



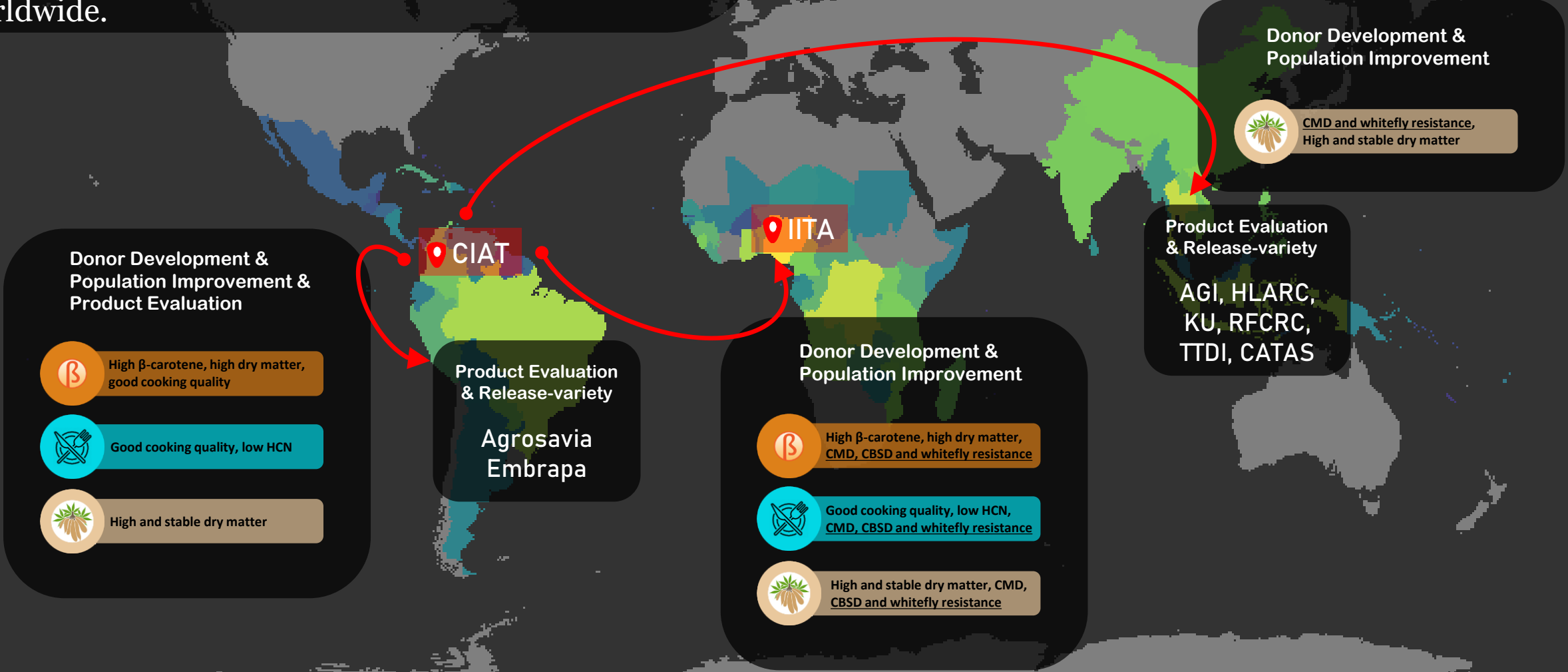
Genomics-assisted Selection in Cassava Breeding

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The Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT) is part of CGIAR – a global research partnership for a food-secure future.

The Cassava breeding program generates development along the cassava chain. Impacting on the main problems and challenges of cassava worldwide.

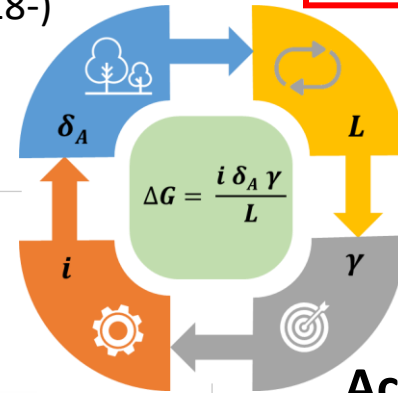
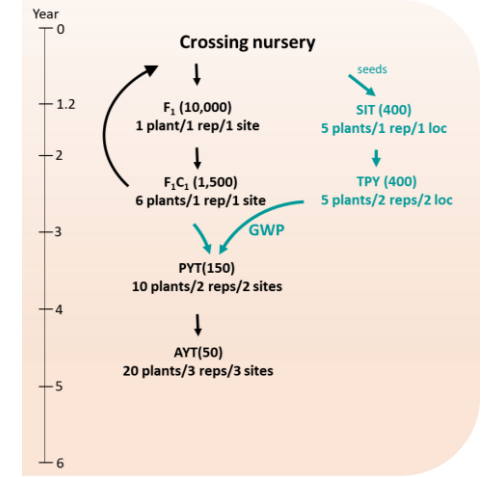


Genetic Diversity

- 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-)

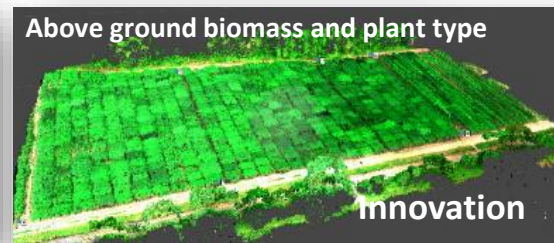
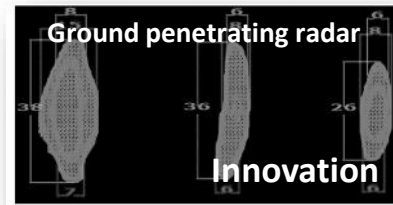


Intensity

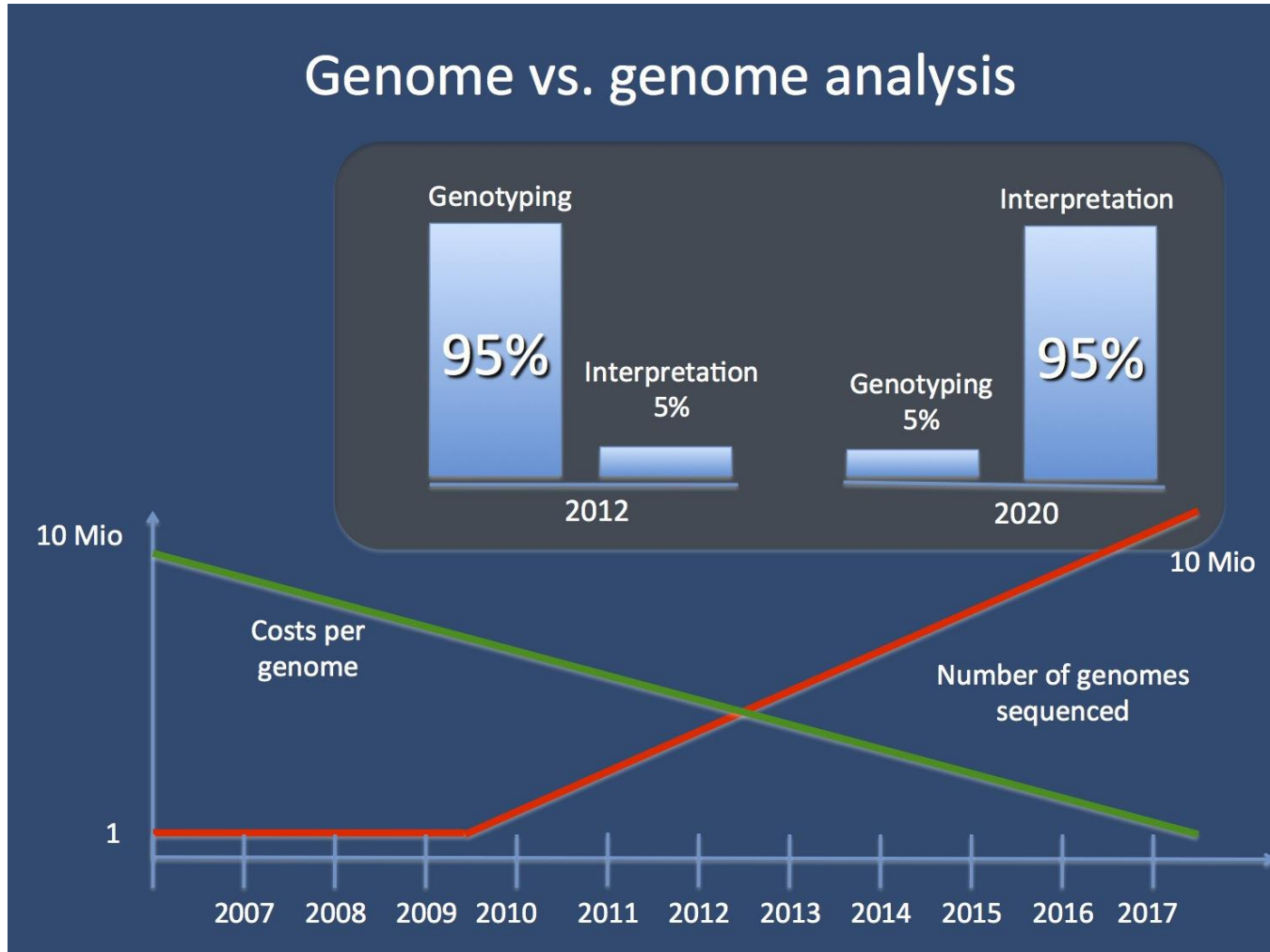
- High throughput phenotyping

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-)



Genetics assisting breeding

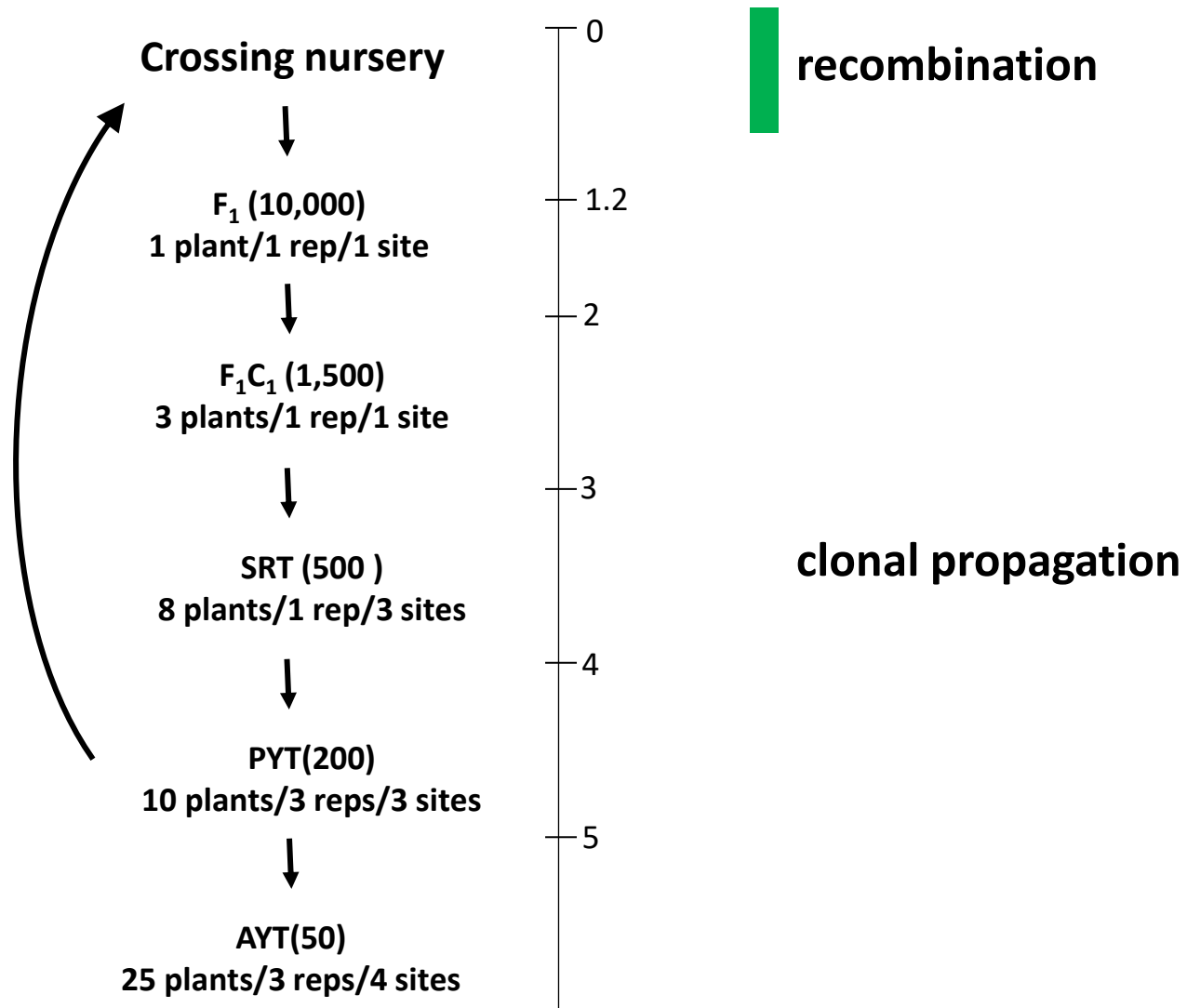


- ❖ In recent years, genomics has become an accessible tool.
- ❖ Compared to other crops such as corn and sorghum, genetic studies and genomics-assisted breeding still lag behind in cassava.

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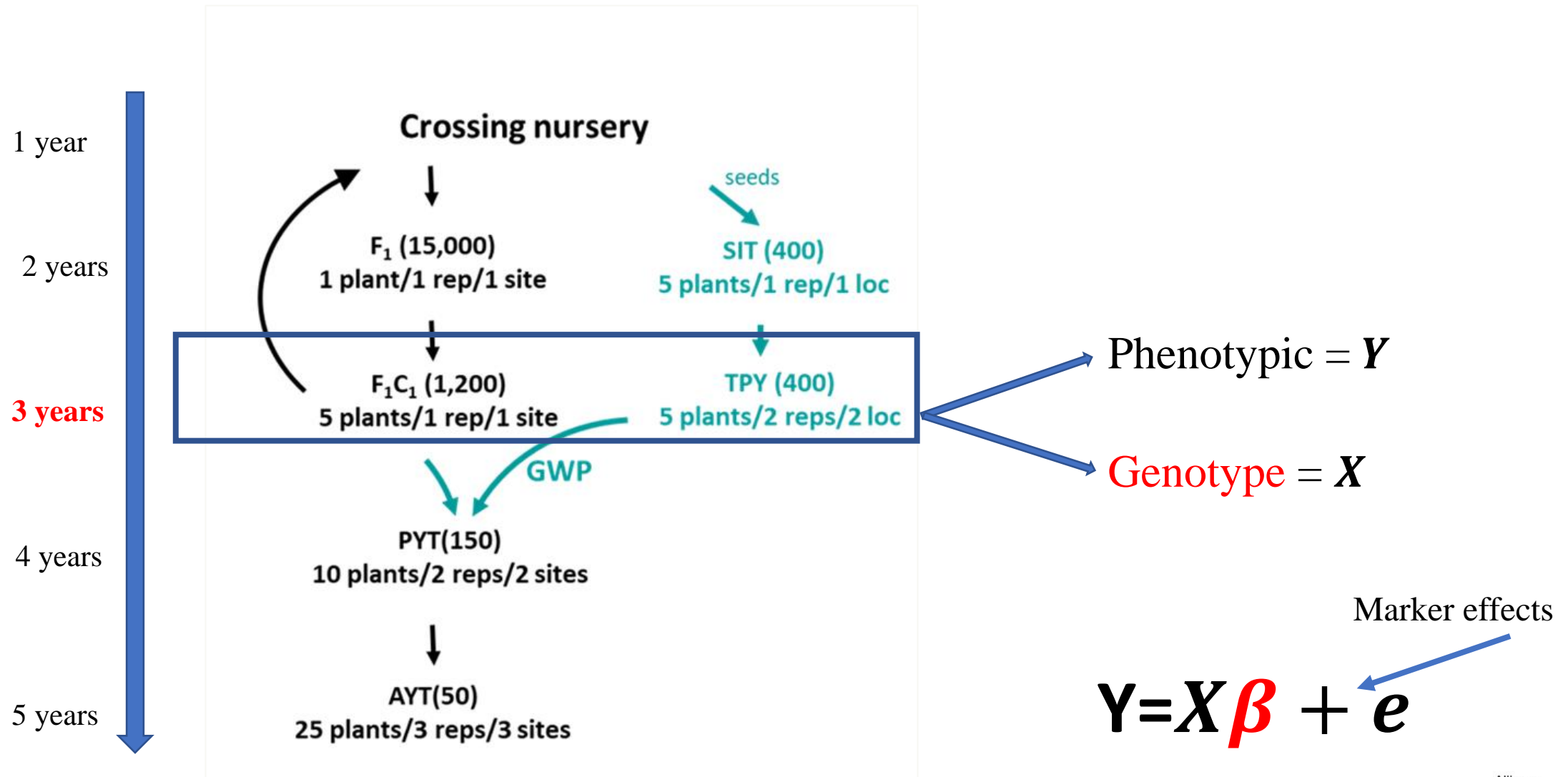


Conventional Cassava Breeding Scheme



- ❖ The recurrent selection method is widely used in cassava.
- ❖ It requires 5 years to be able to start a new breeding cycle.

New Genome-wide Prediction scheme

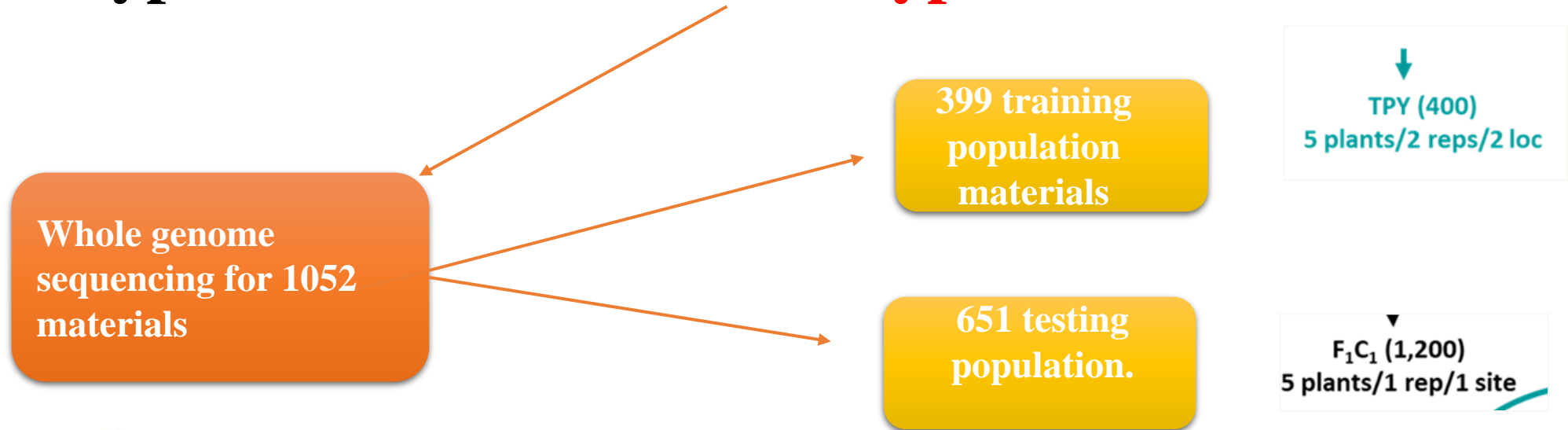


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Genotyping

Phenotype = Environment+ Genotype

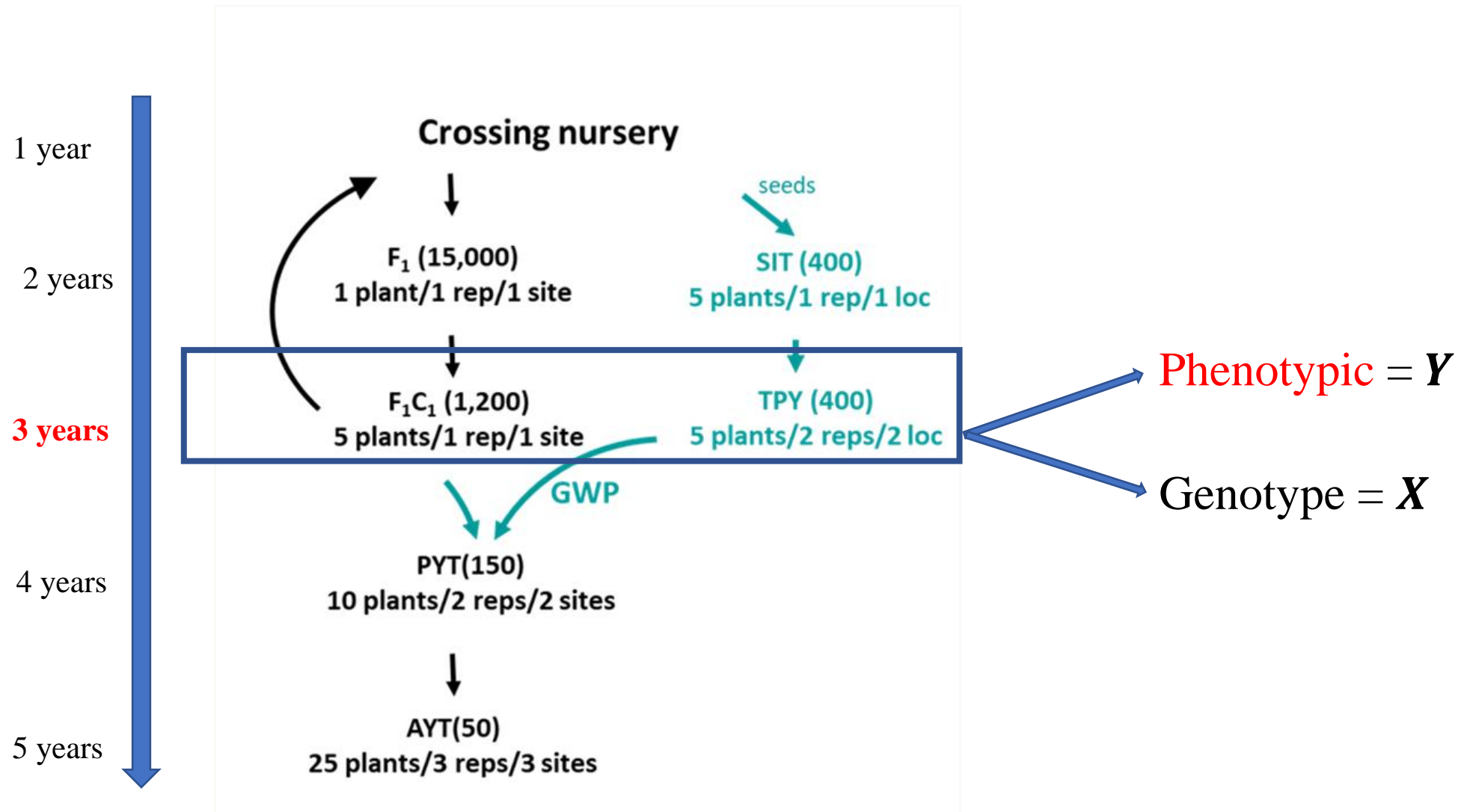


About 230000 high-quality SNPs were selected to compute the genomic estimated breeding values for 21 traits. The same dataset was used to find QTLs using a genome-wide association study (GWAS) analysis.

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New Genome-wide Prediction scheme



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Training population

- ❖ Semi-arid and Sub-Humid environments were evaluated (50% of cassava environments).
- ❖ Multiple traits must be considered when selecting a material
- ❖ Diagonal checks and row and column designs were used in the trials evaluated.



↓
TPY (400)
5 plants/2 reps/2 loc

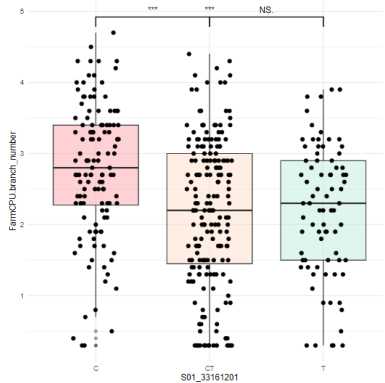
21 Traits were considered



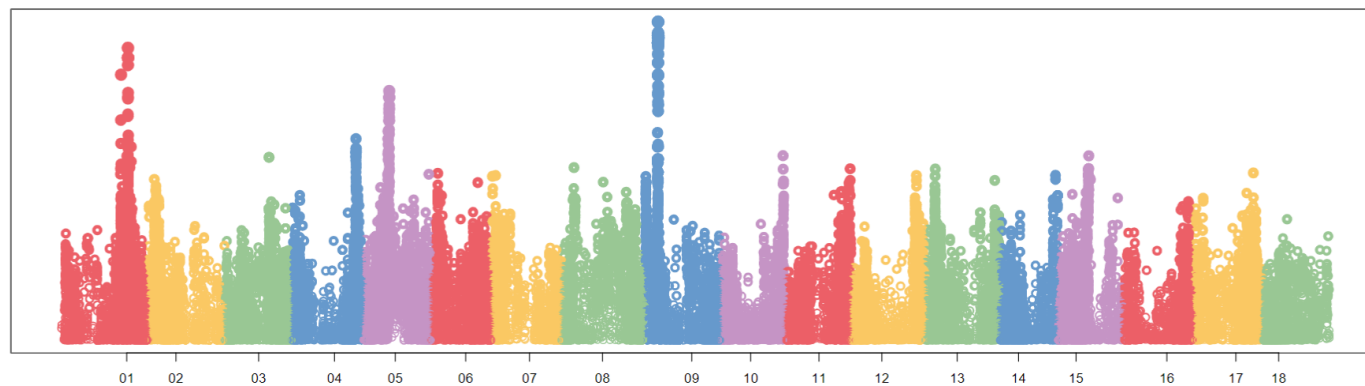
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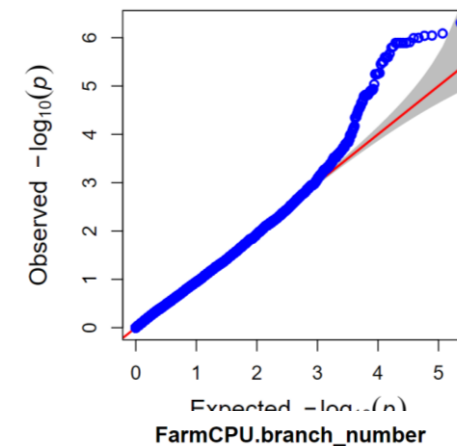
Gwas Results



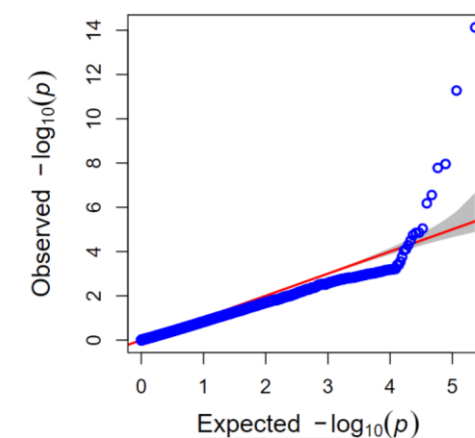
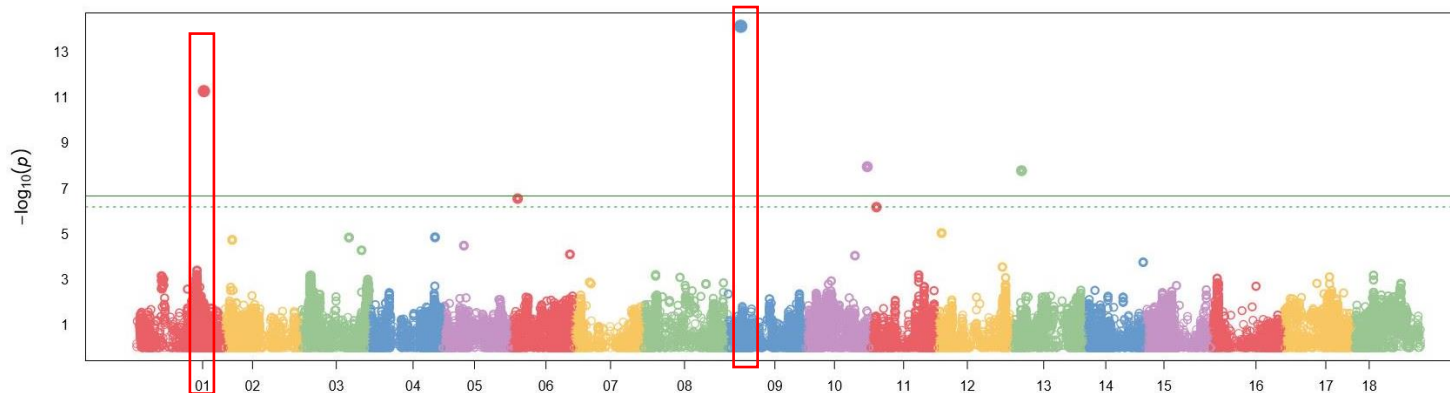
MLM.branch_number



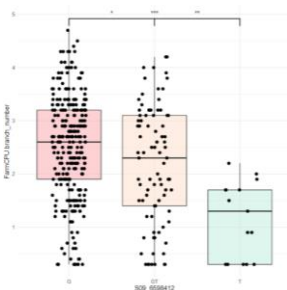
MLM.branch_number



FarmCPU.branch_number



Favorable allele is dominant

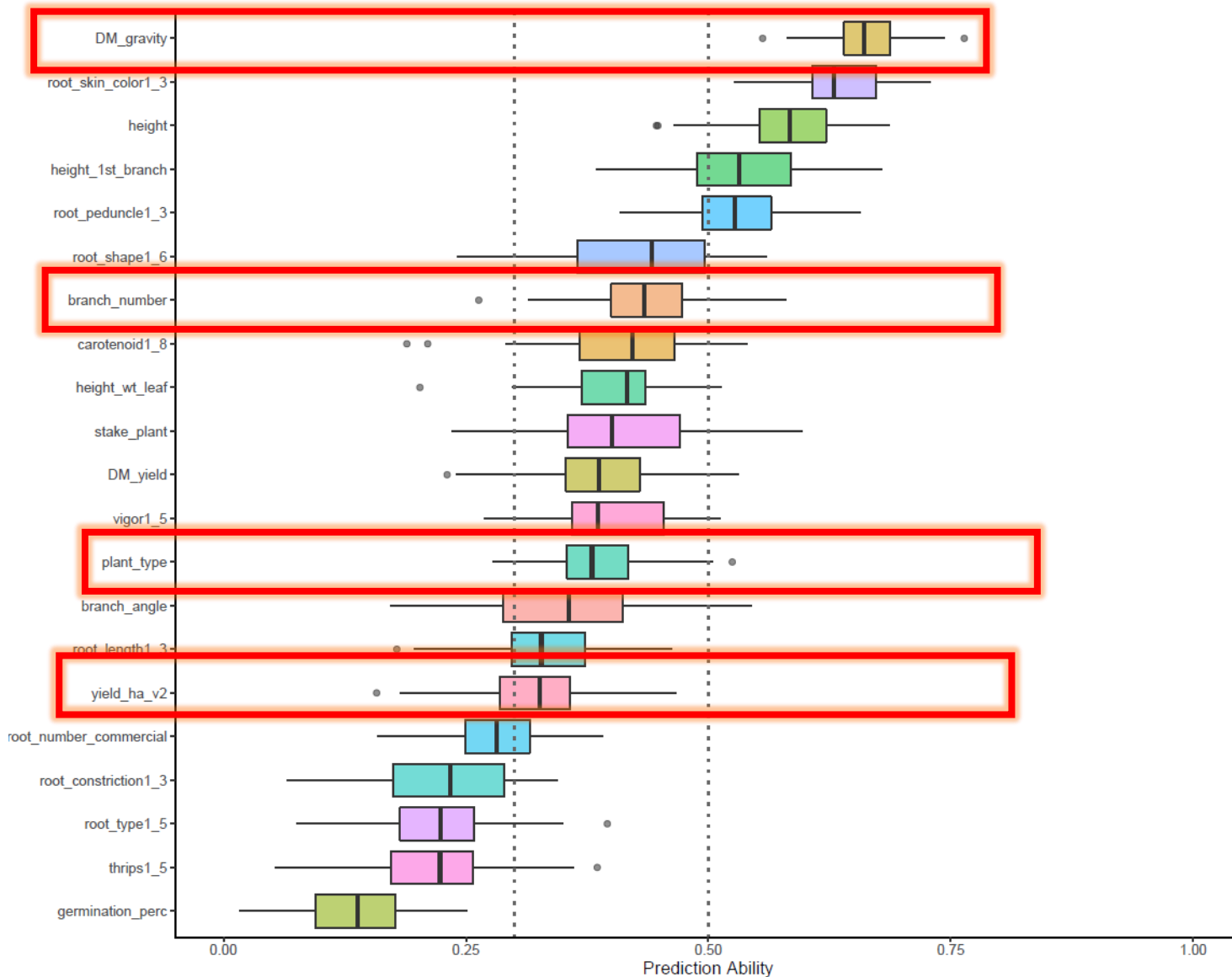


Favorable allele is recessive, but might have high inbreeding depression.

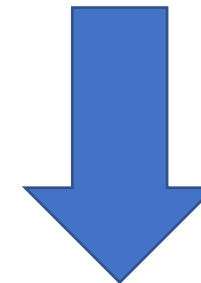
Chr	Pos	P.value	MAF	Effect
1	33,161,201	5.29E-12	0.44	-0.45
9	6,598,412	7.46E-15	0.15	-0.66

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Cross-Validation



- Dry matter, root color and height were the traits with the highest predictive ability.
- Yields are in acceptable ranges (0.35)



Less time for new cycles



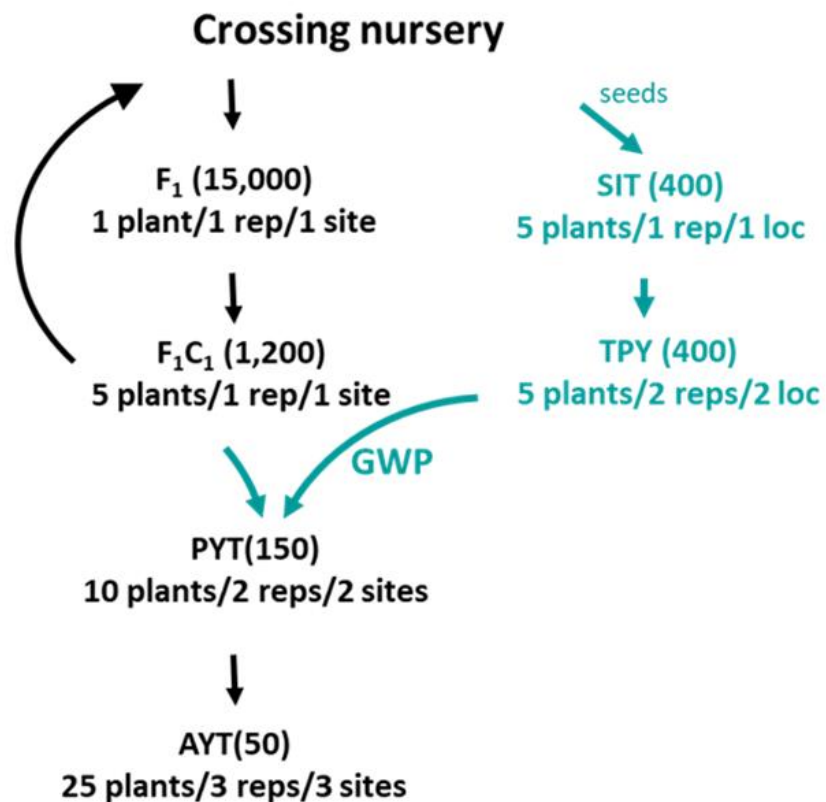
Increase the genetic Gain

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Actual Overview

Crossing nursery



Cycle 1, cohort 1

Apr. 2019 – Apr. 2020, pollination

Apr. – Sep. 2020, Greenhouse
Sep. 2020 – May 2021, Field

Jun. 2021- Apr. 2022, Target env.

Finish

Cycle 1, cohort 2

Apr. 2020 – Apr. 2021, pollination

Apr. – Sep. 2021, Greenhouse
Sep. 2021 – May 2022, Field

Jun. 2022- Apr. 2023, Target env.

Advance

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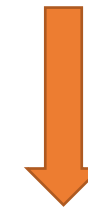


Next Steps

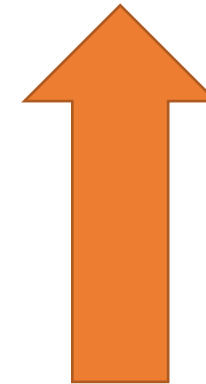
- ❖ Development of an accurate genomic selection model with high predictive values for different traits.
- ❖ Detect the QTLs involved in the expression of different traits.



Time



Cost



Genetic
Gain

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Acknowledgments



NEXTGEN
CASSAVA



CGIAR

华大生命科学研究院
BGI·Research



USAID

FROM THE AMERICAN PEOPLE

BILL & MELINDA
GATES *foundation*

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Thank you!

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