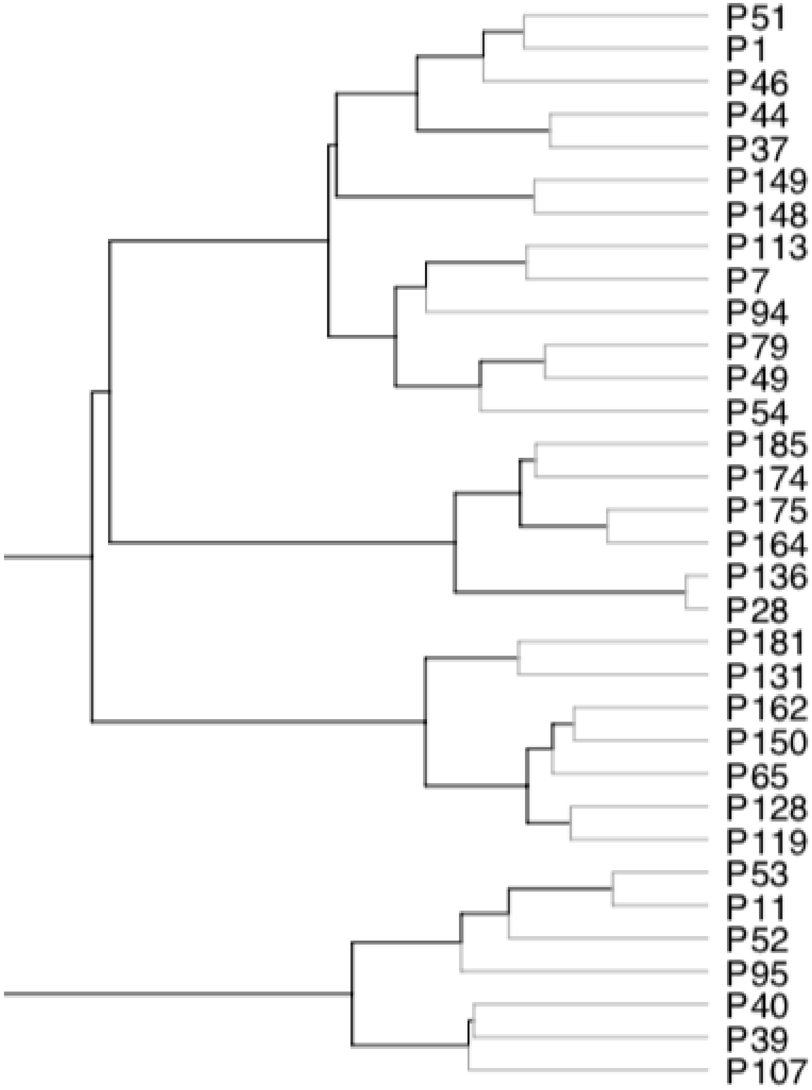
Dorcus C. Gemenet[1*], Bert De Boeck[2], Guilherme Da Silva Pereira[3], Mercy N. Kitavi[1], Reuben T. Ssali[4], Obaiya Utoblo[4], Jolien Swanckaert[5], Edward Carey[4], Wolfgang Gruneberg[2], Benard Yada[6], Craig Yencho[3], Robert O. M. Mwanga[5]

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 QCSNPset for forward breeding and genomic selection

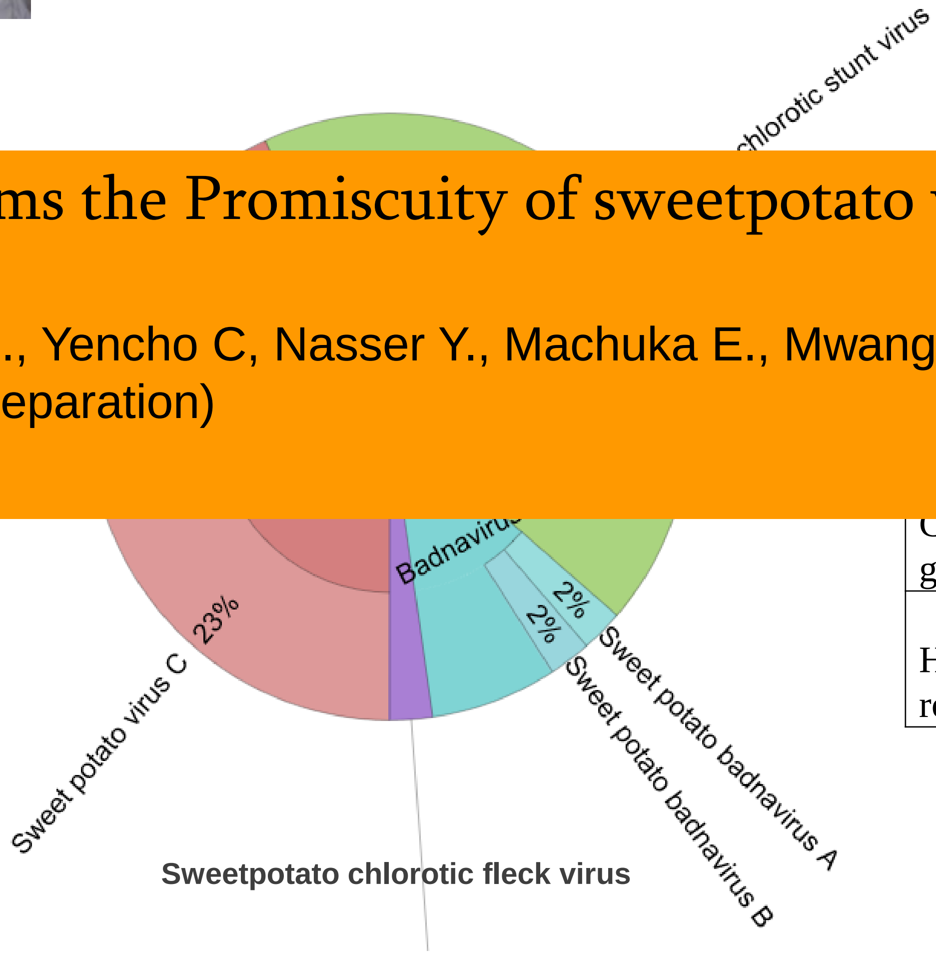




Using genomics to understand taxonomy and distribution of pathogen populations

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)

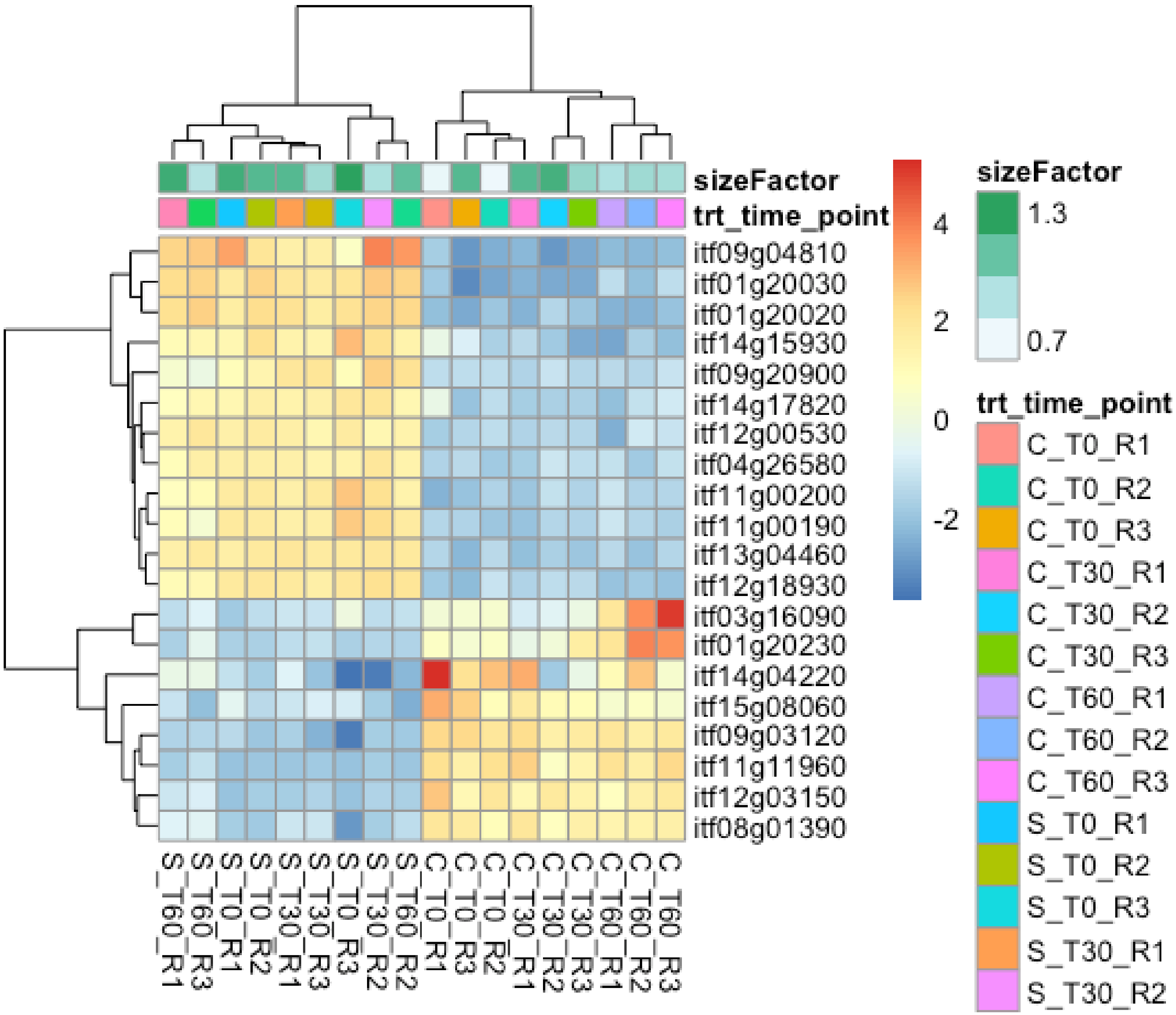


Taxonomic abundance of S.P viruses in Uganda using MiSeq

Crown gall	Agrobacterium tumefaciens
Hairy roots	*Agrobacterium rhizogenes*

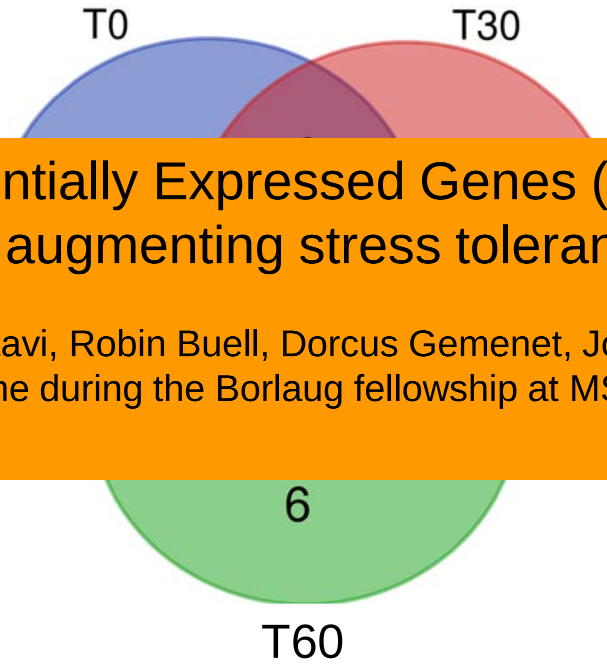
Joanne Adero

Transcriptome studies; heatmap of up and down regulated genes during heat stress in sweetpotato

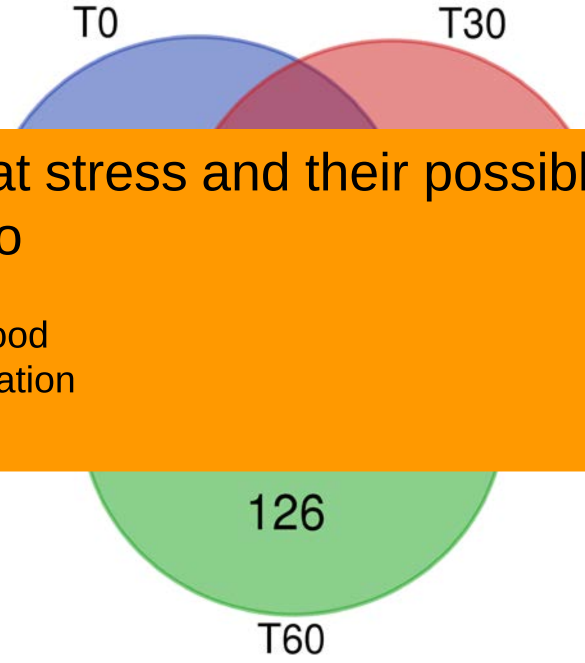


Knowing the differentially expressed genes is important for breeding abiotic and abiotic stresses

Up - Regulated



Down-Regulated

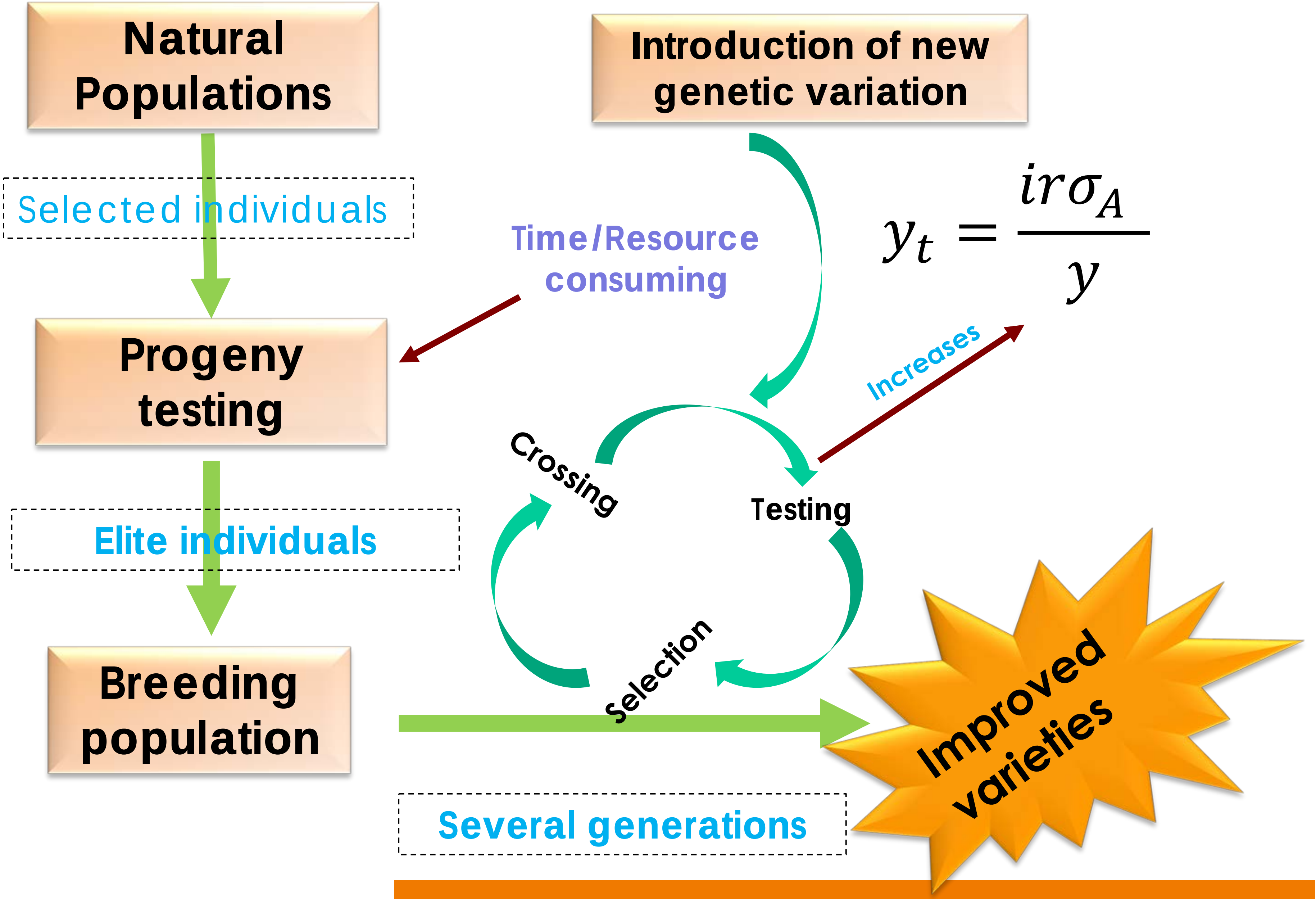


Differentially Expressed Genes (DEGs) during heat stress and their possible role in augmenting stress tolerance in Sweetpotato

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 salicyclic acid pathways

Why genomics enabled breeding?



Natural Populations

Selected individuals

Progeny testing

Elite individuals

Breeding population

Several generations

Introduction of new genetic variation

Time/Resource consuming

$$y_t = \frac{ir\sigma_A}{y}$$

Increases

Crossing

Testing

Selection

Improved varieties

Acknowledgements

GT4SP
GENOMIC TOOLS
FOR SWEETPOTATO
IMPROVEMENT

SASHA
Sweetpotato Action for
Security and Health in Africa

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LIVESTOCK RESEARCH
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The African Biosciences Challenge Fund (ABCF)

Asanteni Sana!

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