A journey from classical to modern cassava breeding: Integrating genomic selection for faster and greater genetic gains

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Cassava Team Meeting

Montería, Colombia | 21st November 2023

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Acknowledgements

Together
Everyone
Achieves
More

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Outline

PART I: Background & context

- Transition from traditional to modern cassava breeding
  - Overview of the traditional cassava breeding method
    - Recurrent phenotypic selection
  - Genomic selection (GS) as a breeding tool
    - What it is? Why implement? How it works?

PART II: Applications & plans

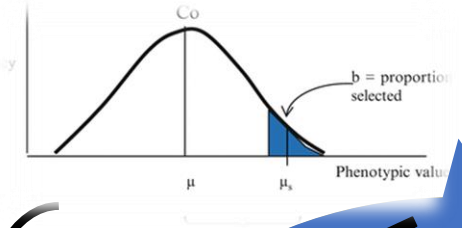
- Incorporating GS in CIAT cassava breeding pipeline
  - Work plan 2023-24, status, challenges & opportunities,
  - Discuss ideas & plans to optimize cassava GS models
  - A glance at the future: Hybrid cassava breeding

Part I

Transition from traditional to modern cassava breeding

The traditional & long cassava breeding cycle

Selections based on phenotypic values



Improve population

SELECT

CROSS

5-YEAR cycle

EVALUATE

Release product (cultivar)

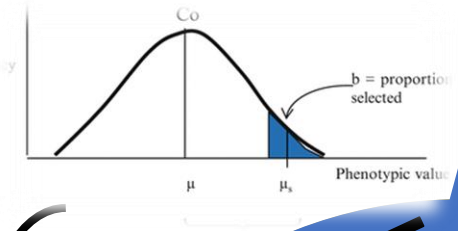
Image credits:
G. Acquaah, 2015; N. Morante; & D. E. Moreta

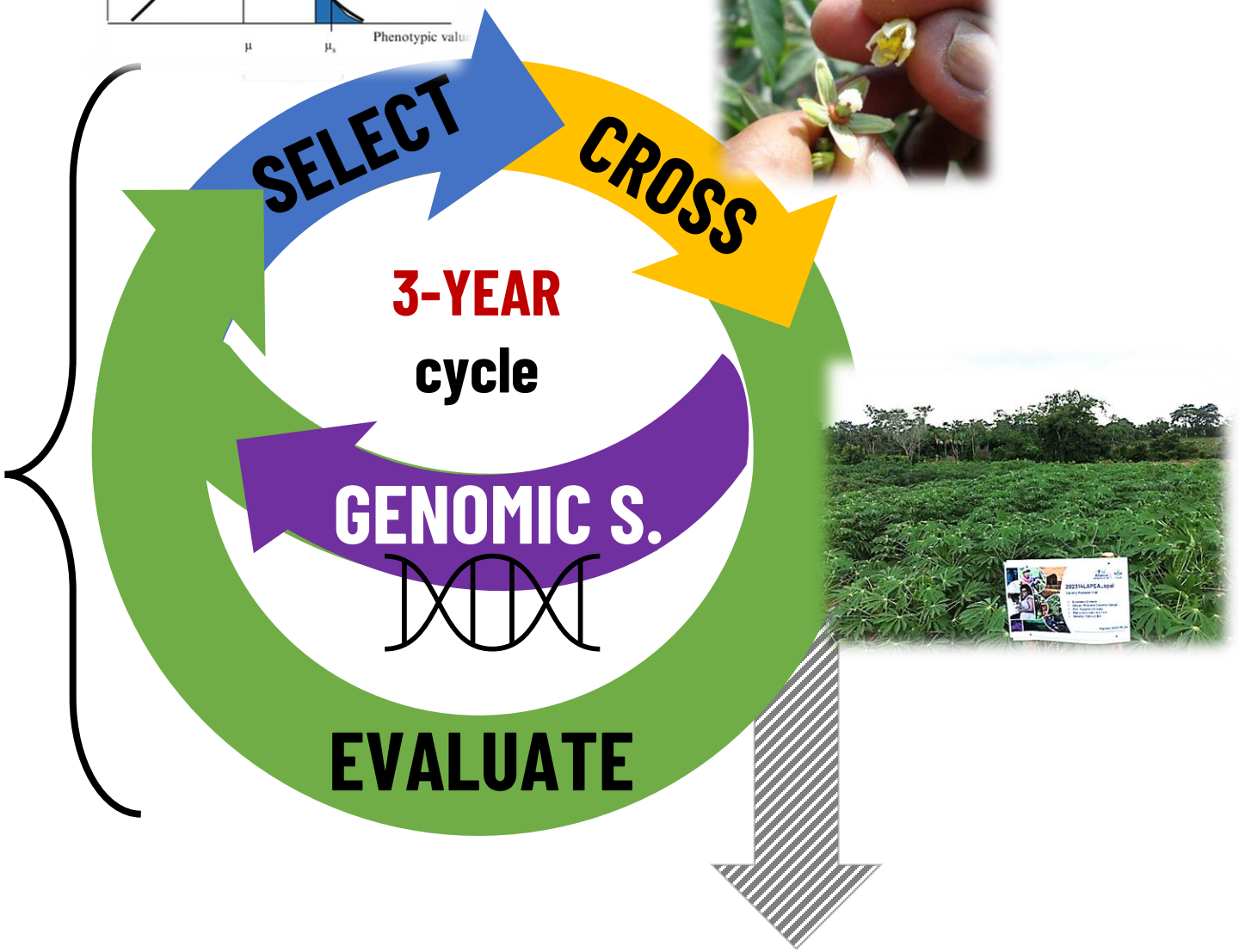
A shorter breeding cycle with genomic selection

Selections based on genomic estimated breeding values (GEBVs)

$$GEBV = f(\text{DNA})$$

Improve population





Release product (cultivar)

Image credits:
G. Acquaah, 2015; N. Morante; & D. E. Moreta

Genomic selection:
The next (r)evolution in plant breeding

$$\Delta G = \frac{i \cdot r \cdot \sigma_a}{t}$$

ΔG: Genetic gain per unit time
i: Intensity of selection
r: Accuracy of selection
σ_a: Additive genetic variation
t: Duration of the breeding cycle

Impacts of GS on the breeder's equation parameters

		Direct impact	Indirect impact
Introducing genomic information	Add genotyping to increase selection accuracy	r	i $1/t$
	Reduce phenotyping effort with genotyping	i $1/t$	
Management of genetic diversity	Better choice of parents to optimize crossbreeding or preserve genetic diversity	r σ_a	

Source: Fugeray-Scarbel et al., 2021

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Accelerated cassava breeding: The major benefit of genomic selection

Genomic Selection (GS, aka genomic prediction, genome-wide selection, genome-wide prediction, etc.) is a genomics-assisted breeding tool.

F_1: seedling nursery
F_1C_1: cloned seedling nursery
SRT: single row trial
PYT: preliminary yield trials
AYT: advanced yield trials
SIT: seed increase trial
TPY: training population yield trials
GWP: genome-wide prediction

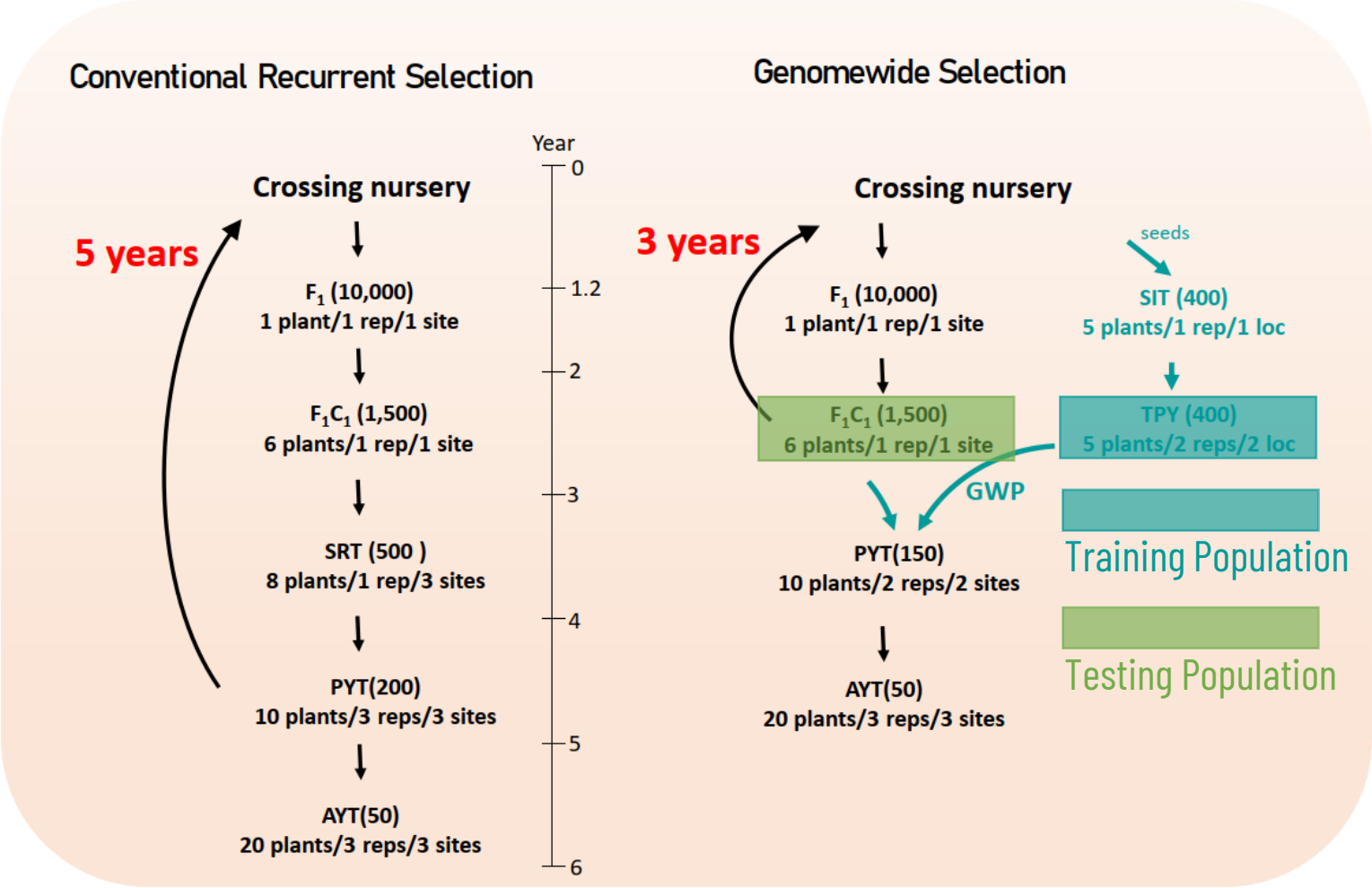


Figure credits: Cassava Breeding Team (Alliance Bioversity-CIAT)

How genomic selection works?

$$GEBVs = f(\text{DNA})$$

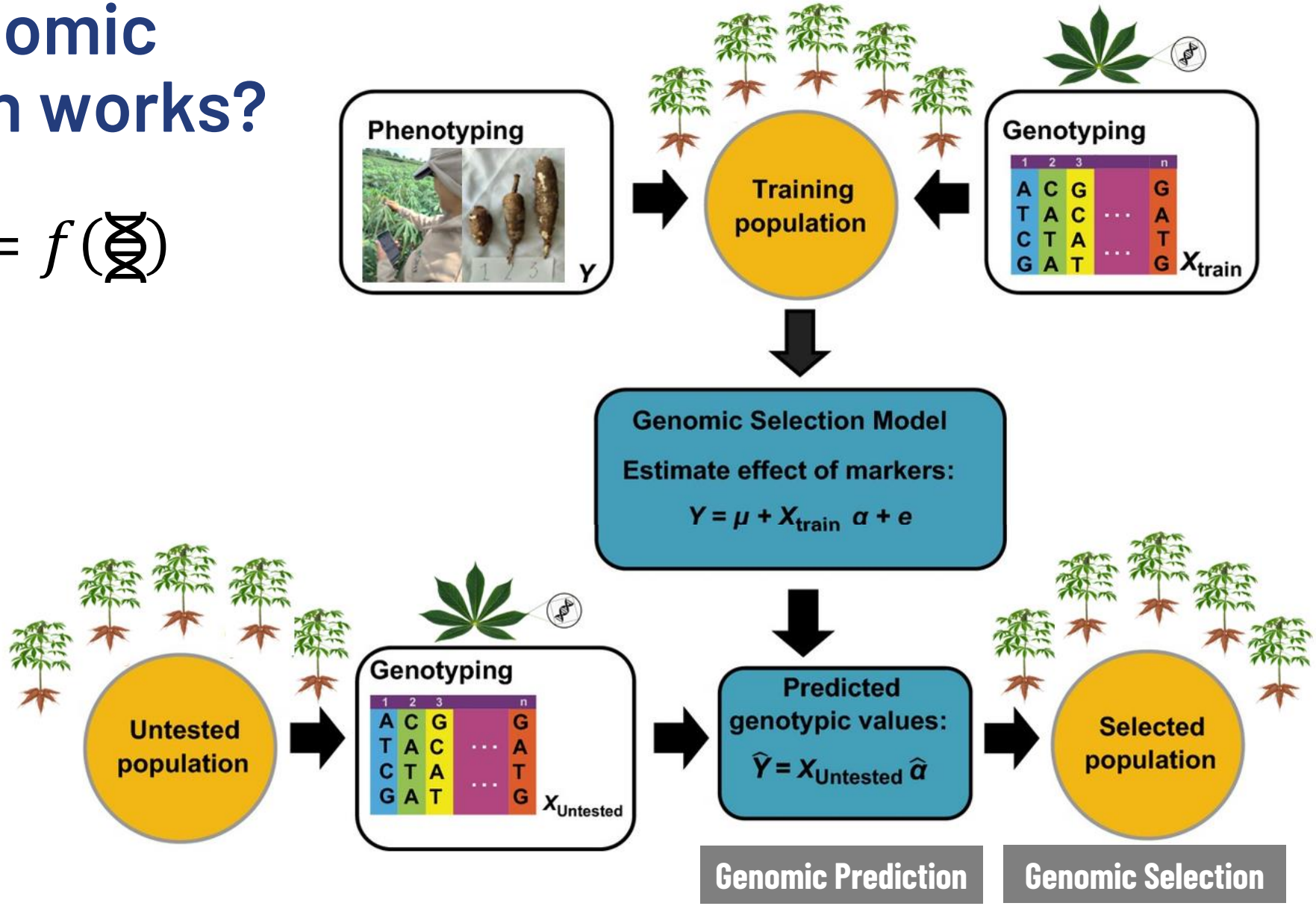


Figure adapted from Zhao et al., 2015 | Photo credits: S. Salazar

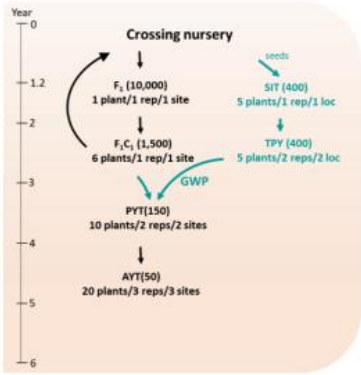
GS as a breeding tool to accelerate cassava genetic gains

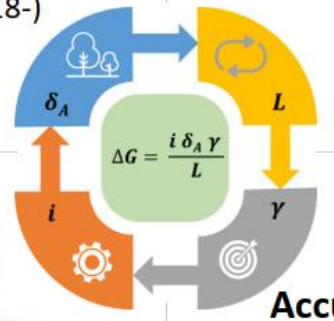
Genetic Diversity

- New traits, e.g., CBSD res., CMD res., good cooking quality et al.
- Sequencing of progenitors (2020-)
- Hybrid Breeding (2018-)

Duration of Selection Cycle

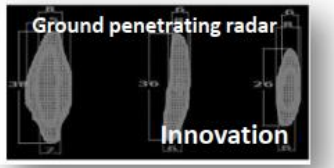
- Flower Inducing (2016-)
- Genomewide Prediction (2019-)





Intensity

- High throughput phenotyping



Accuracy

- CassavaBase, Fieldbook & Barcode (2018-)
- Quality control and MAS (2020-)
- TPE, ≥ 2 Environments (2020-)
- ≥ 5 Checks, BLUP and GBLUP (2020-)
- Selection Index (2012-)
- NIRS & Image Analysis (2012-)
- Stage&Gate System (2020-)
- Operational Excellence (2019-)

Figure credits: X. Zhang

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Why implement genomic selection?

$$GEBV = f(\text{DNA})$$

- Shorten lengthy breeding cycles
- Increase breeding efficiency: greater ΔG per unit time
- Seed shortages
- Discard poor clones earlier
- Reduce manual labor (phenotyping)
- Hard-to-measure traits

What factors affect GS accuracy?

$$\boldsymbol{Accuracy} = corr(phenotype, prediction)$$

- Marker density
- Size & composition of training population
- Number of QTLs
- Heritability
- Linkage disequilibrium (LD)
- Model used

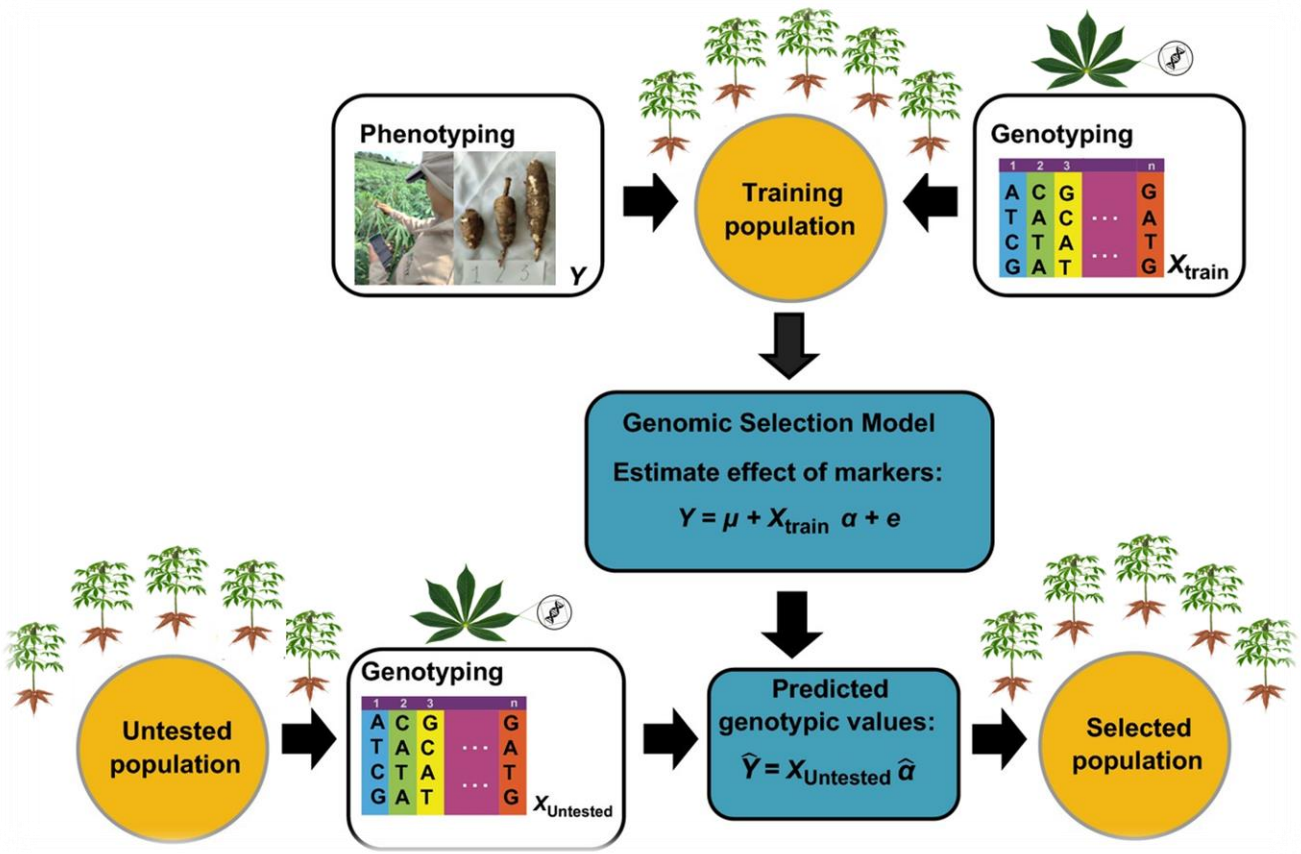


Figure adapted from Zhao et al., 2015 | Photo credits: S. Salazar

Genomic selection models

All models are approximations and hence wrong, but some are useful. ~ George Box

The basic genetic model: $\boldsymbol{P} = G + E + (GxE)$

$$GEBV_{GS} = f(\text{DNA})$$

Ridge-regression best linear unbiased prediction (RR-BLUP)

Assumption: Infinitesimal model of genetic architecture (all markers have an equal effect)

Step 1: Estimate marker effects in training population (TP)

Step 2: Use marker effects & genotypes of selection candidates to predict GEBVs

Genomic best linear unbiased prediction (G-BLUP)

Step 1: Use markers to quantify genomic relationships

Step 2: Use genetic relatedness to TP of unevaluated to predict GEBVs

Bayesian models

- Better model marker effects of differing sizes (Hayes, 2007)
- Separate variance estimated for each marker (Meuwissen et al., 2001)

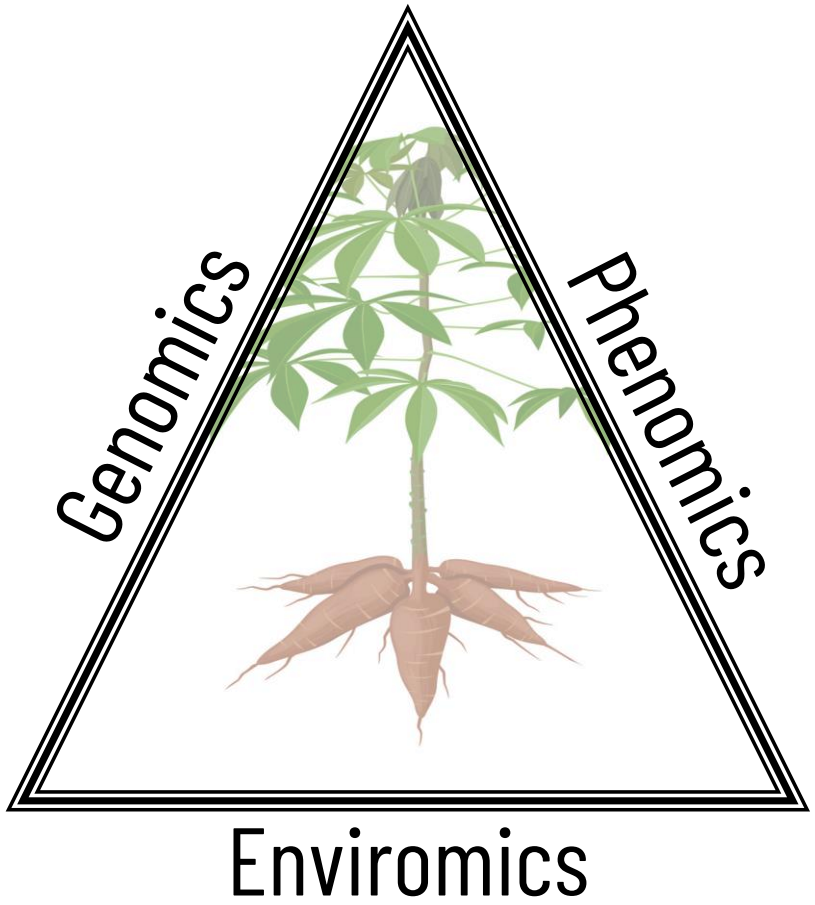
Modern plant breeding beyond molecular markers. Integrating and connecting disciplines

$$P = G + E + (GxE)$$

Phenomics

Genomics

Enviromics

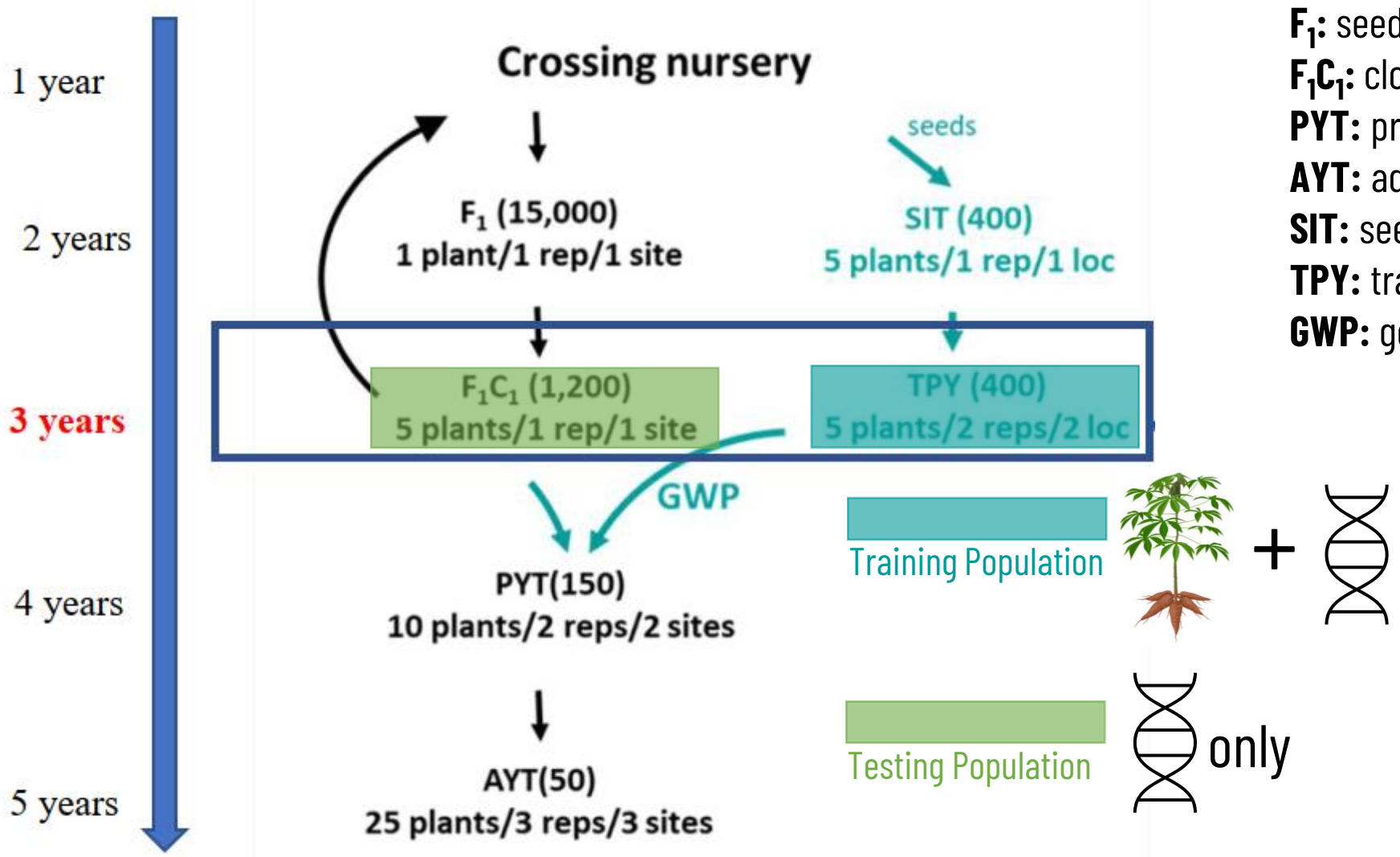


GS will not replace traditional breeding & field work, instead it will help optimize the system.

Part II

Incorporating GS in CIAT cassava breeding pipeline

First steps to implementing GS in the cassava breeding pipeline at CIAT



F_1: seedling nursery
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PYT: preliminary yield trials
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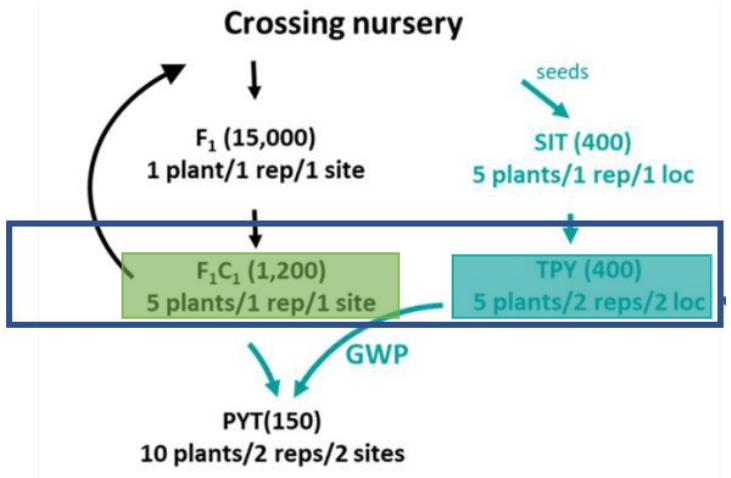
Figure credits: Cassava Breeding Team (Alliance Bioversity-CIAT)

Training & testing (breeding) populations
C1.1 (Cycle 1, Cohort 1) | 2020-2021



Training Population Testing Population

Germplasm: Full-sibs

Trial names: 2021DVGST (n = 399) 2020DVF1C (n = 651)

Locations: 3 locs

2 in north coast*: Repelón, Momil | Ag traits + Pest & disease resistance

1 in Palmira | Only quality traits

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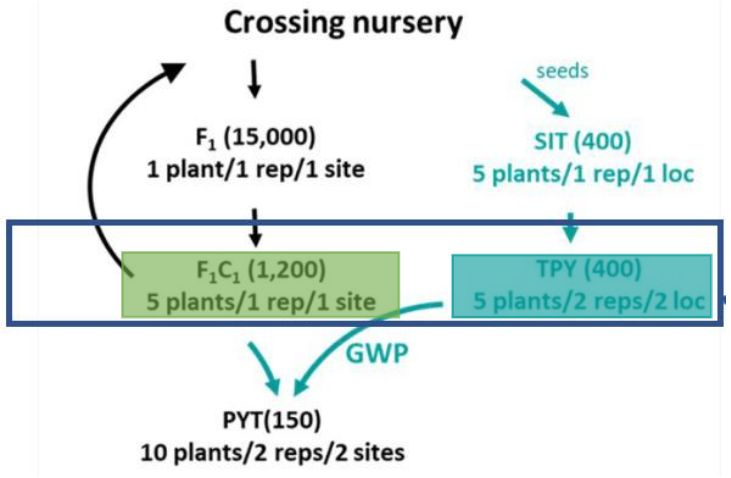
*Semi-arid & sub-humid environments

Training & testing (breeding) populations
C1.2 (Cycle 1, Cohort 2) | 2021-2022

Training Population Testing Population



Germplasm: Full & half-sibs

Trial names: 2022DVGST (n = ~873) 2021DMF1C (n = ~823)
2021CQF1C (n = ~672)

GS for waxy cassava (COMING SOON!)
n = ~200 clones
Ingredion agreement

Locations: 3 locs

2 in north coast*: Santo Tomás, Momil | Ag traits + Pest & disease resistance

1 in Palmira | Only quality traits

---

*Semi-arid & sub-humid environments

Genotyping the training & testing (breeding) populations

C1.1 (Cycle 1, Cohort 1) | 2020-2021

$$Phenotype = Genotype + Environment$$

10X WGS

Whole genome sequencing for 1052 materials

399 training population materials

TPY (400)
5 plants/2 reps/2 loc

651 testing population.

F_1C_1 (1,200)
5 plants/1 rep/1 site

About 230K high-quality SNPs were selected to compute the genomic estimated breeding values (GEBVs) for 21 traits.

Figure credits: C. Vargas

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Prediction ability

C1.1 (Cycle 1, Cohort 1) | 2020-2021

$$Accuracy = corr(phenotype, prediction)$$

Cross-Validation

How well do we predict individuals without phenotypes?

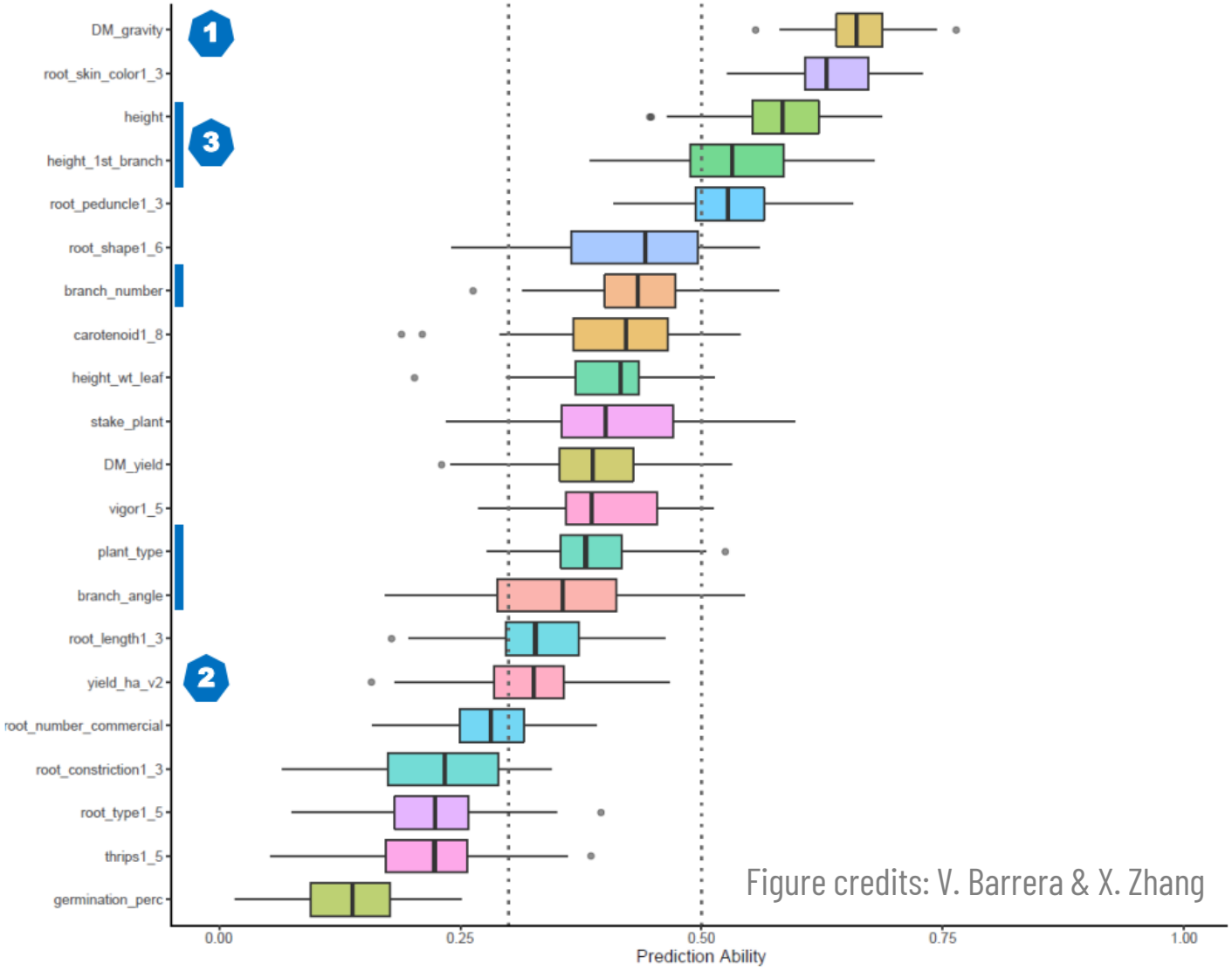
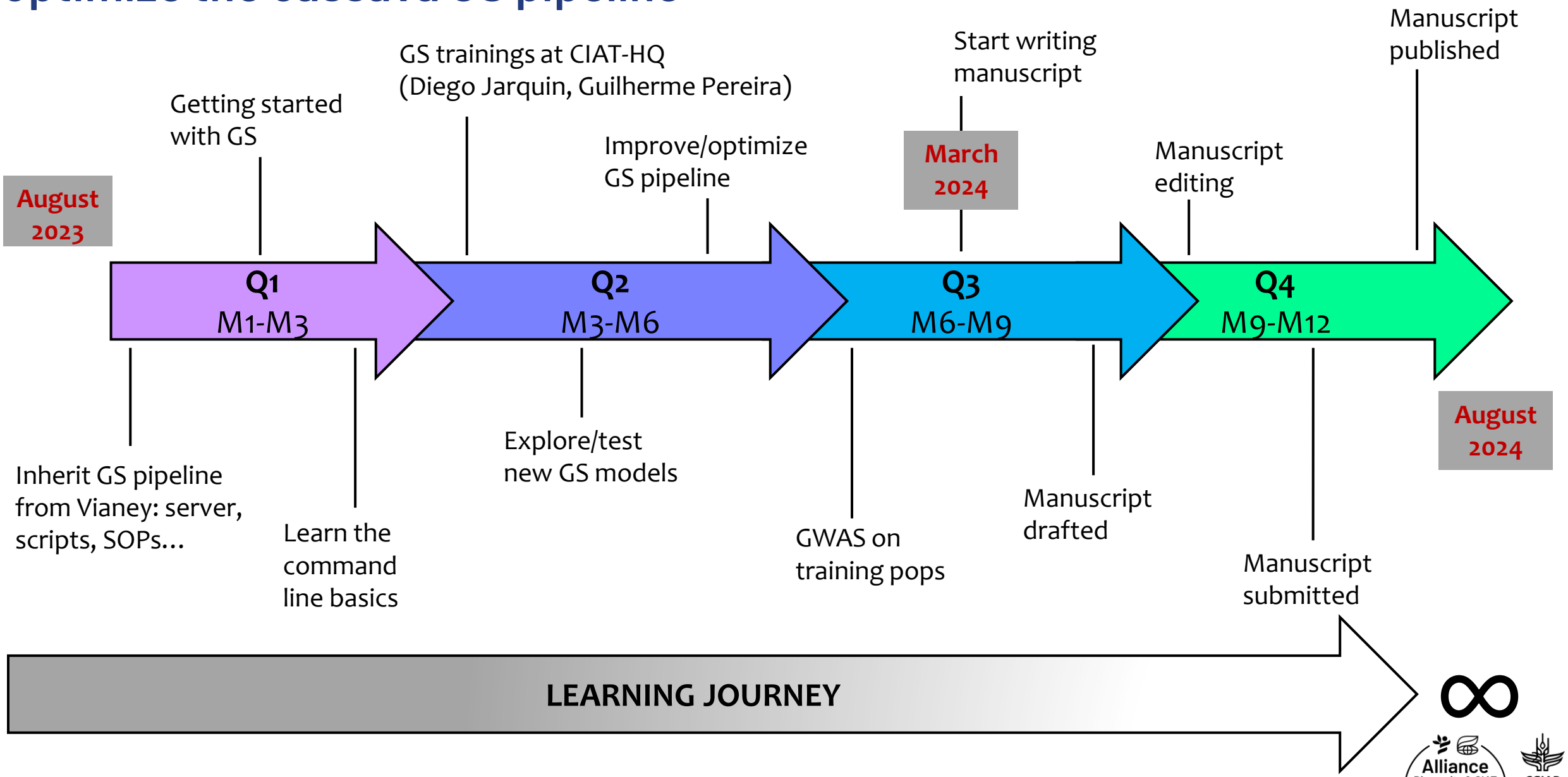


Figure credits: V. Barrera & X. Zhang

My timeline/roadmap to implement & optimize the cassava GS pipeline

Q: quarter of a year (3-month period)
M: month



Status: Trying to reproduce what others did

VCFtutorial_statsVisualization

$dEmc^2$

Cali, CO | 17th October 2023

GUIDE/REFERENCE: https://speciationgenomics.github.io/filtering_vcfs/

$Notes_{dEmc^2}$:

DNA sequencing info

10x whole genome sequencing

VCF file source: **Group1_11.chromosome01.vcf**

$n_{samples}$ = 395

n_{SNPs} = 588,247 (original/raw)

2021: Group 1-8

Group

Genom

Learning by doing!
Running demos & generating reports

GP_GS_demo: rrBLUP

$dEmc^2$

Cali, CO | 25th October 2023

GUIDE/REFERENCE: **GS_GEBVs_Prediction_Tutorial_dEmc2.jpynb**

$Notes_{dEmc^2}$:

Working files

1. $Genotypes_{SNPs}$ = **gs_2023.reduced.txt** | Should contain training (gsT) + breeding pops (gsB)
2. $Phenotypes_{BLUPs}$ = **GS_2023_second_cohort_blups.csv** | Should be only gsT
3. $Accessions_{names}$ = **group12_group12_accessions.csv** | Use to match genos & phenos

NEED TO TRACE BACK ALL THESE FILES IN VIANEY'S FOLDERS. They a

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Operational challenges & opportunities

Challenges	Opportunities
Unorganized files on server (hard to track and find)	Systematic organization of files on server
Lack of repository for GS scripts and related	Feed/update **Cassava2050 GitHub repository** (reproducible research)
IT micromanagement & lack of communication with researchers	Creation of a **server committee**: “Cassava byters” (Sean, Xiaofei, Winnie, Camilo, Danilo)

Ideas to optimize (make it more accurate) the cassava GS models

$$\boldsymbol{P} = G + E + (GxE)$$

Let's not miss these parts!

$$GEBV_{GS} = f(\text{DNA})$$

Phenos & environment

- Plug environmental covariates: weather & soil
- Account for GxE effects x
- Combine populations to increase power
- Include secondary traits (easier to predict?)
  - Relative yield
  - Total disease resistance
  - Harvest index, etc.
- High-throughput phenotyping for better model training (ongoing collab. w/ Mike Selvaraj)

DNA markers

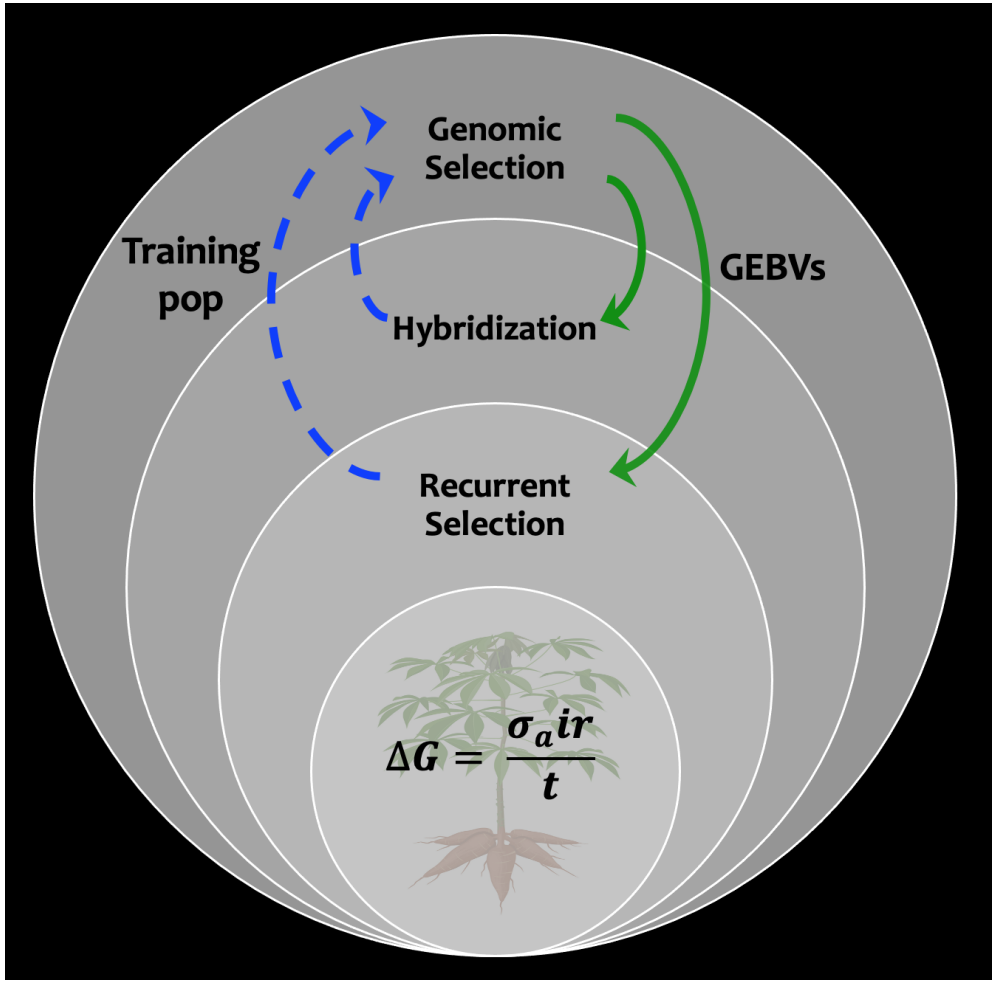
- Try different TP sizes & number of markers
- Dual purpose of TP: predictions + association (GWAS)
- Special treatment to some markers
  - Most significant & GWAS hits as fixed effects

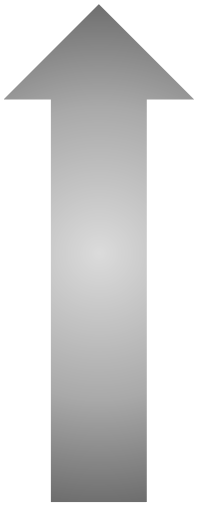
Moving up cassava improvement & production to the next level through hybrid breeding

How can GS help achieve this?

Inbreds: Combining ability

Hybrids: Performance





Efficacy of ΔG per unit time and cost

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Thanks!