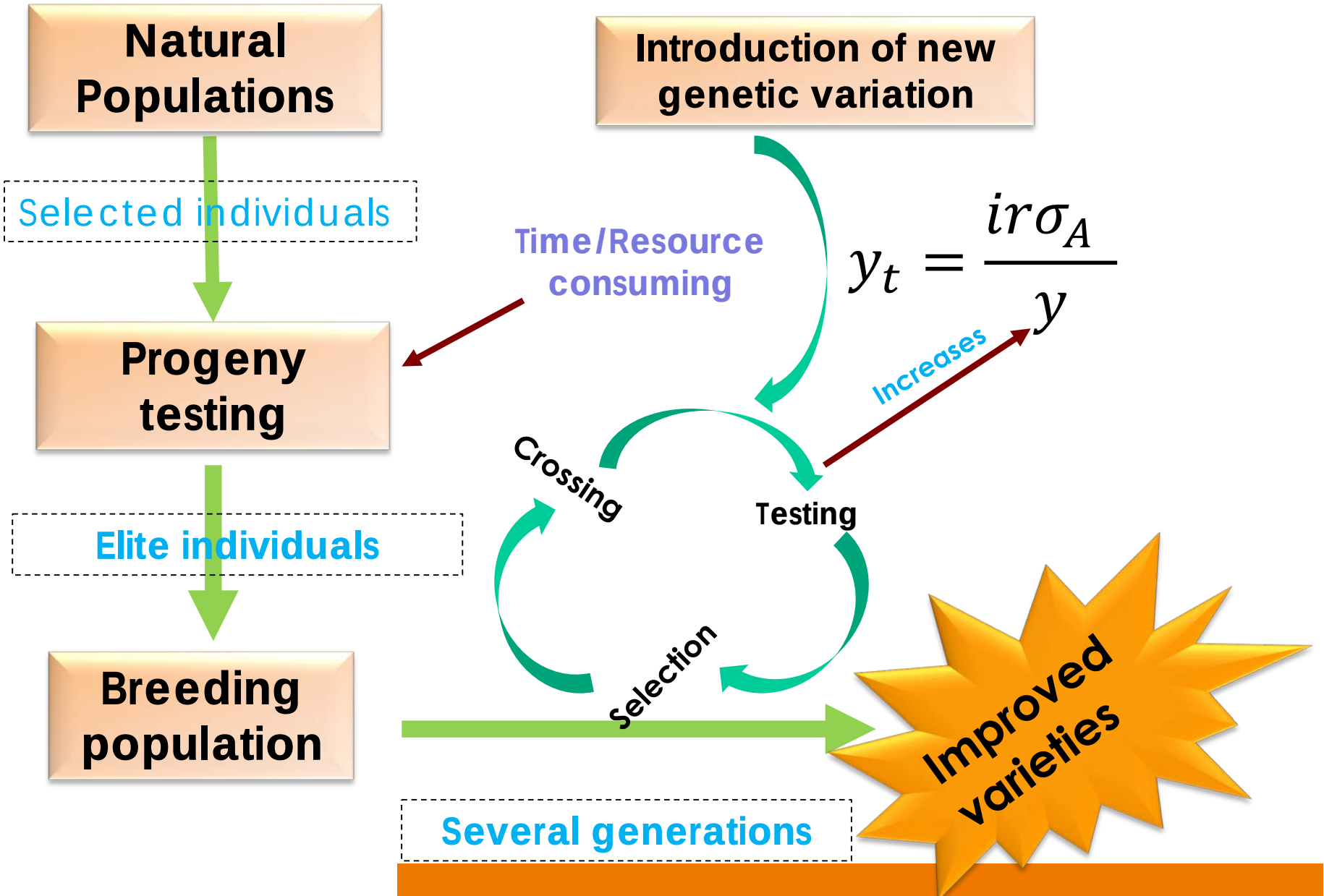
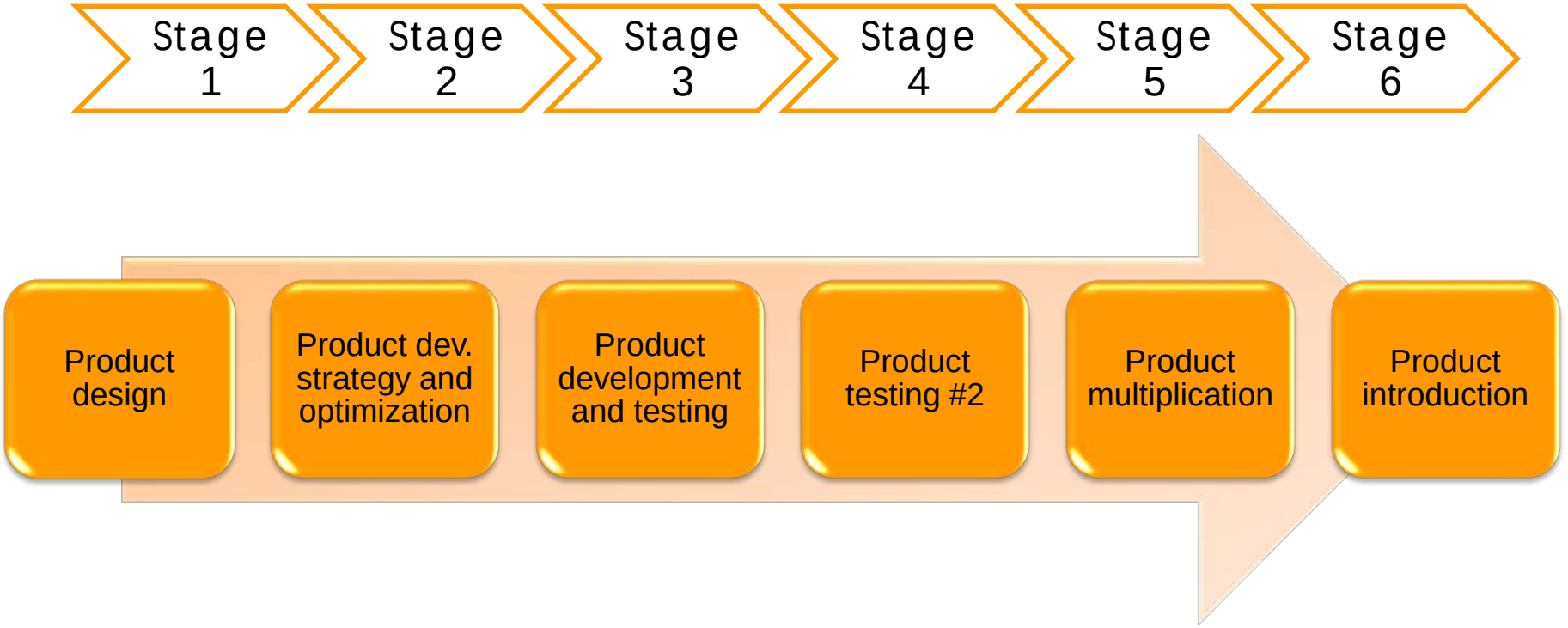
# Towards Genomics-Assisted Breeding in Sweetpotato at CIP: Product Advancement Process

17TH SPEEDBREEDERS' MEETING_DGEMENET_JUNE 07, 2018_NAIROBI

# The breeding process

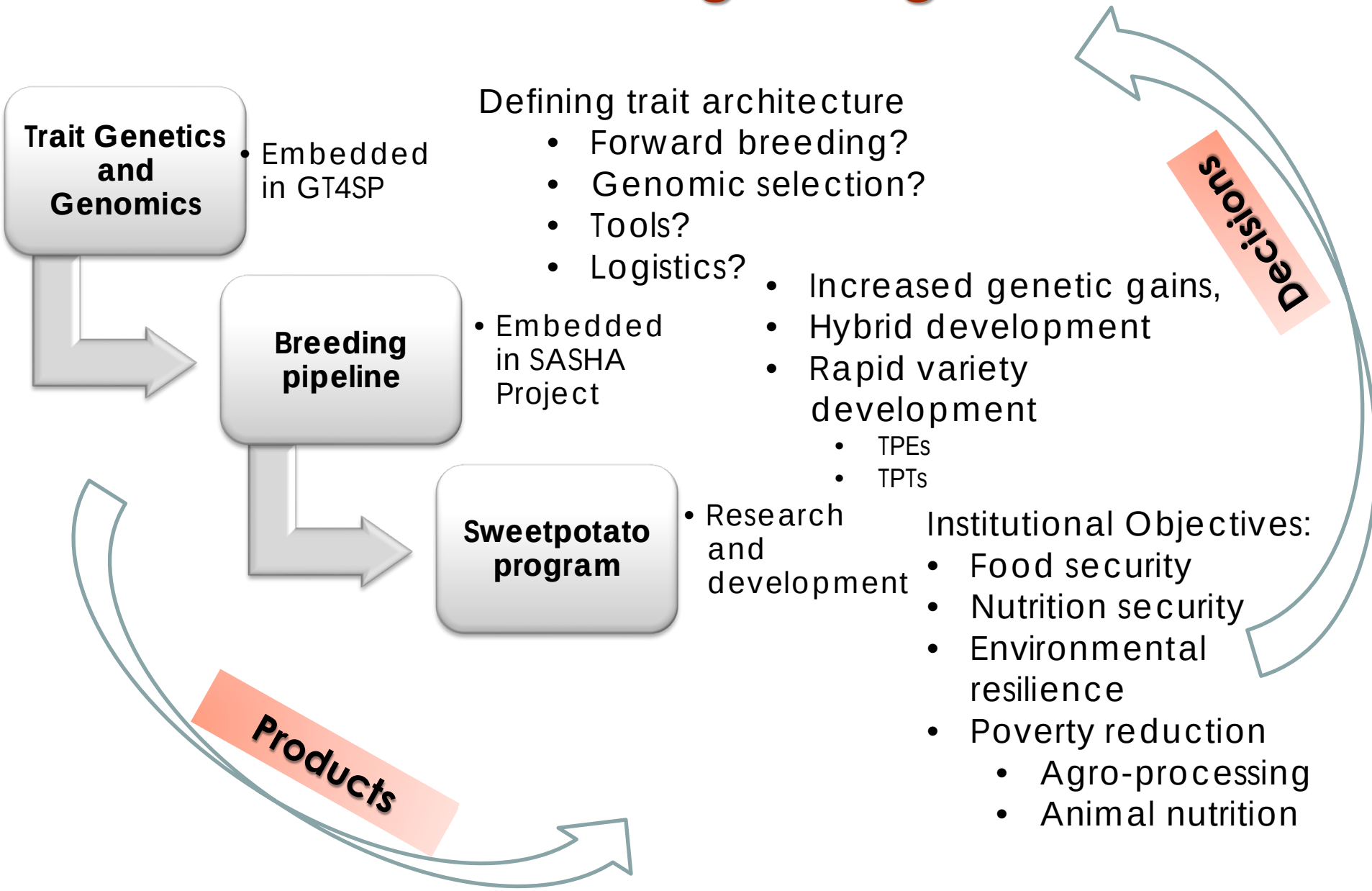


# Product Advancement Stages

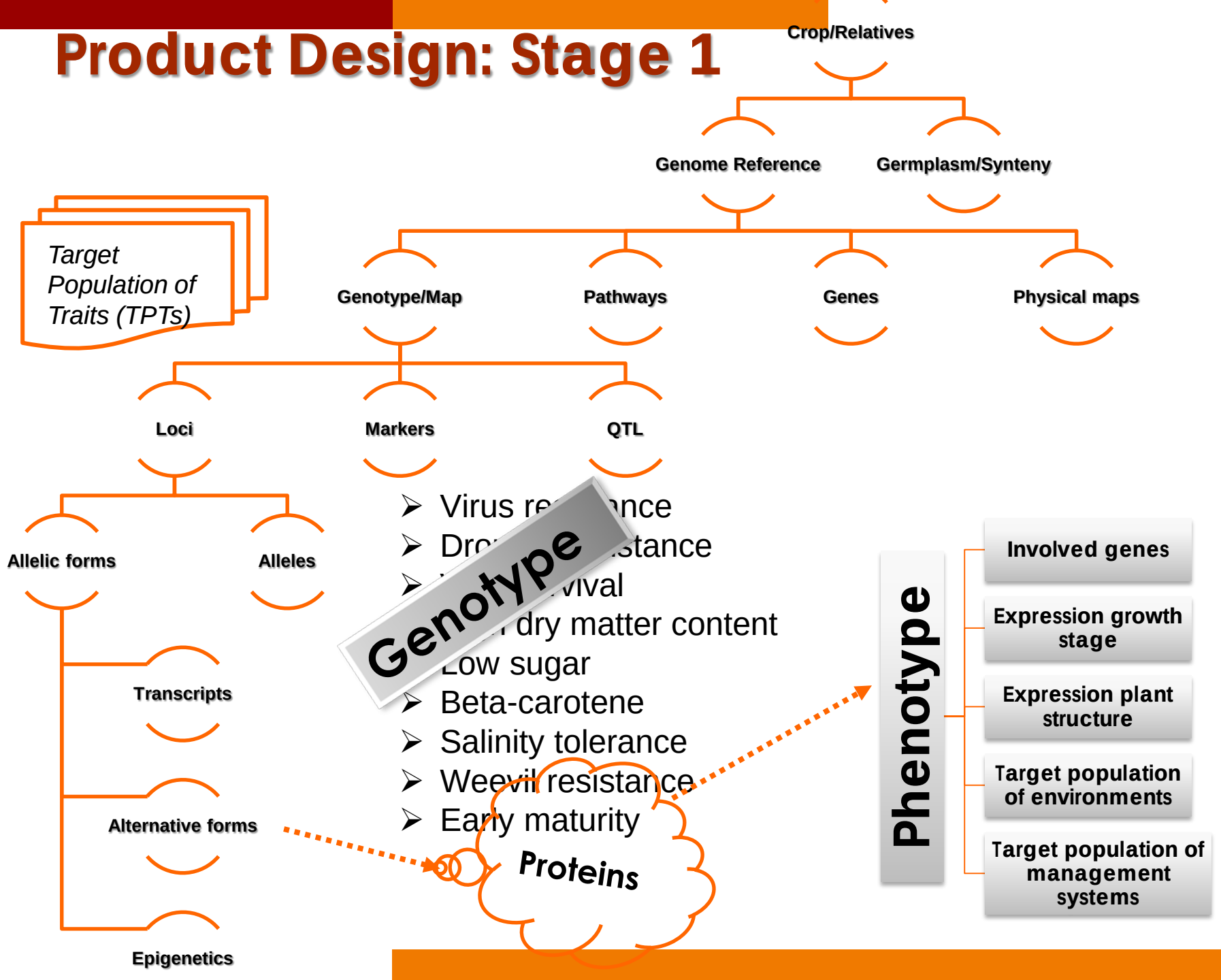



Modelled after the CGIAR's EiB platform.

# Product Design: Stage 1



# Product Design: Stage 1



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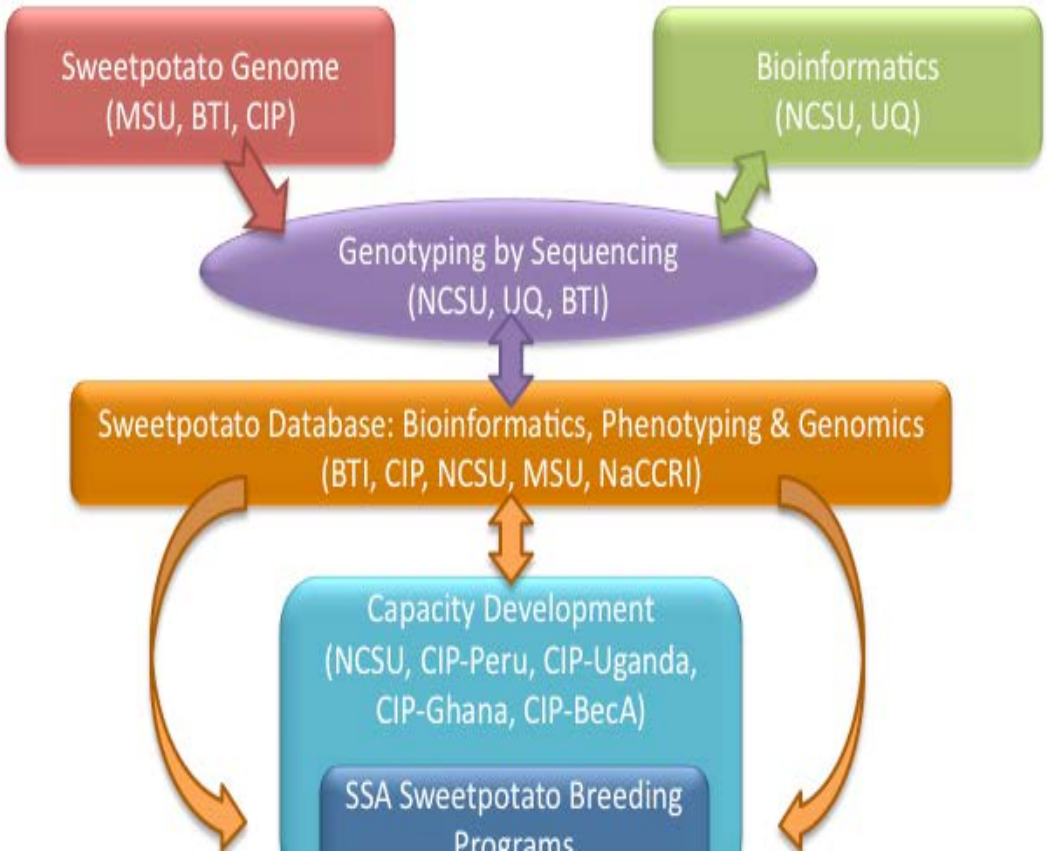
# The Genomic Tools for Sweetpotato Improvement (GT4SP) Project

A new four year investment to develop genomic and genetic resources for sweetpotato improvement has been launched with the goal of establishing a molecular marker-assisted breeding program in sweetpotato.



# Product development and testing: Stage 3

## Product: Genomic and Genetic Resources

1. Two reference genomes (anchored and annotated: ***Ipomoea trifida*** and ***Ipomoea triloba***

2. Phasing and linkage mapping methods for polyploids: **MapPoly**

3. Quantitative trait loci (QTL) mapping methods for polyploids: **PolyQTL**

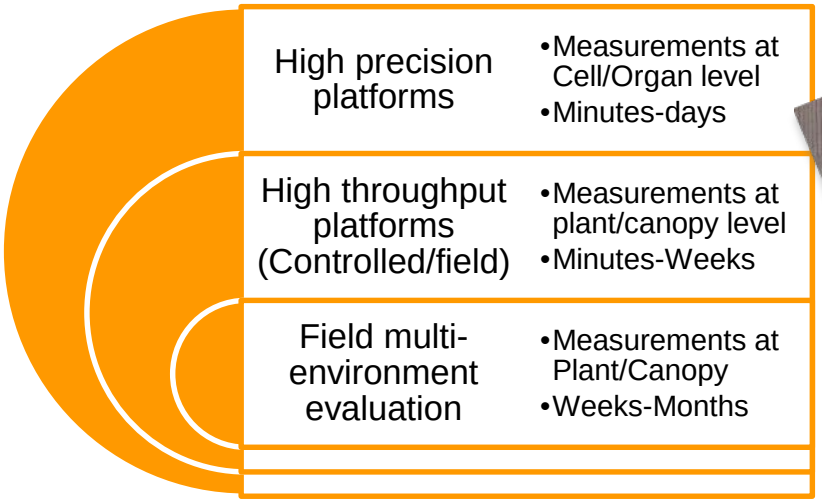
4. Optimized genotyping methods for dosage calling and phasing: **GBSpoly**

5. A database: **SweetpotatoBase**

# Product development and testing: Stage 3

## Product: Trait Dissection Experiments (TDE)

Multiscale-phenomics is the best approach to trait dissection




Tardieu et al 2017, Current Biology

# Product development and testing: Stage 3

## Product: Trait Dissection Experiments (TDE)





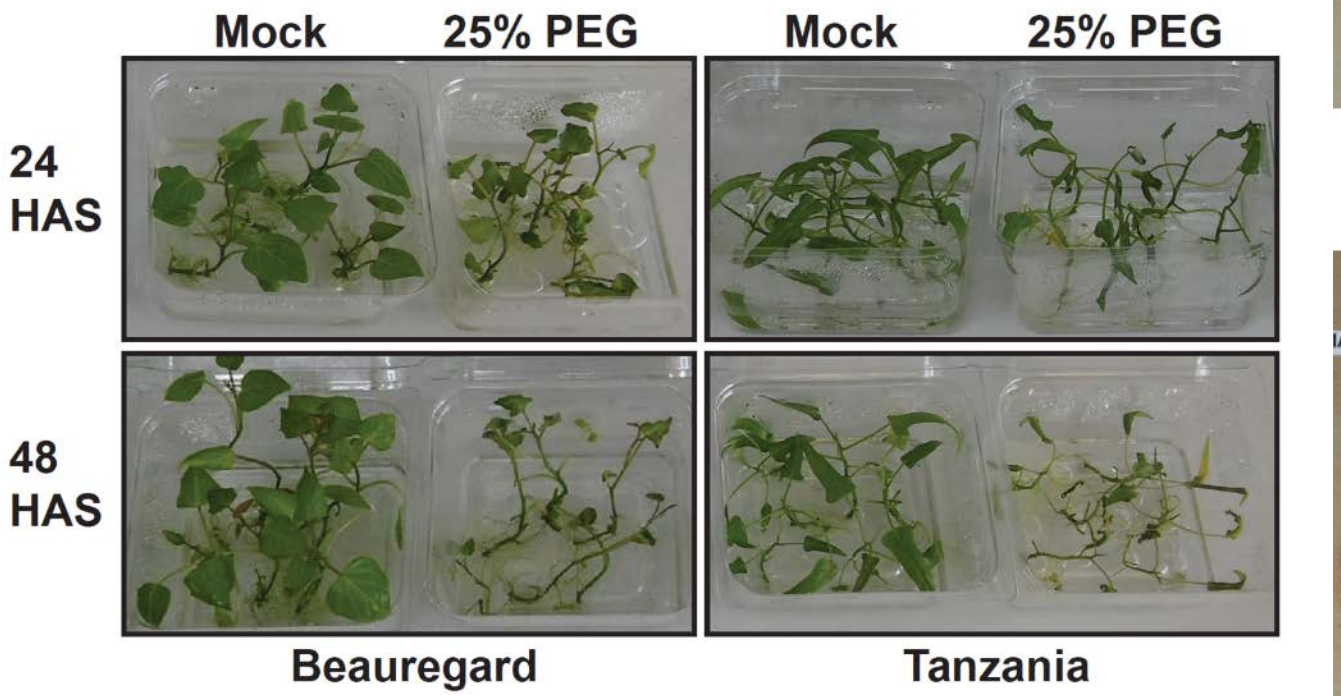
Strategic high precision and/or high throughput phenotyping networks need be cultivated

# Product development and testing: Stage 3

## Product: Trait Dissection Experiments (TDE)








# Product development and testing: Stage 3

Beauregard

x

Tanzania

# Product development and testing: Stage 3

## Product: Trait Dissection Experiments (TDE)

- 20 Field environments for the hexaploid mapping population (Peru, Ghana, Uganda)
  - Agronomic/quality traits
  - Performance under drought
  - Sweetpotato virus disease (SPVD)
  - Morpho-Physiological traits

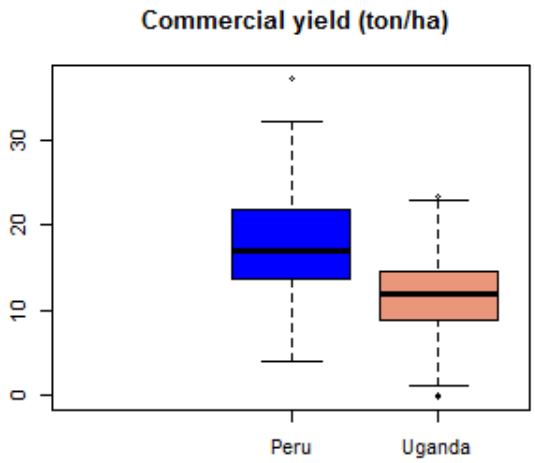
- 6 Screen house experiments for sweetpotato
  - Root system architecture under abiotic stress

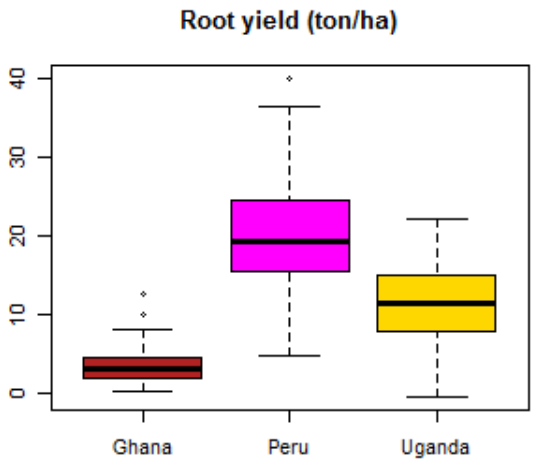
- 3 RNAseq experiments for sweetpotato
  - Storage root development
  - Abiotic stress: Drought, Heat and Salinity
  - Sweetpotato virus disease

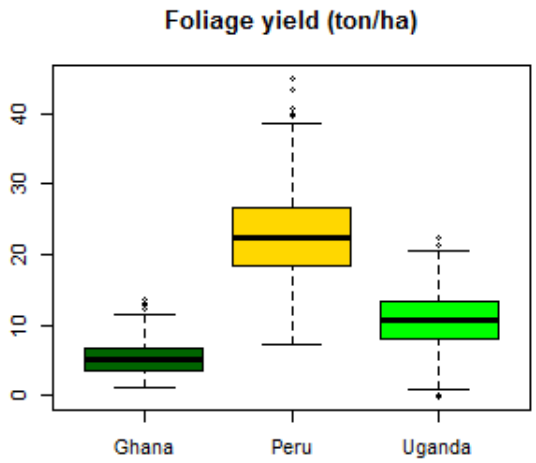
- 2 Experiments for the diploid *I. trifida*

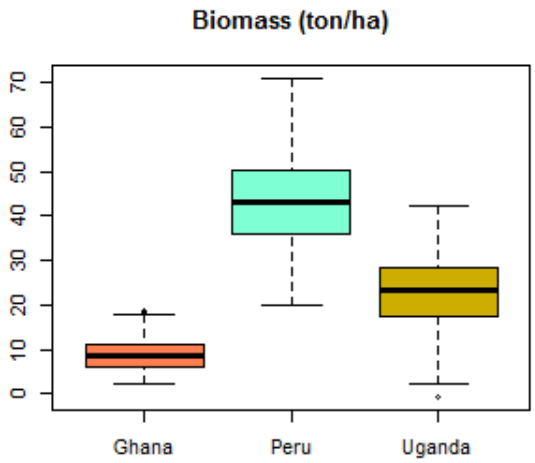
# Product development and testing: Stage 3

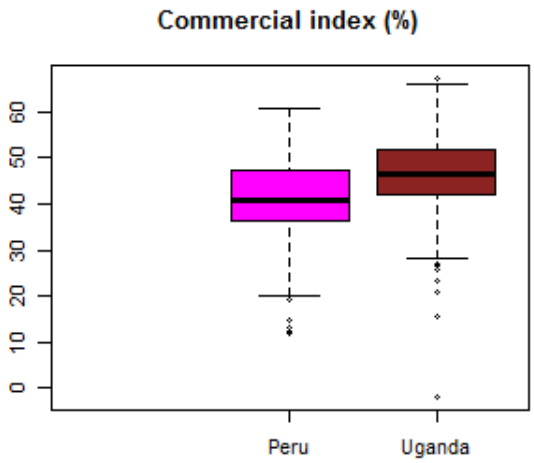
## Output (TDE): Combined Results Summaries

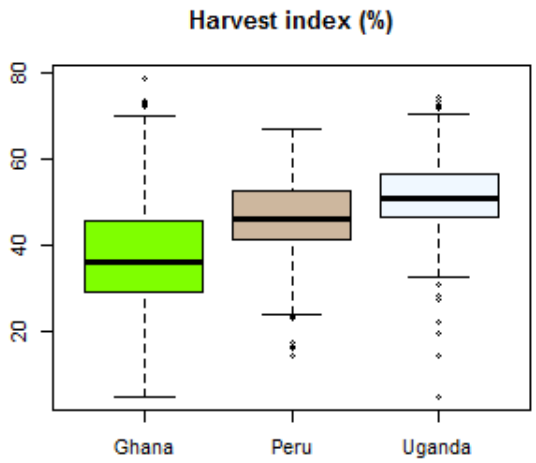


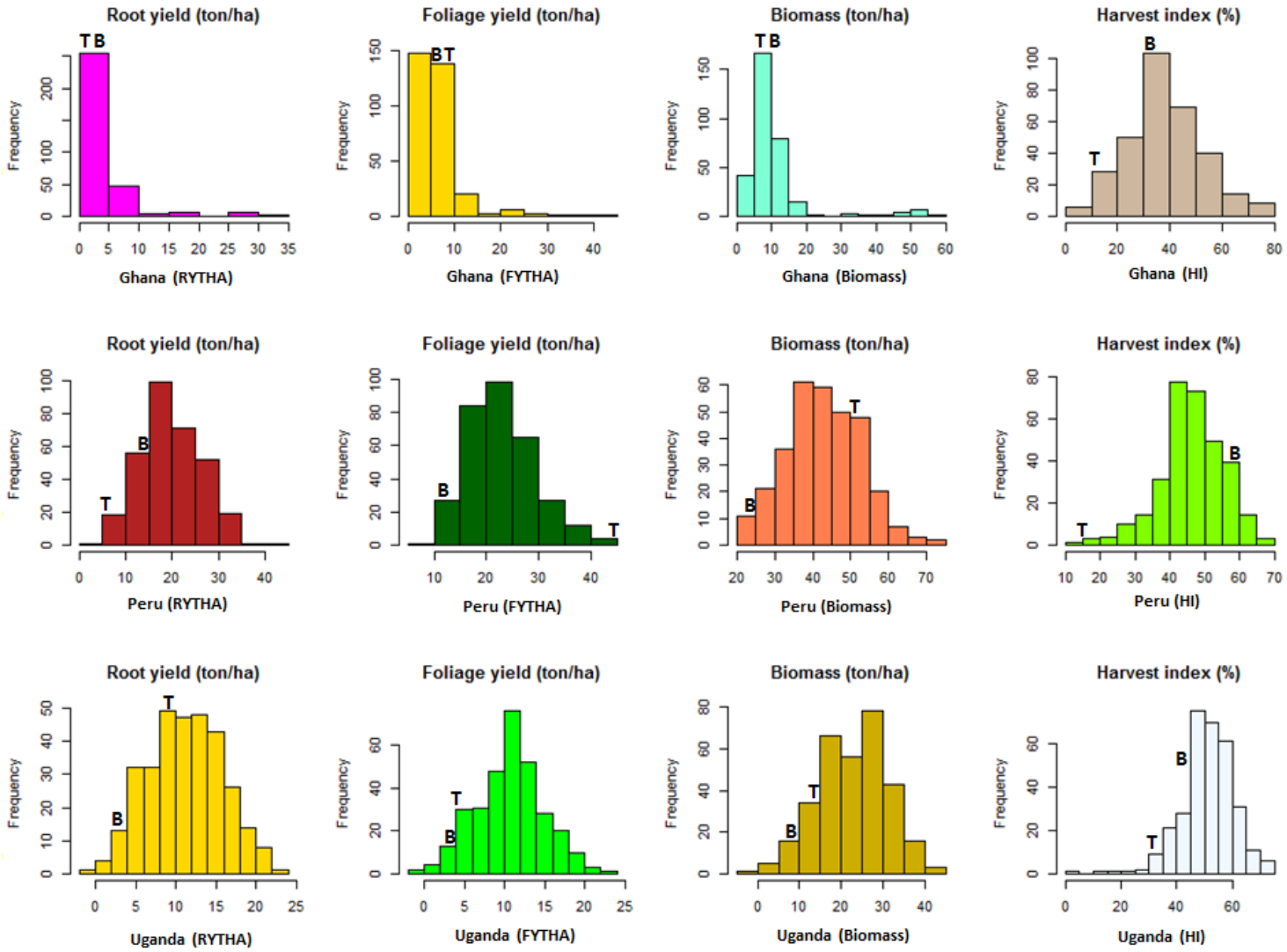



# Product development and testing: Stage 3

## Output (TDE): Combined Results Summaries



# Product development and testing: Stage 3

## Output (TDE): Validating Methods for Applied Breeding

**Potential of genomics-assisted breeding given new genomic tools: Mapping QTL for Quality-Related Traits and Inferring Candidate Genes based on a Diploid Reference Genome.**

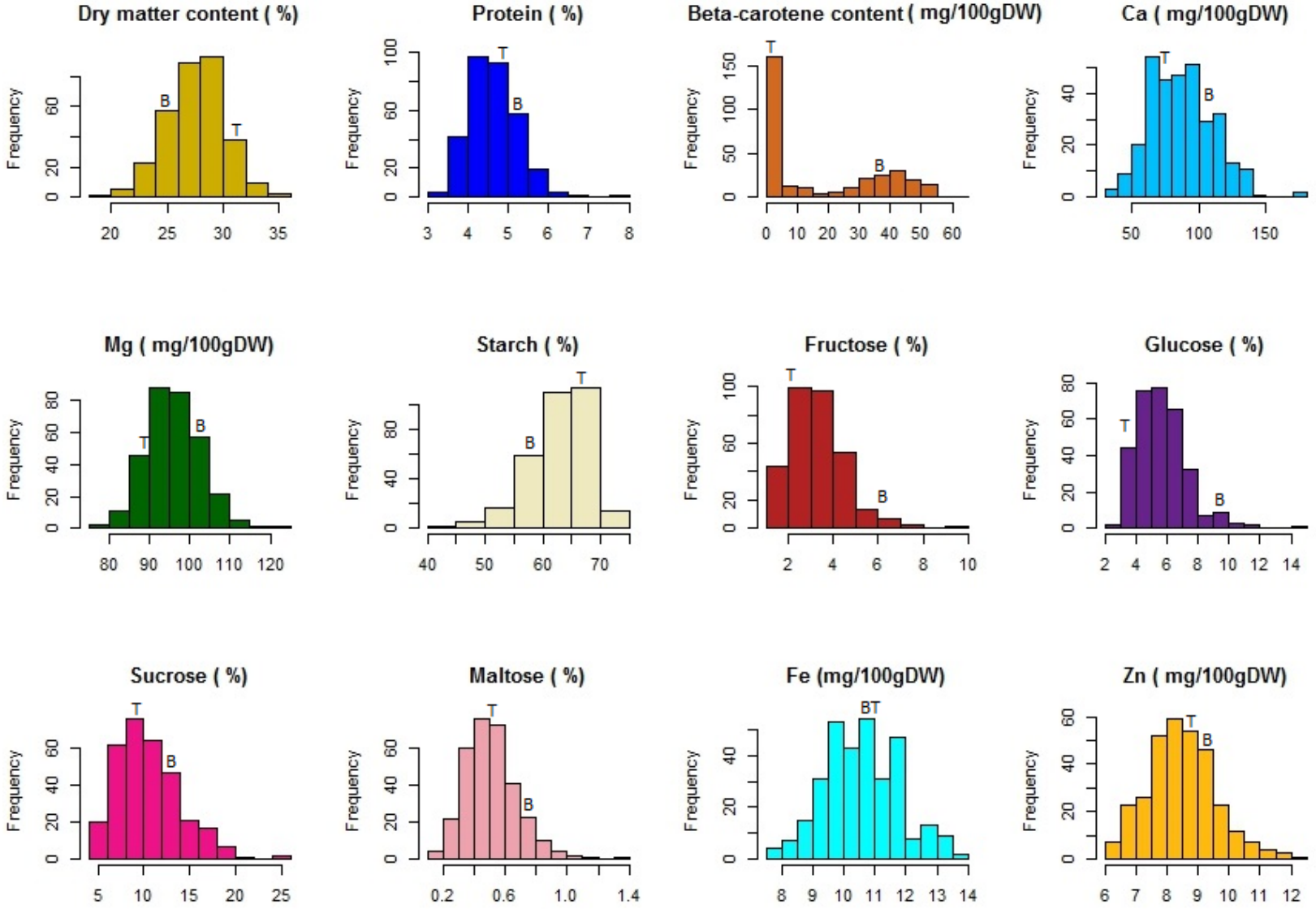
Dorcus C. Gemenet, Guilherme Da Silva Pereira, Federico Diaz, ……

**Five environments**

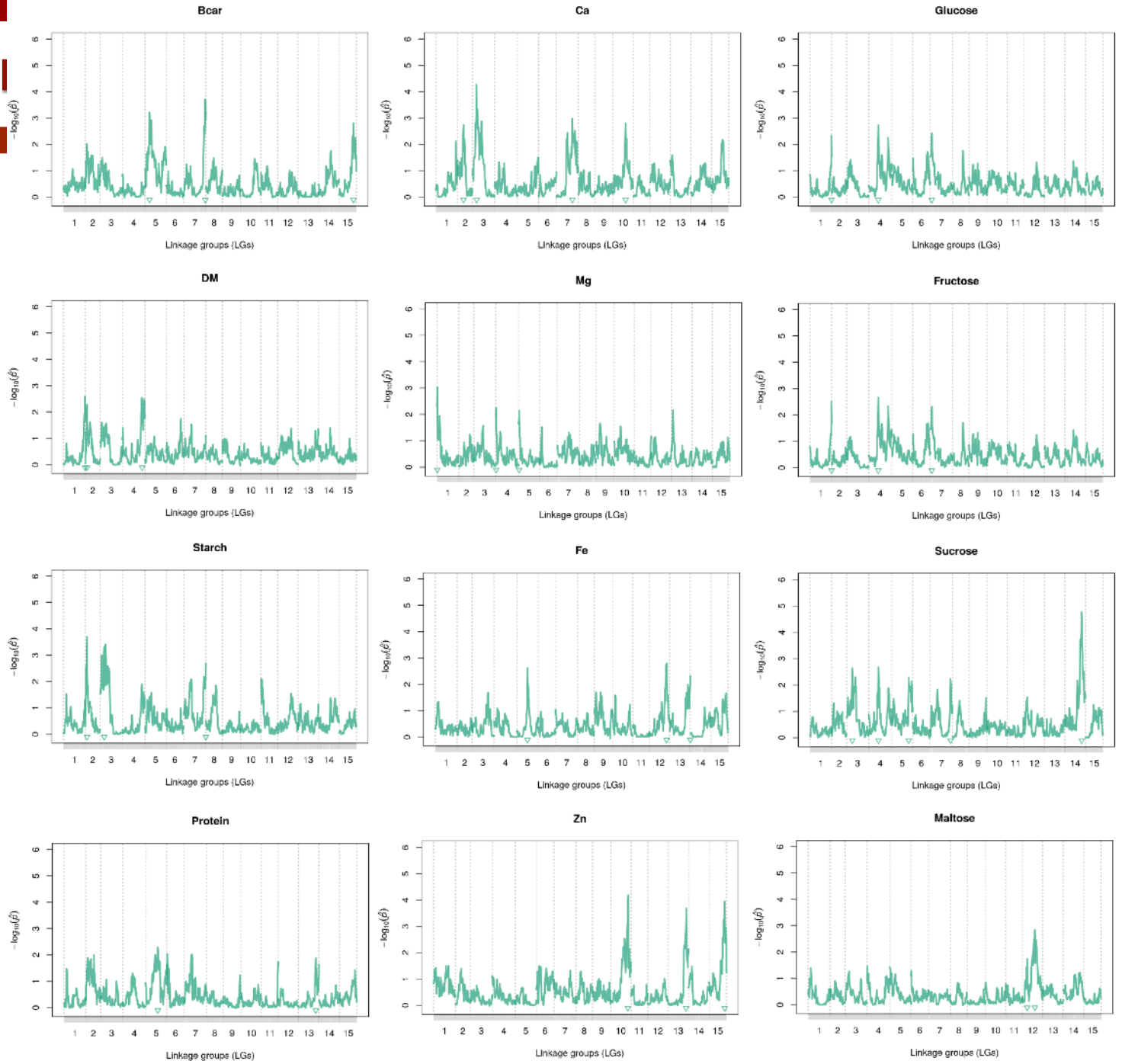
- Dry matter
- Starch
- Beta carotene
- Flesh color
- Protein
- Calcium
- Magnesium
- Iron
- Zinc
- Glucose
- Fructose
- Sucrose
- Maltose

# Product development and testing: Stage 3

## Output (TDE): Validating Methods for Applied Breeding



# Pl
# Ou ng


Bcar
Ca
Glucose
DM
Mg
Fructose
Starch
Fe
Sucrose
Protein
Zn
Maltose
Linkage groups (LGs)
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
0 1 2 3 4 5 6

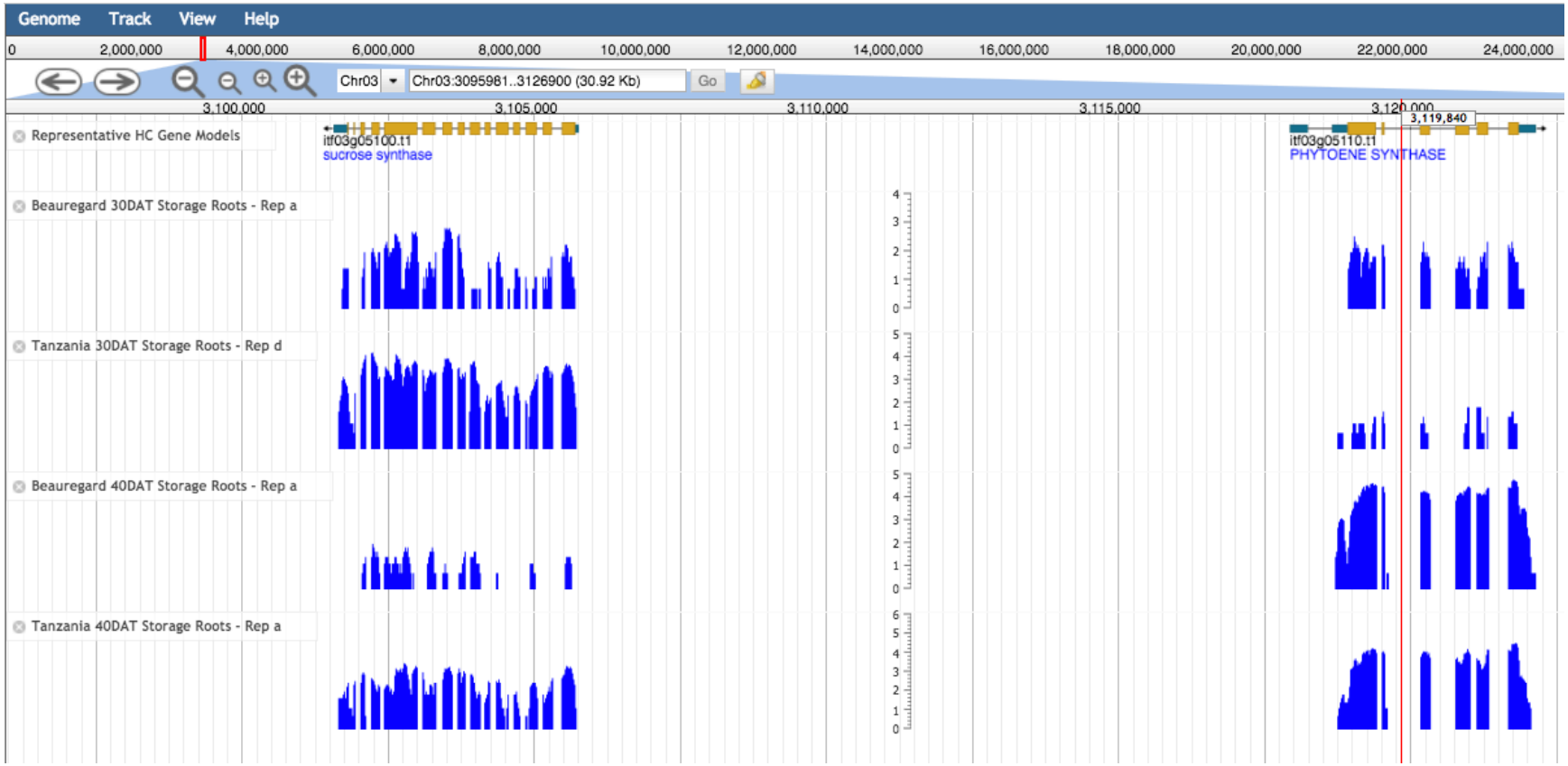
# Product development and testing: Stage 3

## Output (TDE): Validating Methods for Applied Breeding

| | | Mrk | LG | Position | $\sigma^2$ (%) | Pval | Gene ID | Gene |
|---|---|---|---|---|---|---|---|---|
| Bcar | 1 | S5_8626252 | 5 | 20.13 | 9.4 | 0.0005 | itf05g07990.t1 | plantacyanin |
| | 2 | S7_23088888 | 7 | 96.04 | 12.1 | 0.0001 | itf07g22960.t1 | DEA(D/H)-box RNA helicase family protein |
| | 3 | S15_11473599 | 15 | 64.01 | 10.2 | 0.001 | itf15g14400.t1 | Carbohydrate-binding X8 domain superfamily protein |
| Starch | 1 | S2_3909445 | 2 | 8.07 | 14.6 | 0.002 | itf02g02850.t1 | conserved hypothetical protein |
| | 2 | S3_3120245 | 3 | 18.07 | 13 | 0.0001 | itf03g05110.t1 | PHYTOENE SYNTHASE |
| | 3 | S7_23613033 | 7 | 98.31 | 8.6 | 0.002 | itf07g23680.t1 | Transport protein particle (TRAPP) component |
| Flesh col | 1 | S2_9472161 | 2 | 46.14 | 4.7 | 0.003 | itf02g11040.t1 | cellulose synthase-like B |
| | 2 | S3_3813045 | 3 | 24.01 | 7.5 | 0.004 | itf03g05900.t2 | Protein kinase superfamily protein |
| | 3 | S5_19816275 | 5 | 45.35 | 7 | 0.002 | itf05g17260.t1 | Protein of unknown function (DUF1162) |
| | 4 | S7_22098473 | 7 | 90.09 | 10.8 | 0.0004 | itf07g21700.t1 | Argonaute family protein |
| | 5 | S8_5331289 | 8 | 45.31 | 5.5 | 0.004 | itf08g07360.t1 | DNA glycosylase superfamily protein |
| | 6 | S15_20064142 | 15 | 72.11 | 8.4 | 0.0008 | itf15g20960.t1 | RNApolymerase sigma-subunit C |

# Product development and testing: Stage 3

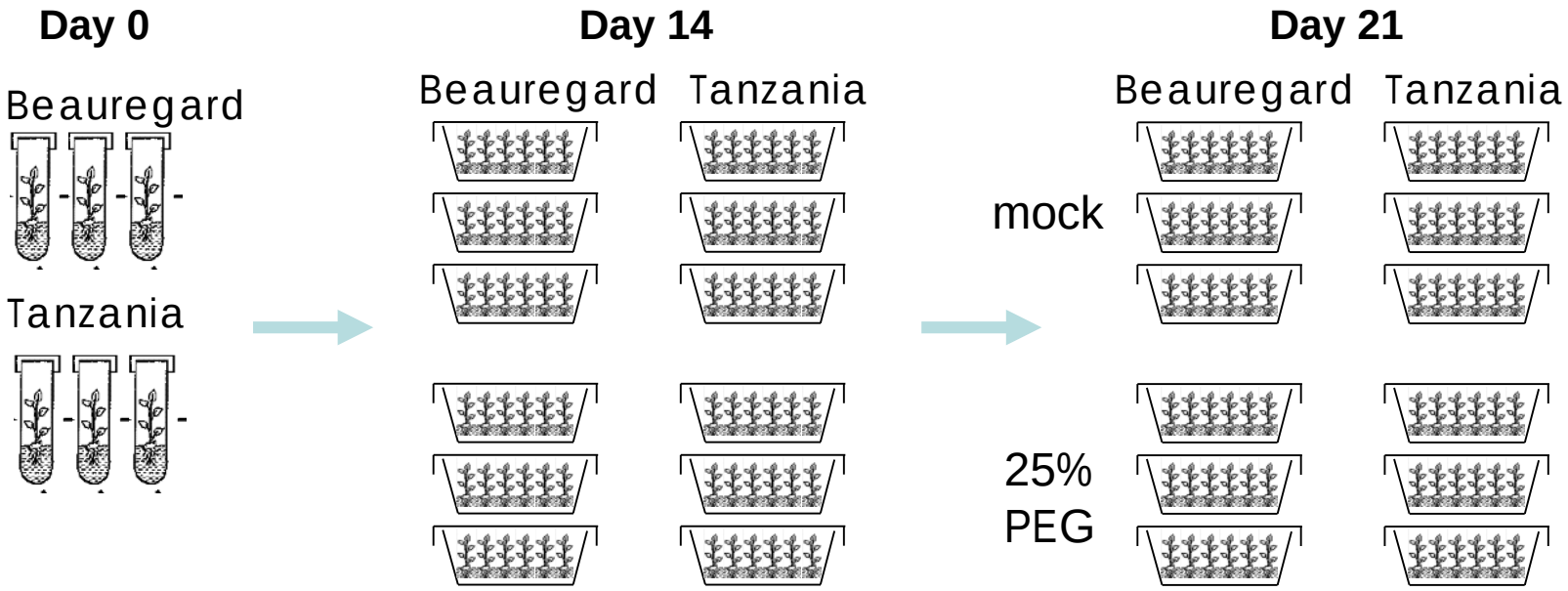
## Output (TDE): Validating Methods for Applied Breeding



# Product development and testing: Stage 3

## Output (TDE): Transcriptomics and gene expression

Kin Lau, Dorcus C. Gemenet, Rosario Herrera…




**Initial growth in solid media.**

- 1 single node / tube.

**Transfer to vessels with liquid media.**

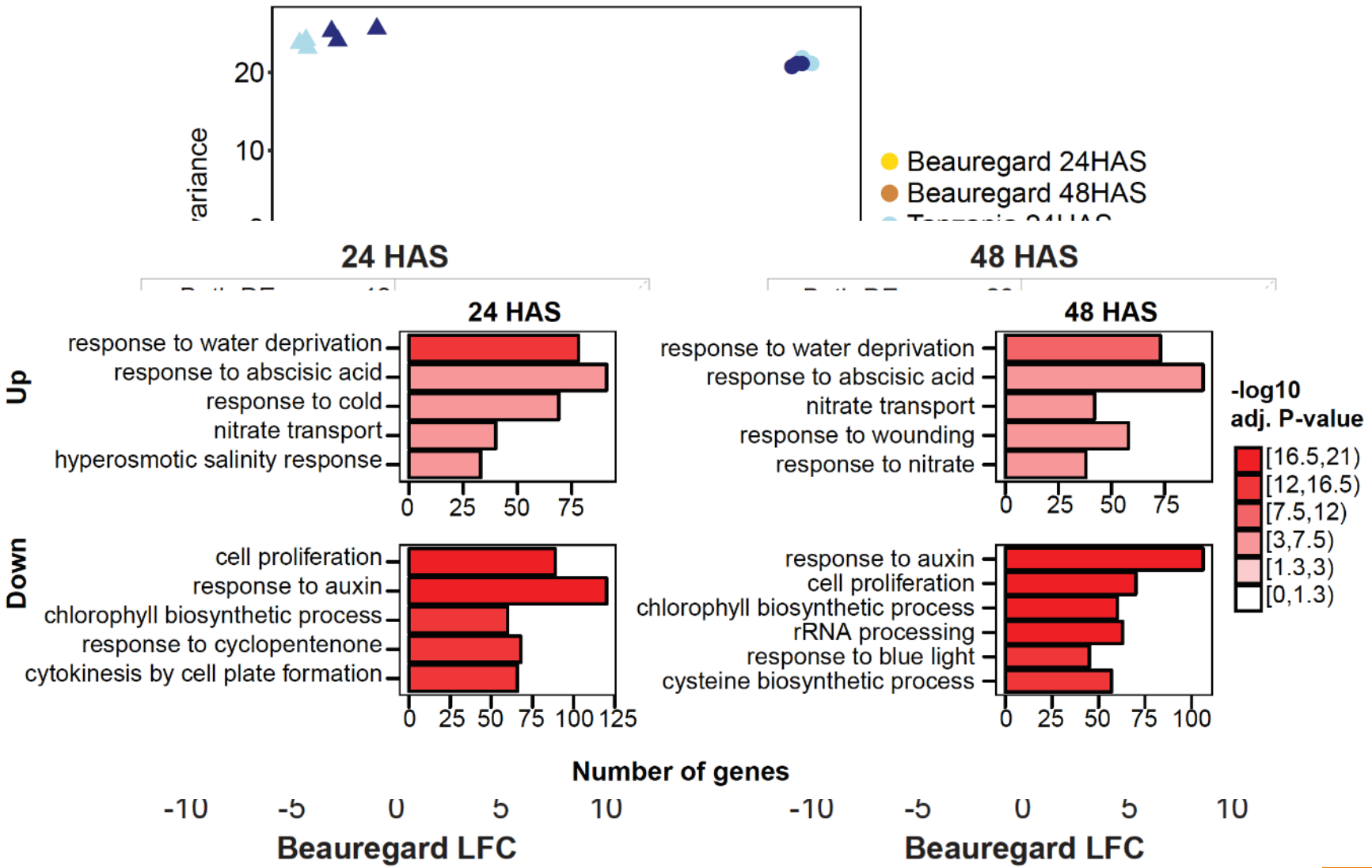
- 6 plants / box.
- 6 boxes / genotype.

**Stress imposition.**

- Add 25% PEG to 3 random boxes.
- Sampled for RNA at 24 and 48 hours after stress (HAS).

# Product development and testing: Stage 3

## Output (TDE): Transcriptomics and gene expression



# Product development and testing: Stage 3

## Output (TDE): Transcriptomics and gene expression

- Tight clustering of replicates and enrichment of drought-related GO terms indicate a high quality drought response dataset
- A group of ~20 LRR kinases are down-regulated at 24 HAS specifically
- *SLAC1* and *LHCB6* are candidates for over-expression experiments
- Four co-regulated gene clusters with higher expression in Beauregard may contribute to higher chlorophyll content resiliency

# Product development and testing: Stage 3

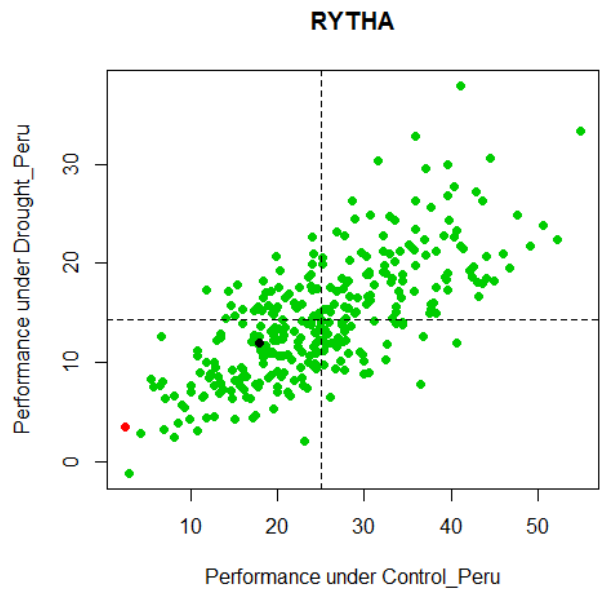
## Output (TDE): Genomic regions for performance under drought

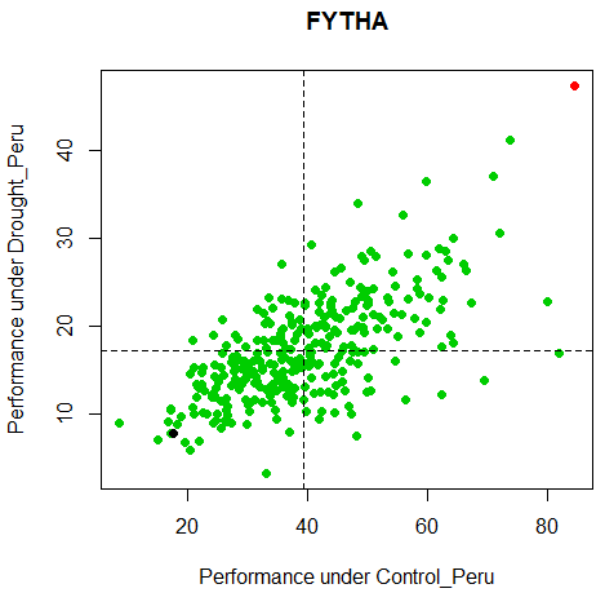
**Trait *per se* versus tolerance indices for selection under drought conditions: QTL mapping for drought tolerance in sweetpotato (*Ipomoea batatas* (L.) Lam)**

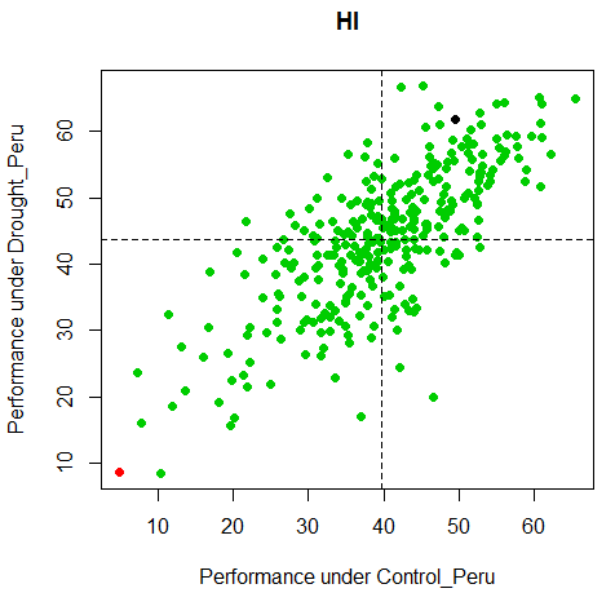
Dorcus C. Gemenet, Guilherme Da Silva Perreira, Veronica Mosquera, Obaiya Utoblo, ...

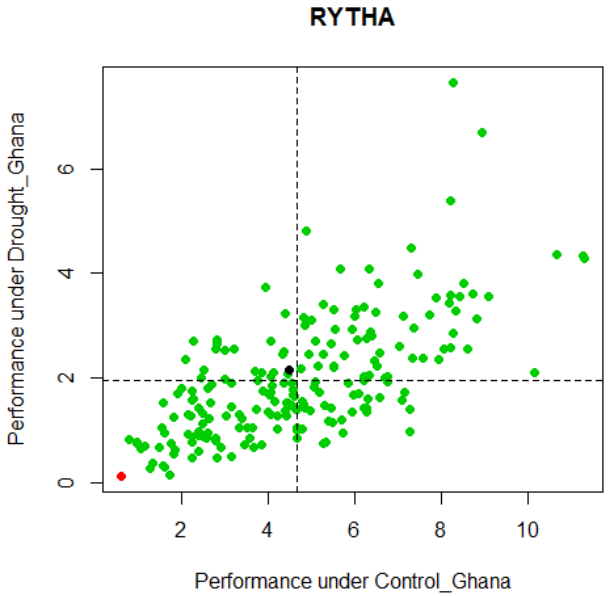
5 drought and 5 control conditions in Peru and Ghana

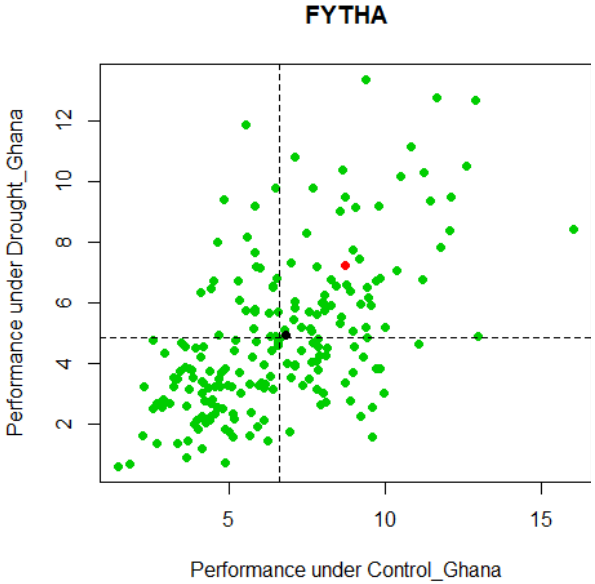
# Product development and testing: Stage 3

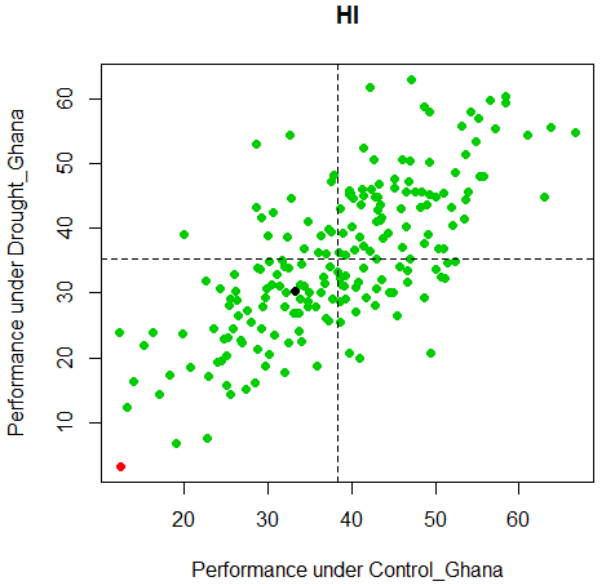


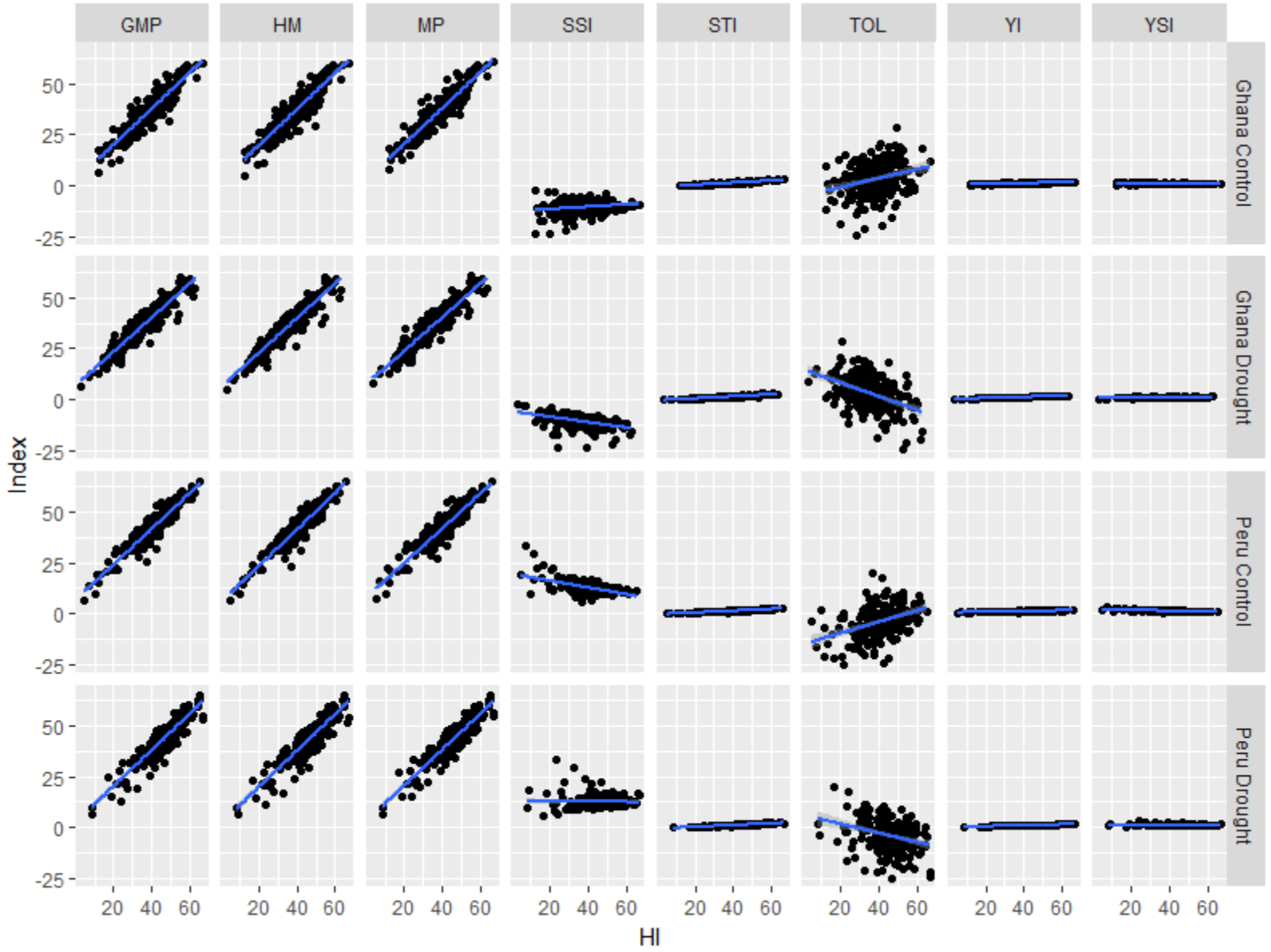



# Product development and testing: Stage 3

## Outp nder

| | Control | | | Drought | | |
|---|---|---|---|---|---|---|
| RYTHA(56.9 : 34.9%) | LG | Posn | Vrnc% | LG | Posn | Vrnc% |
| | 1 | 192.64 | 6.7 | 3 | 37.18 | 10.3 |
| | 3 | 73.12 | 11.8 | 11 | 147.54 | 9.5 |
| | 4 | 48.11 | 6.6 | 15 | 3.55 | 15 |
| | 11 | 212.68 | 9.8 | | | |
| | 13 | 129.11 | 9 | | | |
| | 15 | 57.43 | 13.1 | | | |
| | | | | | | |
| FYTHA(46.4 : 43.7%) | 4 | 186.07 | 11.9 | 4 | 0 | 17 |
| | 7 | 126.59 | 7 | 7 | 150.82 | 8.1 |
| | 10 | 117.38 | 8.2 | 10 | 54.07 | 9.9 |
| | 13 | 60.23 | 10.1 | 14 | 6.13 | 8.7 |
| | 14 | 165.11 | 9.2 | | | |
| | | | | | | |
| HI(77.2 : 52.1%) | 1 | 234.87 | 7.1 | 1 | 195.11 | 8.3 |
| | 3 | 69.25 | 11.5 | 3 | 9.31 | 13.8 |
| | 4 | 90.02 | 8.8 | 4 | 144.1 | 10.1 |
| | 5 | 0 | 4.1 | 7 | 30.03 | 12.2 |
| | 8 | 72.31 | 5.4 | 13 | 108.3 | 7.7 |
| | 11 | 135.31 | 8.4 | | | |
| | 12 | 141.11 | 6.5 | | | |
| | 13 | 28.25 | 8.4 | | | |
| | 13 | 129.11 | 6 | | | |
| | 15 | 30.19 | 11.1 | | | |

# Product development and testing: Stage 3

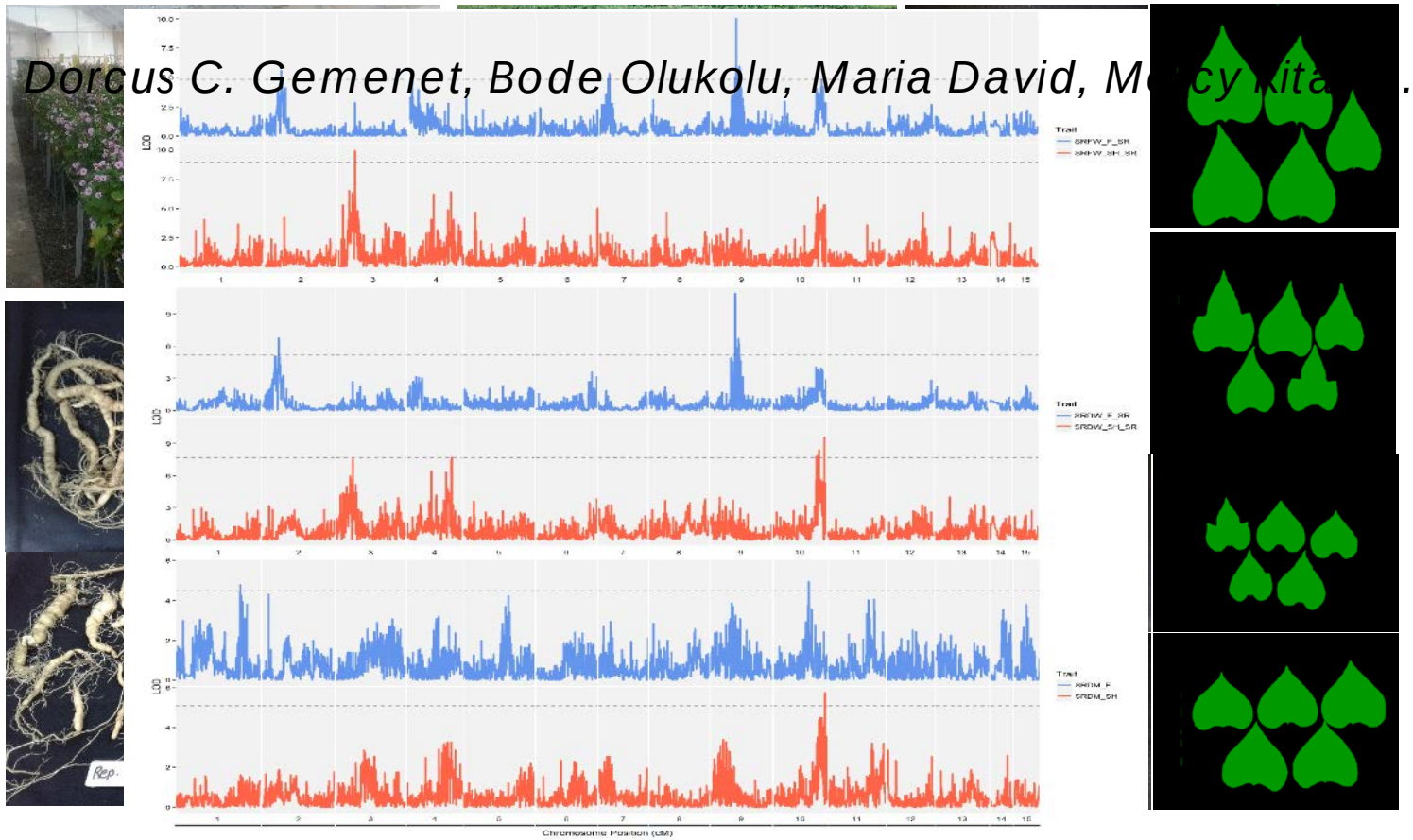


# Product development and testing: Stage 3

## Output (TDE): Comparative mapping btn diploid and hexaploid

Comparative QTL mapping between diploid *Ipomoea trifida* and hexaploid sweetpotato [*Ipomoea batatas* (L.) Lam]

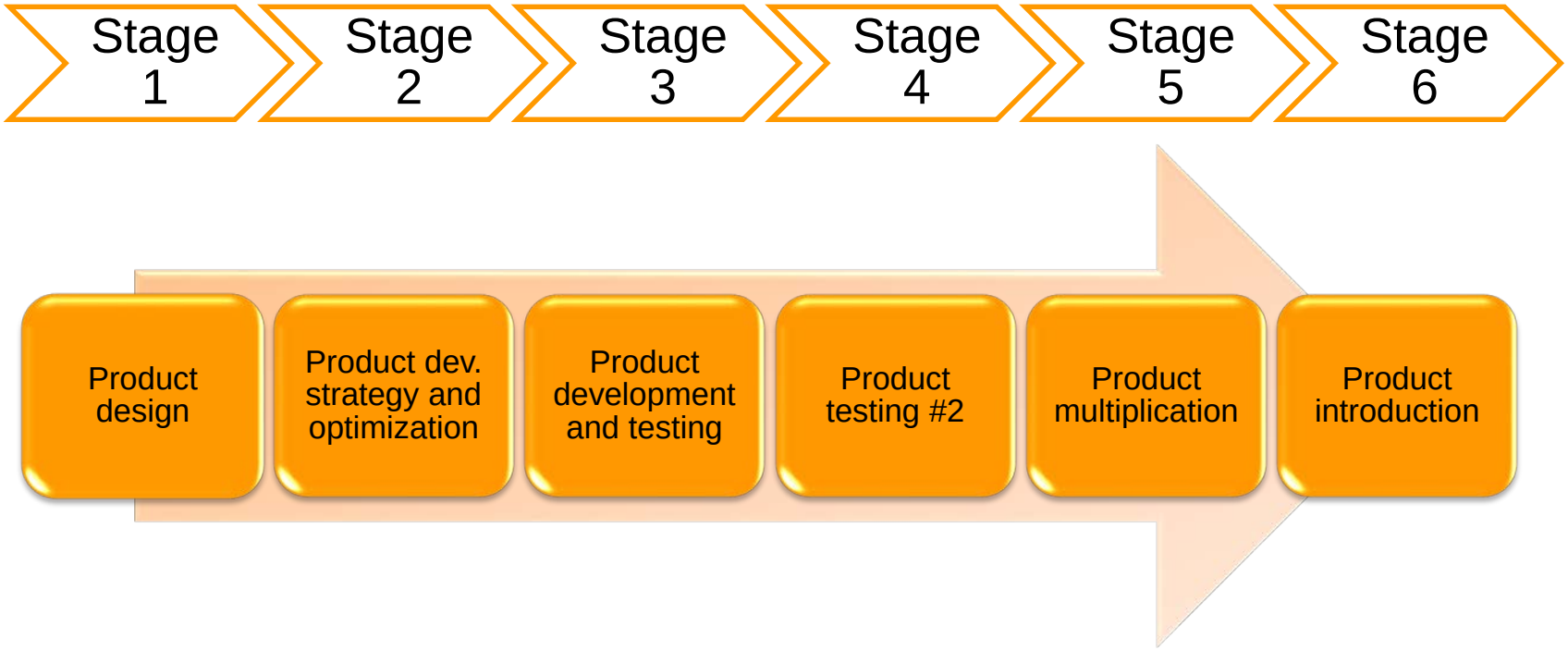
*Dorcus C. Gemenet, Bode Olukolu, Maria David, Mercy Kitavi.*



# Product testing #2: Stage 4

- Biparental population
- Genetic backgrounds
- Breeding sub-populations

# Product Advancement Stages




**Variety = Market Value + Reliable Production**

# Product Advancement Stages

## Product Profiles Towards Variety replacement and Market Changing Strategies

### Framework for defining and managing traits for RTB strategic value chains

1. Portfolio of priority traits is dynamic
2. Next- and end-user knowledge, interests and expectations are central
3. Prioritization process need be fully interdisciplinary and participatory
4. Traits must be measurable and heritable
5. Traits should be defined as packages for adoption; meet specific demands
6. Traits of interest to only a small end-user population not justifiable for breeding
7. Number of target traits for breeding is low
8. Maintenance traits are part of product profile
9. Trait expression determined under well defined conditions
10. Genetic gains measured against well-defined baselines.

Hershey et al., 2017.

# Product Advancement Stages

## Product Profiles Towards Variety replacement and Market Changing Strategies

**Table Quality**

- DM content
- Nutritional value
- Storability
- Color
- Cooking time
- Sweetness
- Texture
- After-cooking quality

**Baking Quality**

- Sweetness
- Color
- Nutritional value
- Sugars (Browning of crust)
- Bread shelf-life
- Starch profiles
- Cell wall structure for water binding
- DM content

**Processing/Industrial**

- Shape and size
- Food safety e.g. acrylamides
- After-cooking quality
- Sweetness
- Texture (starch distribution)

**Reliable Production**

- Yield and component traits
- Environmental resilience
- Planting material
- Management systems

Tawanda Muzhingi, 2018

# Needs Assessment

i) A Budget

ii) Current Business Partners (GT4SP and SASHA)

iii) EiB, esp. Module 3 and 4

iv) FTO

# Acknowledgements





BILL & MELINDA GATES foundation