

Plant breeding through the lens of quantitative genetics

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April 9, 2024

About me



Map from R/maps

1. Malaysia
2. Indiana (BSc Biotech, Maths)
3. Wisconsin (PhD Genetics)
4. Freising, DE (Postdoc)
5. Edinburgh, UK (Postdoc)

Talk outline

Introduction

Research experience

- Crop domestication
- Genetic diversity and pre-breeding

Research vision and plans

Summary

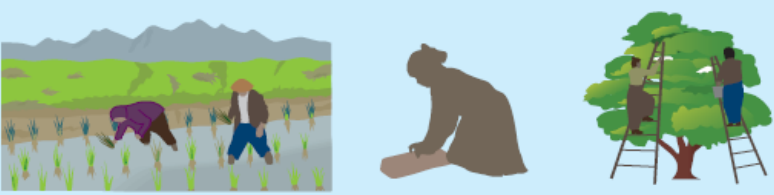
Introduction

Plant breeding, complex traits and genetic gain

Plant Breeding

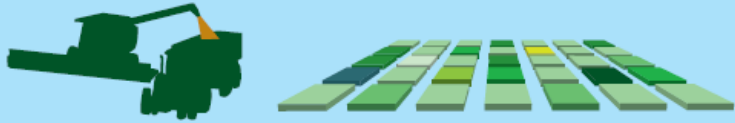
BREEDING 1.0

Incidental selection by farmers



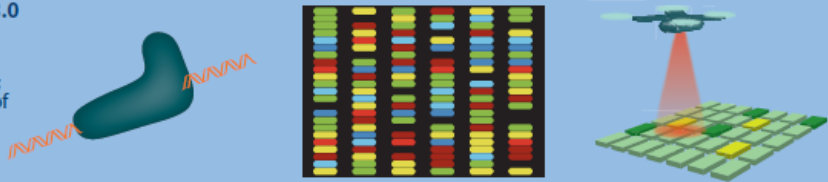
BREEDING 2.0

Statistical and experimental design to improve selection effort



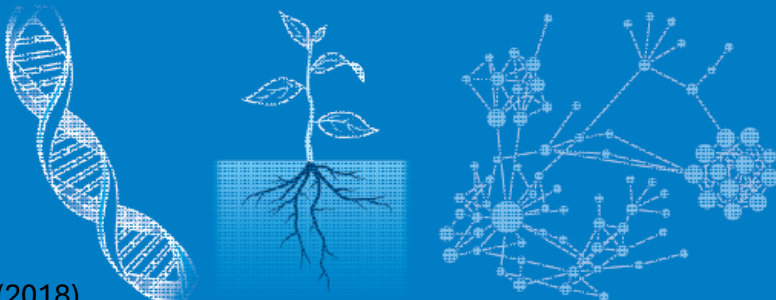
BREEDING 3.0

Integration of genetic and genomic data; current state of the art



BREEDING 4.0

Ability to combine any known alleles into optimal combinations; will be reached soon for some crops

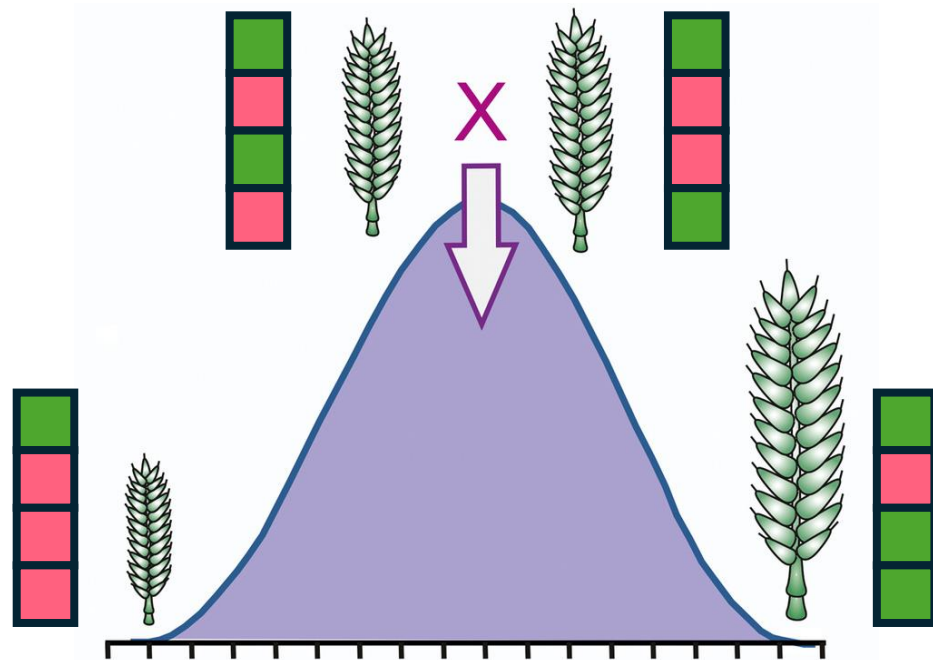


Wallace et al (2018)

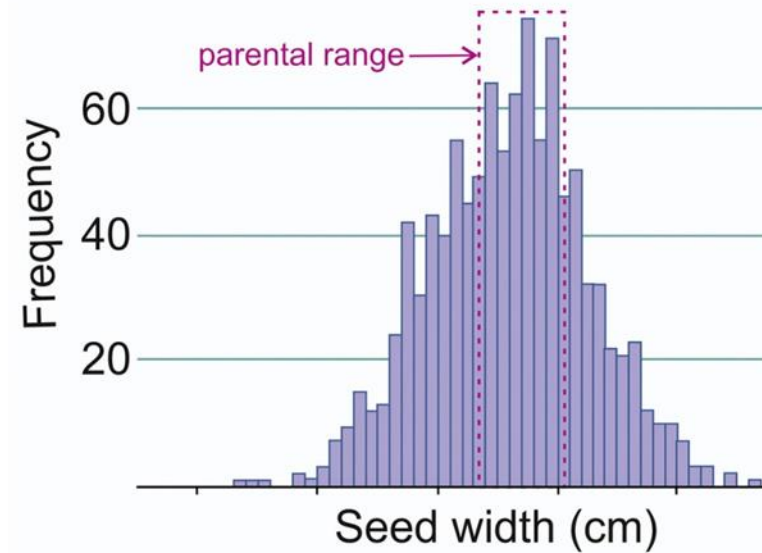
- Domestication
- Improvement
- Experimental design
- Marker assisted selection (MAS)
- Genomic/Phenomic selection (GS/PS)
- Biology-Breeding
- Gene editing (GE)
- Functional variants
- Machine learning (ML/AI)

Success in line breeding

Transgressive segregation: recombination and shuffling of causative genetic loci.



(d) Transgressive segregation for seed width in 'NIAB Elite MAGIC'



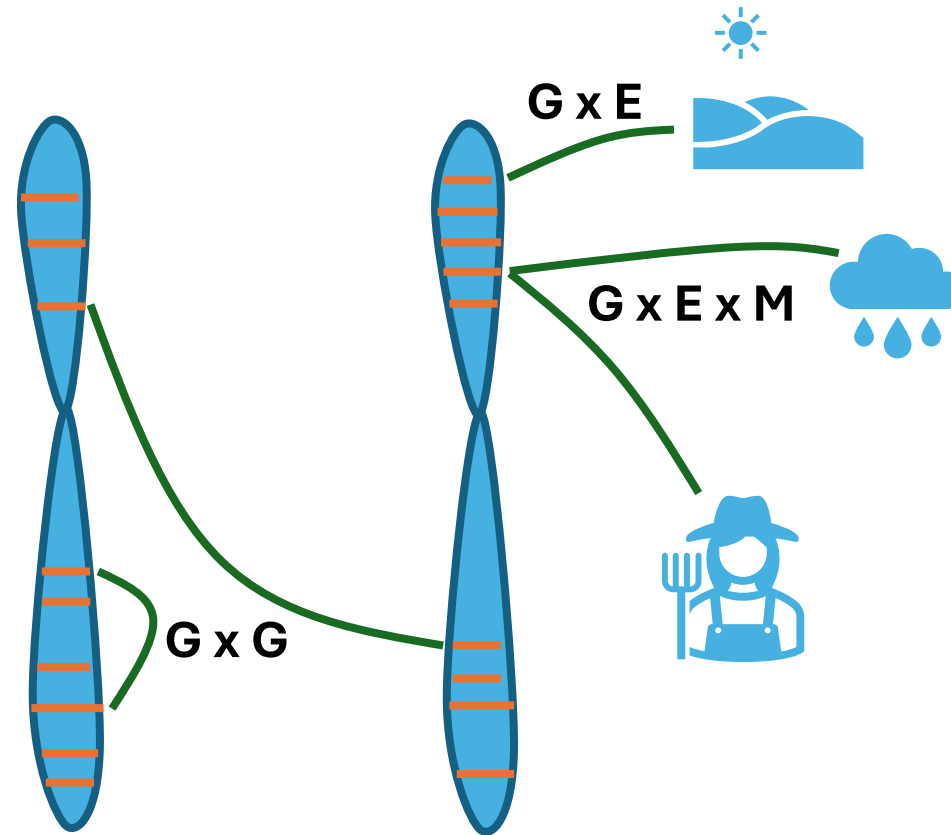
Mackay et al (2021)

Complex traits

Breeding targets: yield, flowering time, plant architecture, resource use efficiencies.

Quantitative/polygenic traits

Working model:



Genetic Gain

Breeder's equation
(Lush 1937)

$$R = h^2 S$$

$$R = \frac{\sigma_g^2}{\sigma_p^2} \sigma_p i$$

$$R = \frac{\sigma_g}{\sigma_p} \sigma_g i$$

$$R = h \sigma_g i$$

Rate of genetic gain

$$\Delta R = \frac{h \sigma_g i}{t}$$

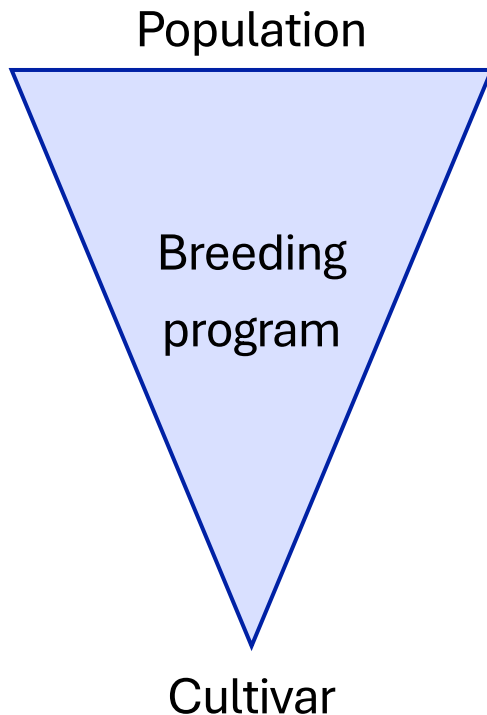
$$\Delta R = \frac{\text{sel. accuracy} \times \text{genetic variation} \times \text{sel. intensity}}{\text{time}}$$



Framework for quantitative genetics

Improving ΔR

$$\Delta R = \frac{\textit{sel. accuracy} \times \textit{genetic variation} \times \textit{sel. intensity}}{\textit{time}}$$



- Multiparental population, mutation, pre-breeding.
- MAS, GS, GE, phenomics.
- Larger/efficient trials.
- Rapid cycling, speed breeding (SB/RGA).

Research experience

Project 1: crop domestication

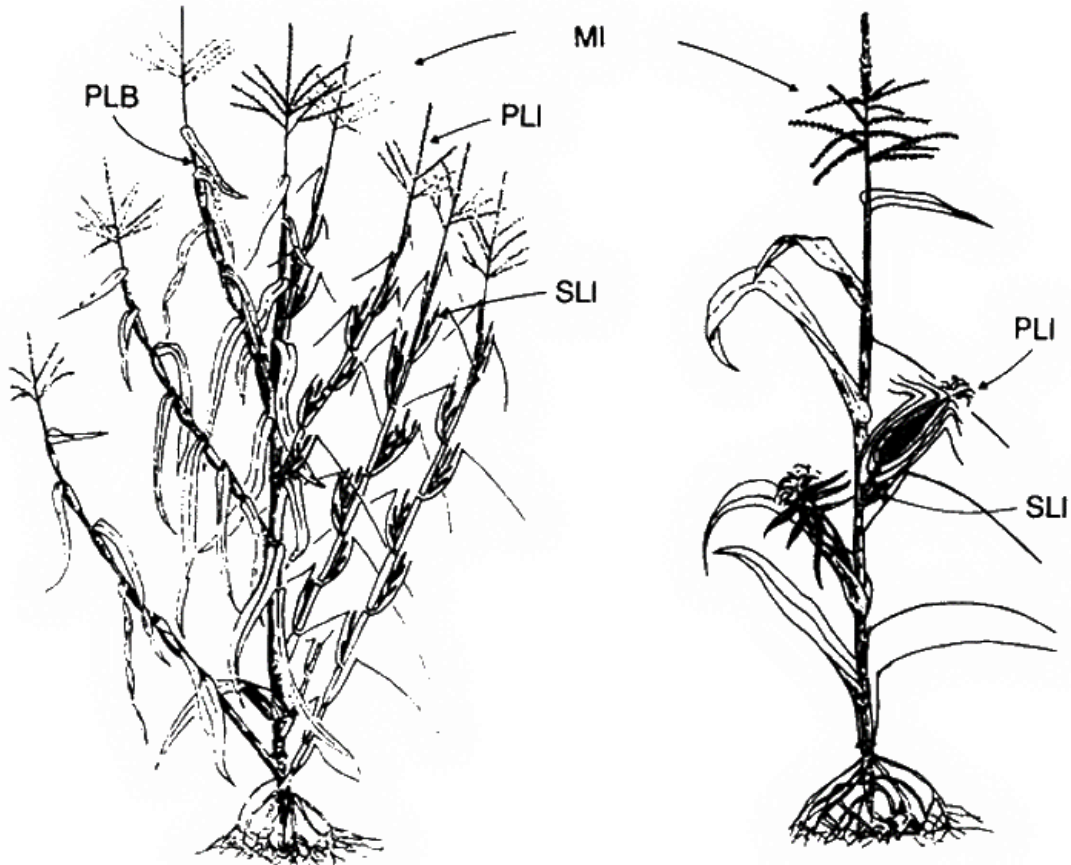
Project 2: genetic diversity and pre-breeding

Domestication

This earliest form of plant breeding is known as domestication, where plants were selected to be more productive, easier to harvest, or more aesthetically or gastronomically pleasing (Flint-Garcia 2013).

Maize-teosinte model

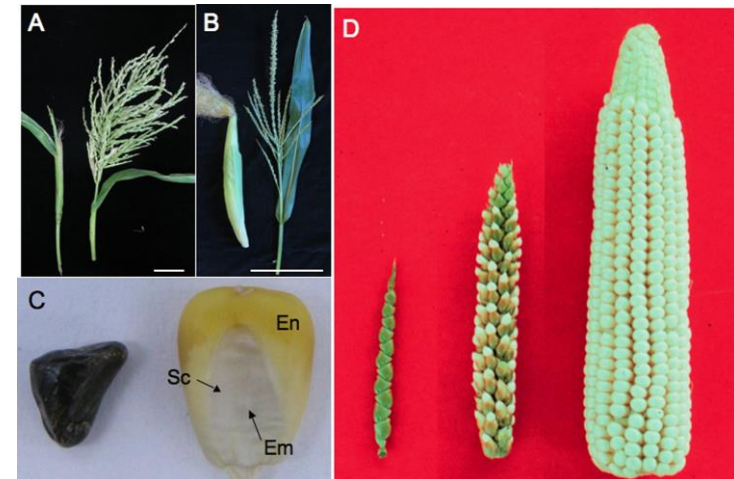
- Tillers
- Lateral branches
- Terminal inflorescence
- Ear length/diameter/number
- Kernel number/size/glume



TEOSINTE

MAIZE

Doebley et al (1990)



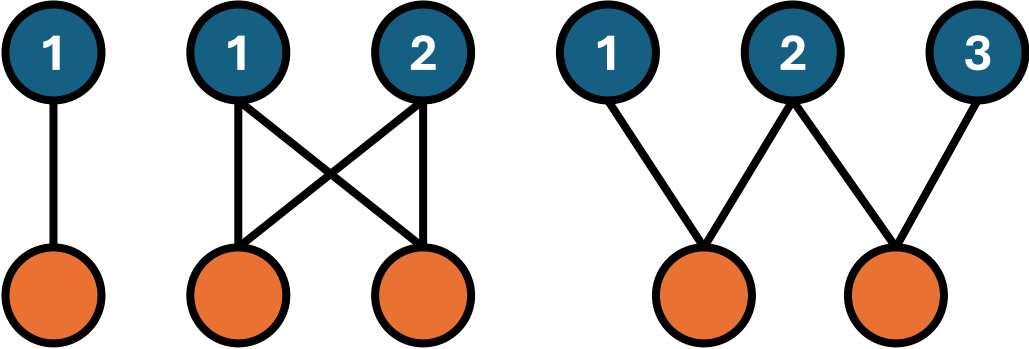
Hake and Ross-Ibarra (2015)

Study population

50 parents from Palmar Chico – Rio Balsas



Crossing schemes



Field trials

- Homestead, FL, 2013 – 2017
- 3,000 plants/year, randomized
- 18 domestication traits
- GBS: Genotype-by-Sequencing, WGS: Whole Genome Sequencing



Field trials

- Homestead, FL, 2013 – 2017
- 3,000 plants/year, randomized
- 18 domestication traits
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Variance/covariance partitioning

Fitted standard mixed linear model $y = X\beta + a + d + ay + e$

*Trait = Fixed + Additive + Dominance + Additive * Year + Residual*

$$a \sim N(0, K_A \sigma_A^2)$$

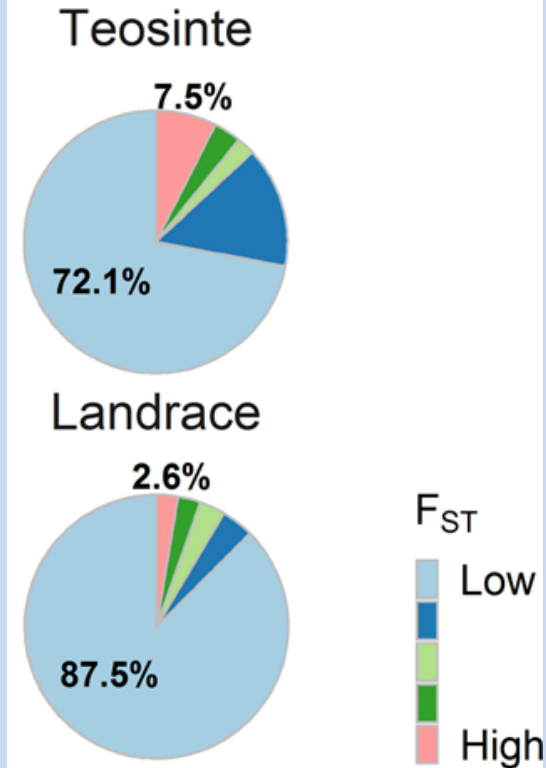
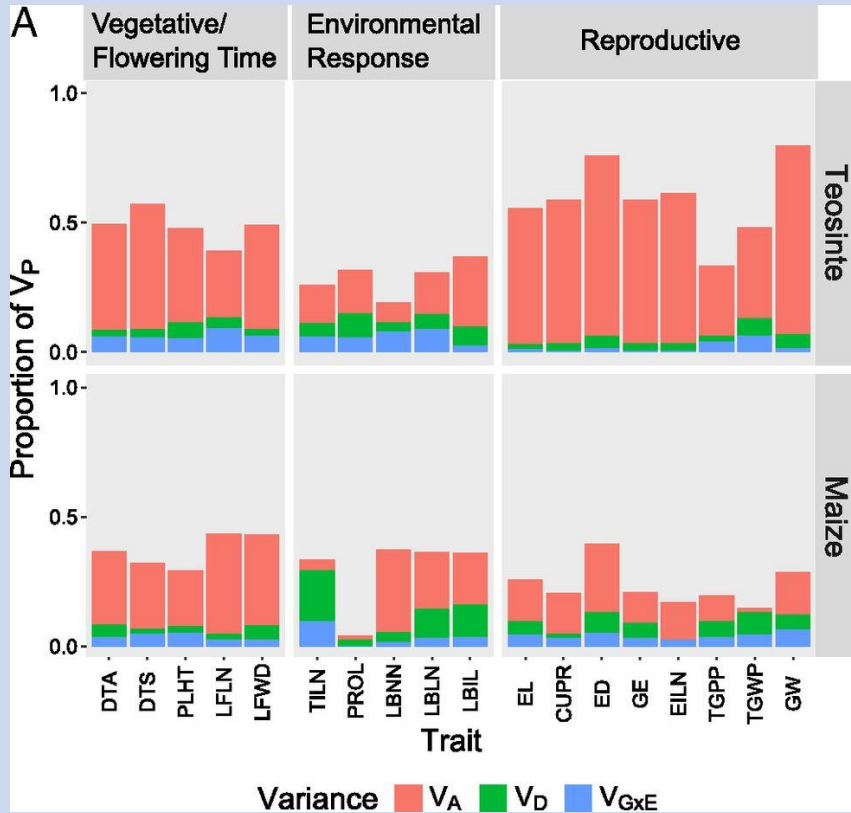
$$d \sim N(0, K_D \sigma_D^2)$$

$$ay \sim N(0, K_{AY} \sigma_{AY}^2)$$

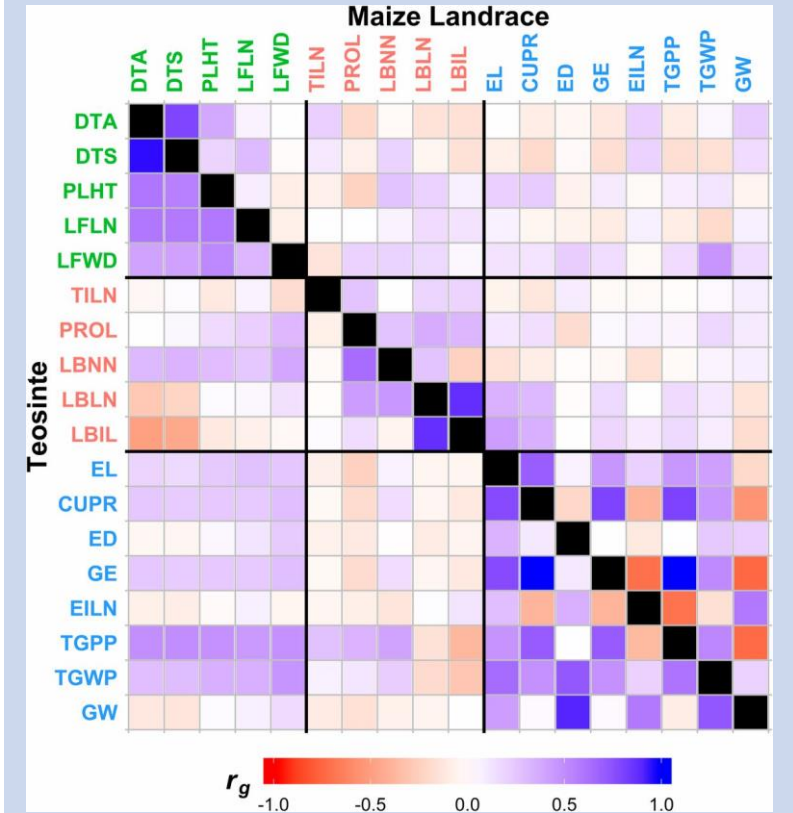
Only the additive term was fitted in the bivariate model.

QG modelling of domestication

Reduction in genetic variances (in high F_{ST} regions).



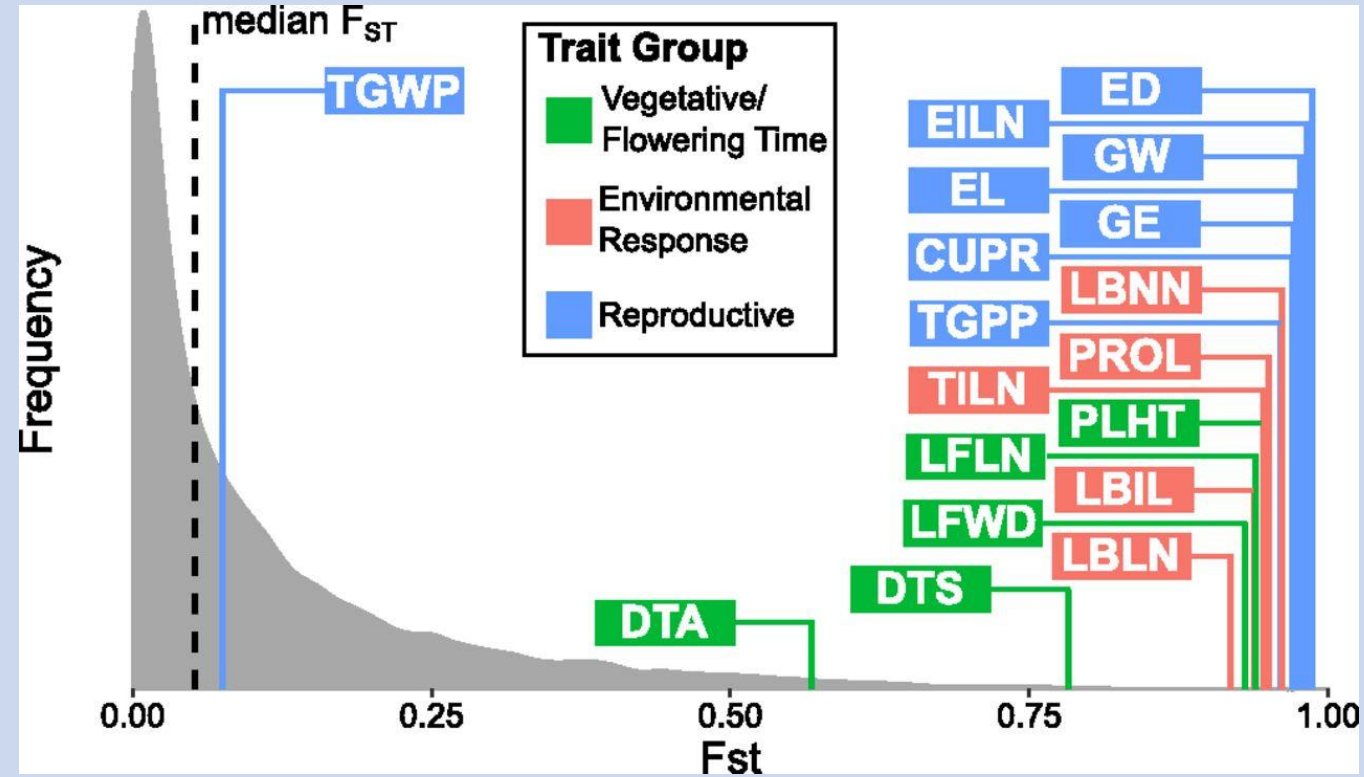
Change in genetic correlations.



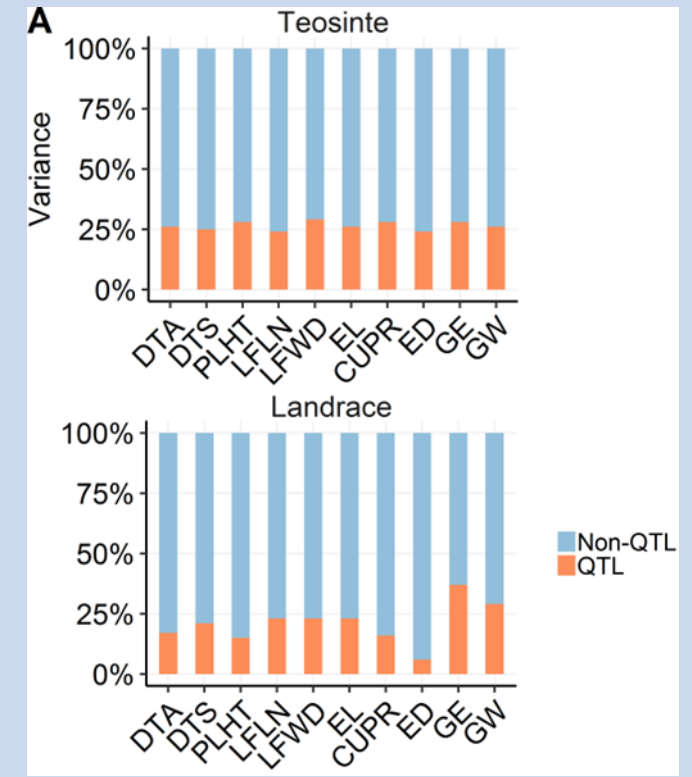
Yang et al (2019), Chen et al (2020, 2021)

QG modelling of domestication

Divergence in traits (Qst-Fst)



Importance of small effect QTLs.



Yang et al (2019), Chen et al (2020, 2021)

Research experience

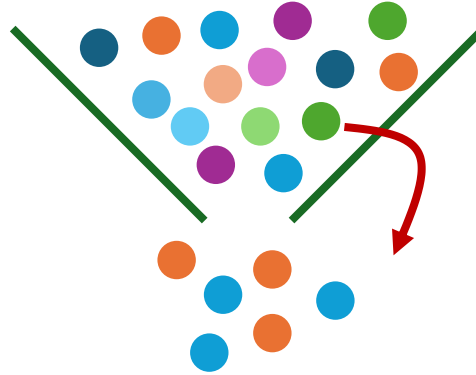
Project 1: crop domestication

Project 2: genetic diversity and pre-breeding

Shuffling genetic diversity

Domestication/Improvement

- Bottleneck
- Selection



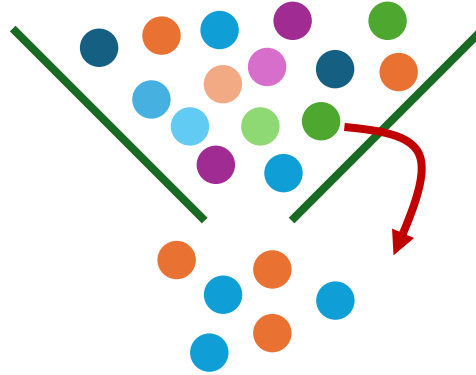
Marker assisted selection (MAS)

- Great for oligogenic traits.
- E.g. disease resistance.
- Inefficient for polygenic traits.

Shuffling genetic diversity

Domestication/Improvement

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Marker assisted selection (MAS)

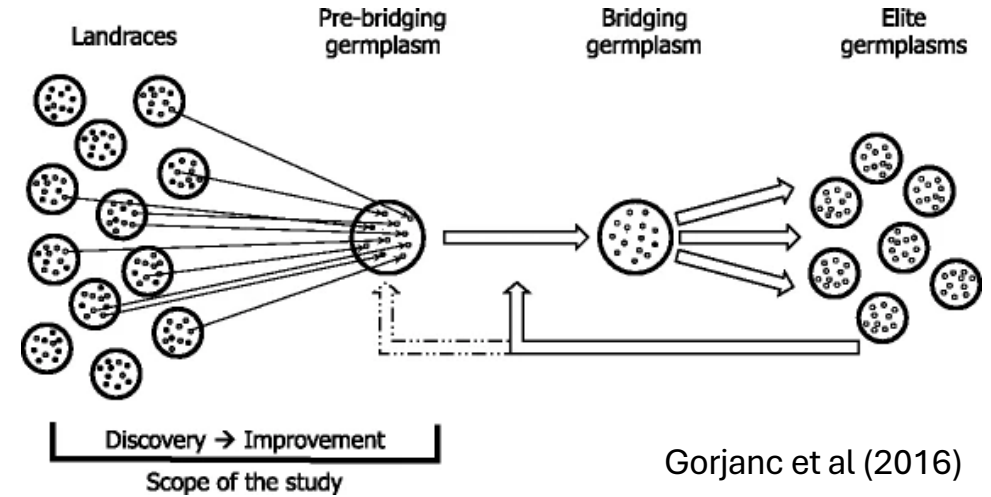
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Polygenic introgression is challenging – why?

Pre-breeding



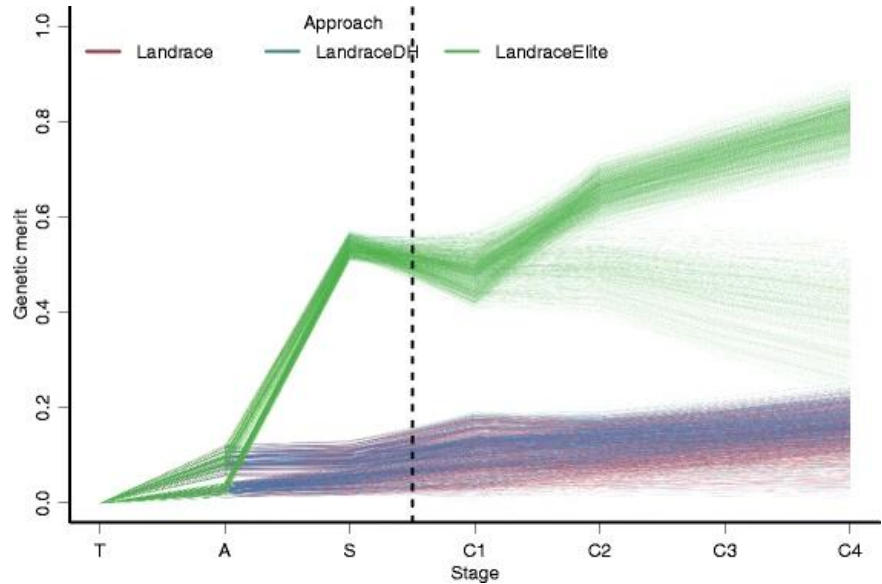
Seeds of Discovery (SeeD) studies and characterizes maize and wheat genetic diversity for use in breeding programs, which develop wheat varieties and maize hybrids improved through conventional technologies. These hybrids are better adapted to climate change, more resistant to pests and diseases and have higher yield potential.



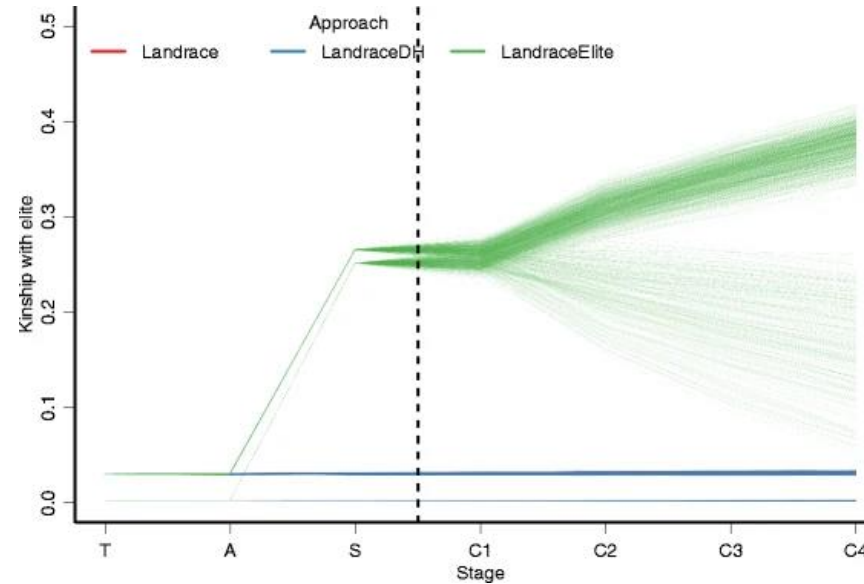
- Bridging population with elite-exotic crosses.
- Improve in elite-exotic first, then introduce into elite population.

Selection bias in pre-breeding (simulation)

Breeding value



Kinship with elite parents



Elite x Exotic

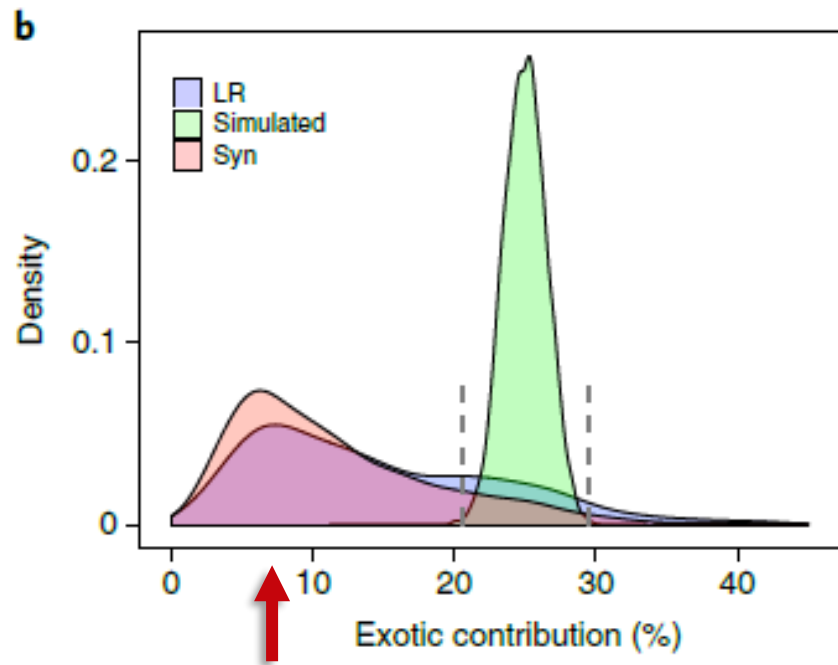
Exotic (landrace)

Gorjanc et al (2016)

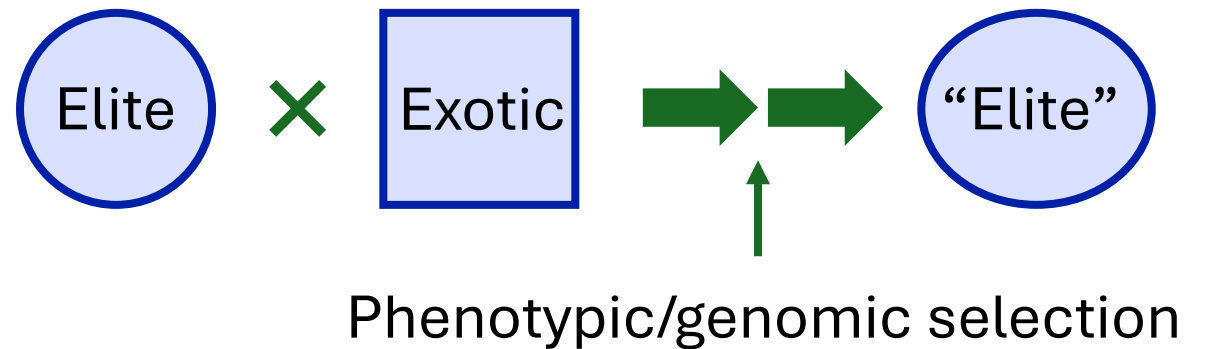
- Selection within exotic is slower than elite-exotic.
- Selection within elite-exotic reconstitutes the elite parent genome.

Selection bias in pre-breeding (observed)

- Elite 2 x (Elite 1 x Exotic)
- Distribution of exotic parent genome after applying phenotypic selection.
- Validation of simulation outcomes in experimental observation.

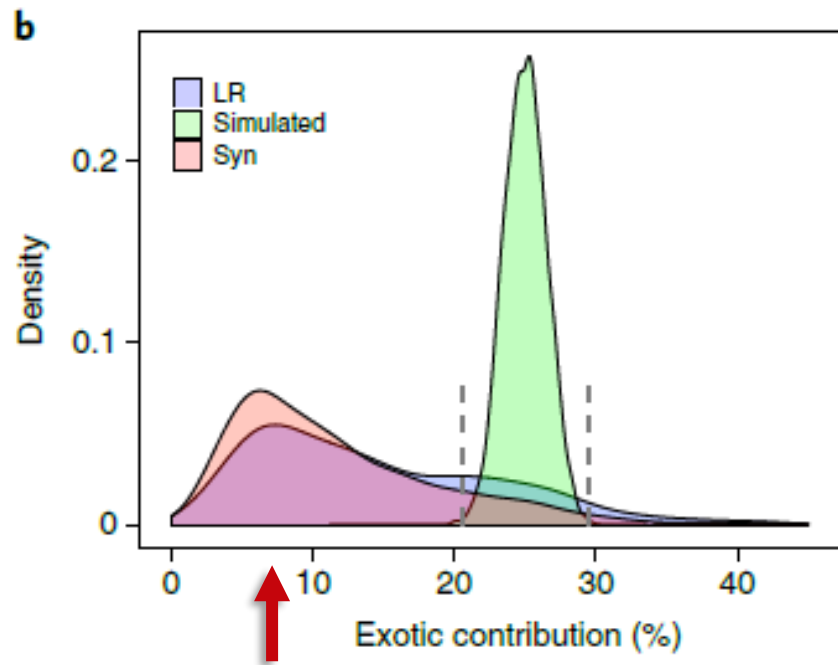


Singh et al (2021)



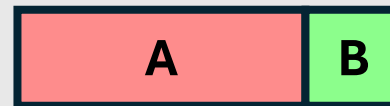
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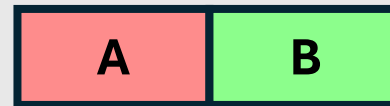


Singh et al (2021)

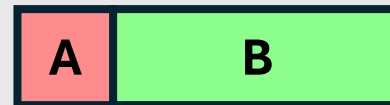
Example: Favorable allele in elite(A):exotic(B) = 6:4



$$BV = 0.75 * 0.6 + 0.25 * 0.4 = 0.55$$



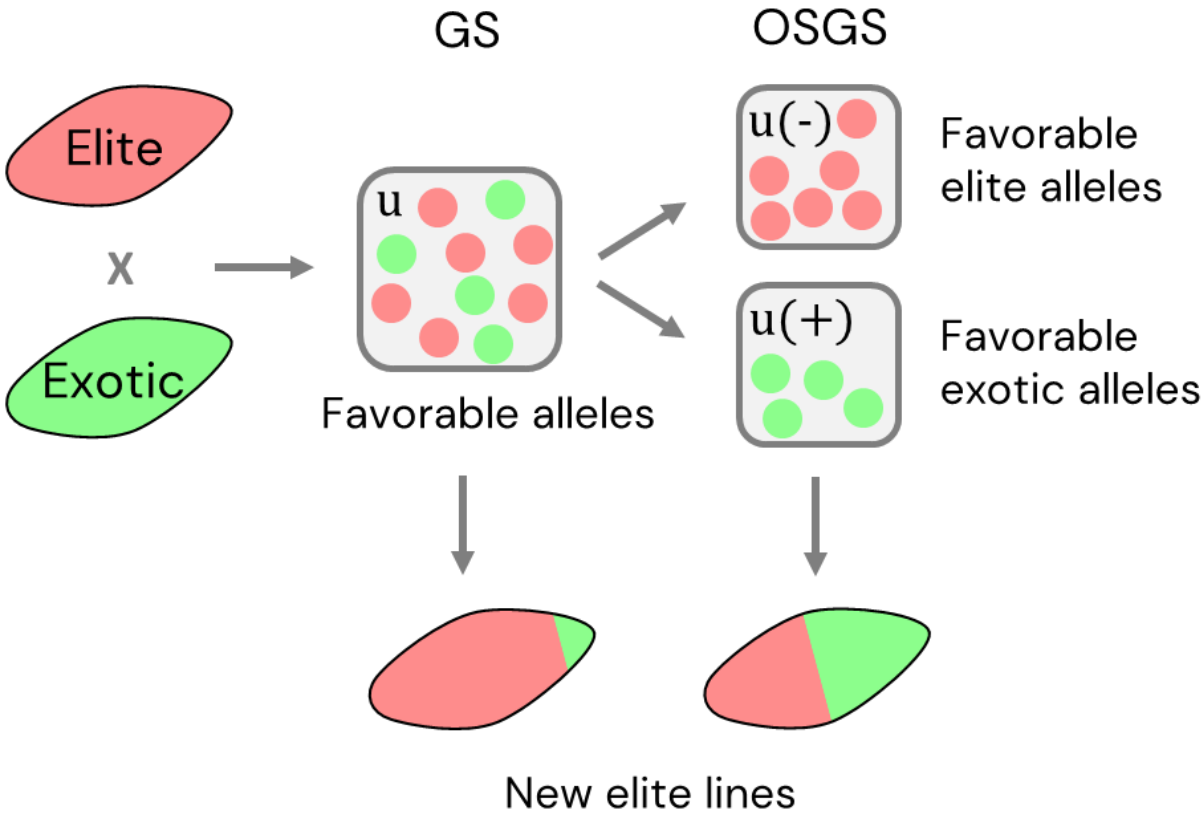
$$BV = 0.50 * 0.6 + 0.50 * 0.4 = 0.50$$



$$BV = 0.25 * 0.6 + 0.75 * 0.4 = 0.45$$

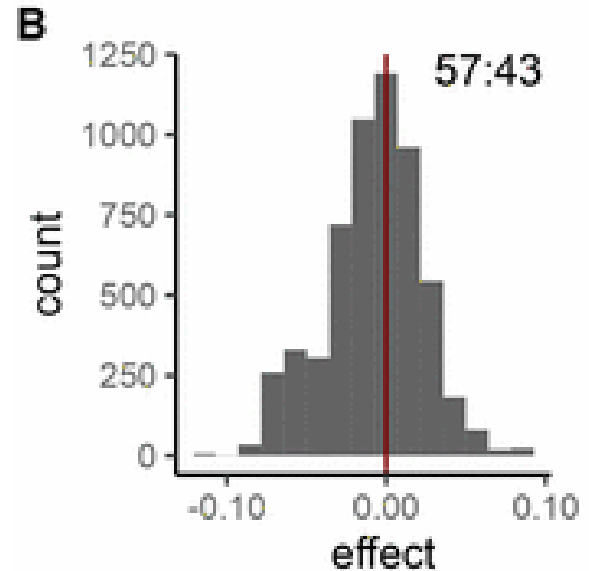
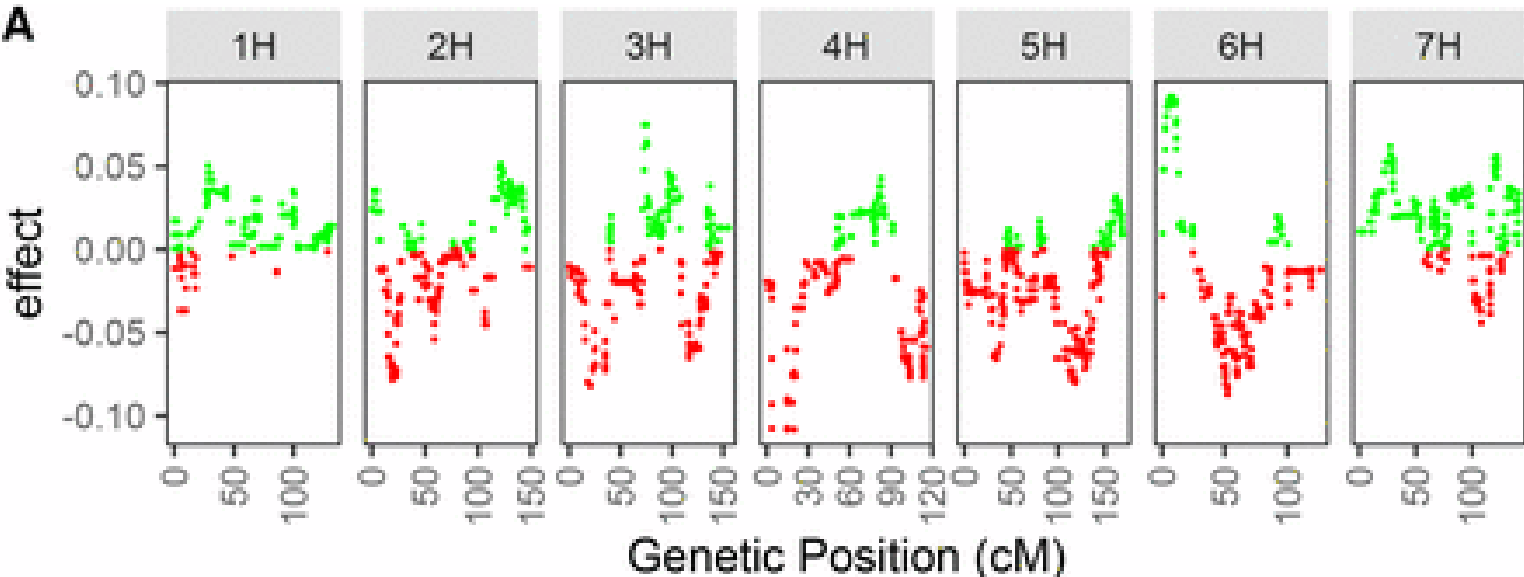
Origin specific genomic selection (OSGS)

OSGS: isolate and select on favorable parental contribution.



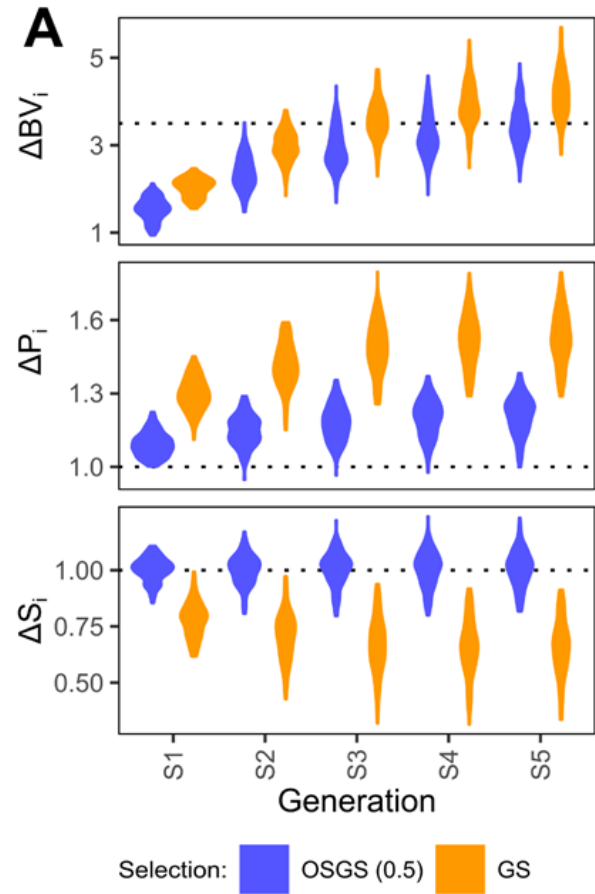
OSGS in barley NAM (yield)

Partitioning favorable parental contributions.



Yang et al (2020)

OSGS in simulated data



Yang et al (2020)

- OSGS vs GS in F2.
- Weighted selection in OSGS.
- Comparable breeding values.
- OSGS maintains elite-exotic balance.

Research vision

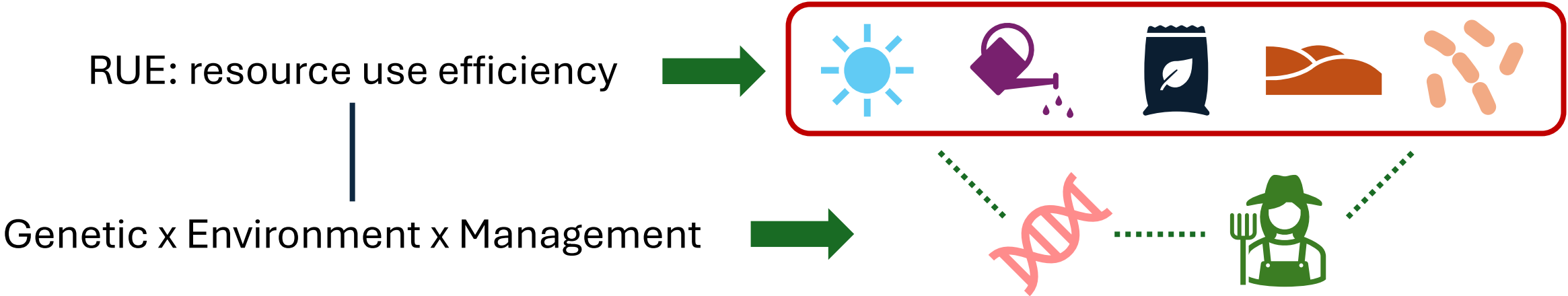
- Quantitative genetics
- Genetic x Environment x Management (GEM) interaction
- Resource Use Efficiency (RUE).

Research vision

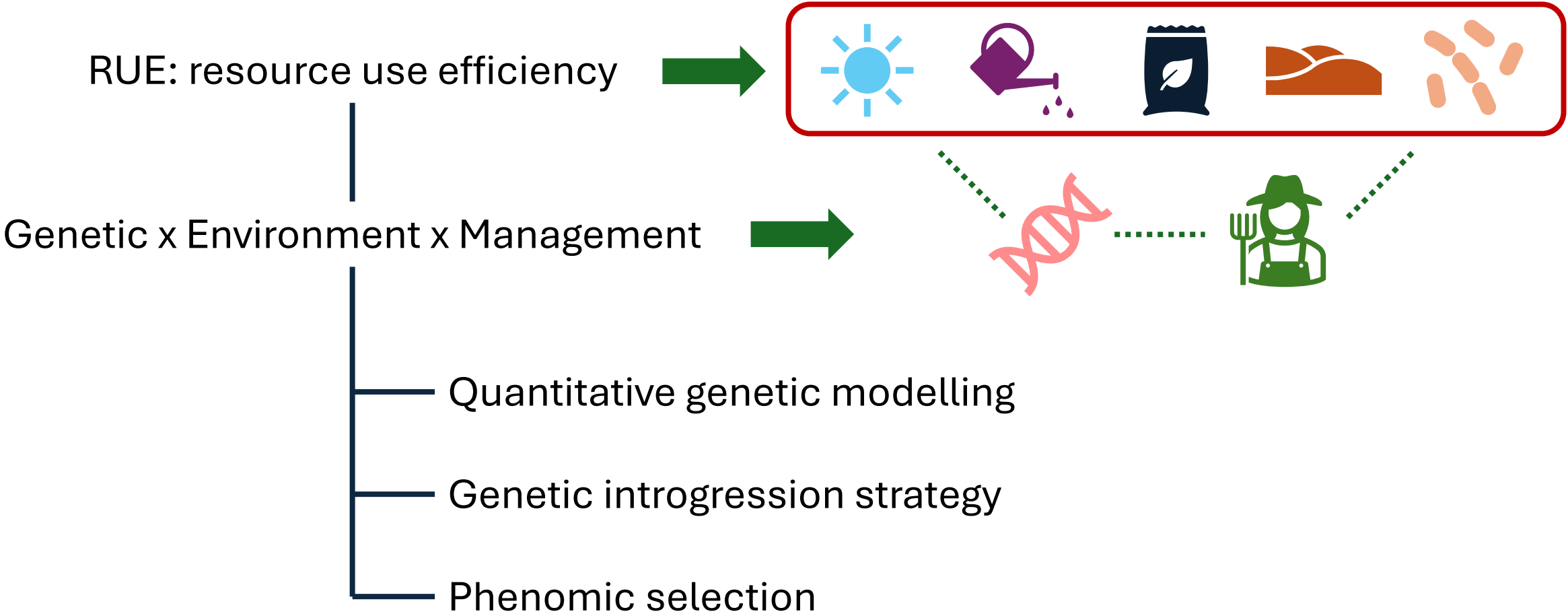
RUE: resource use efficiency



Research vision



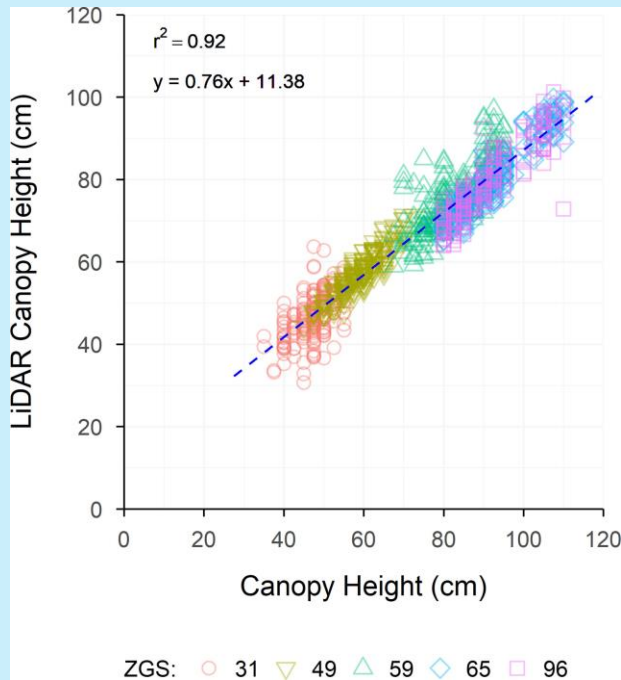
Research vision and plans



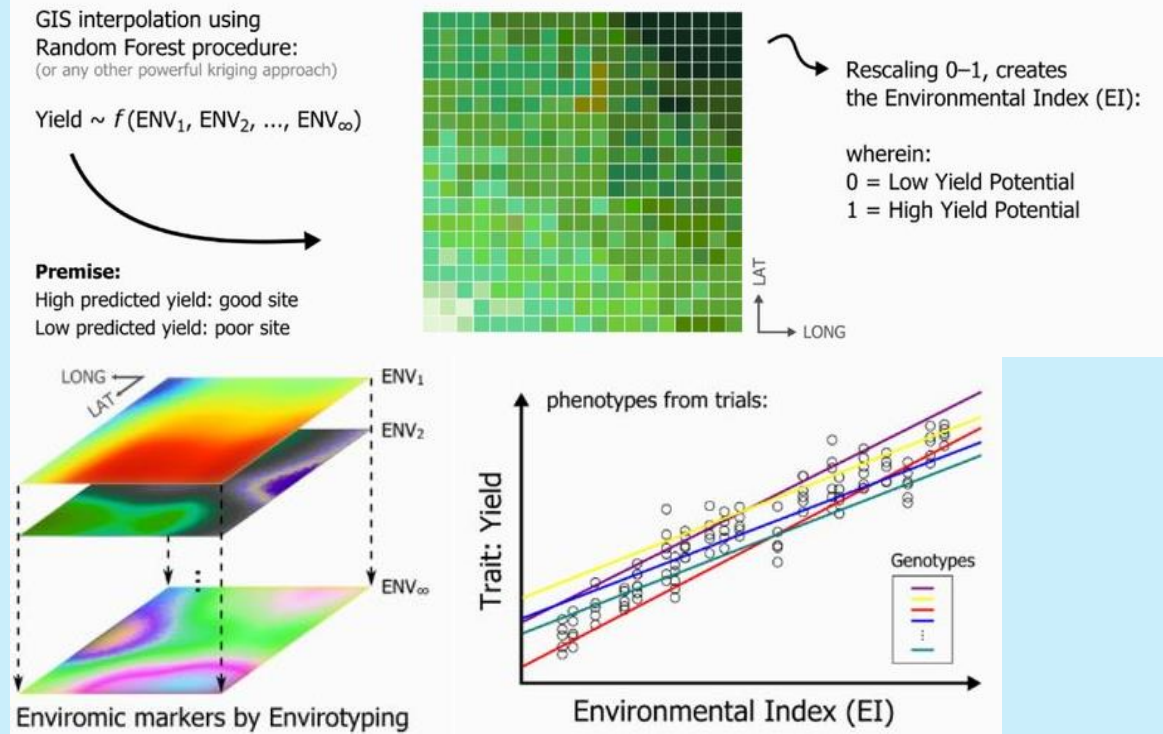
Clarification on phenomic selection

Phenome is not new – it is normally used as a proxy trait or an environmental measure.

$$\text{Trait} \sim \text{Genetic} + \text{Environment} + \text{Residual}$$



Walter et al (2019)



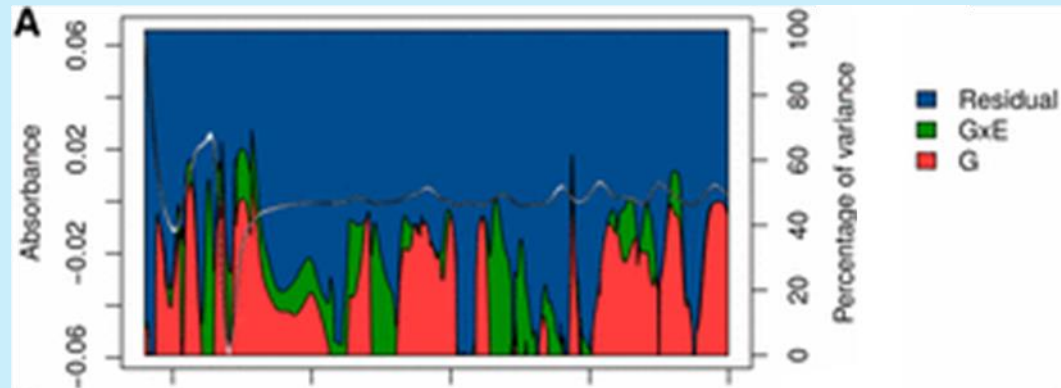
Resende et al (2020)

Clarification on phenomic selection

We are interested in using phenome to instead capture the genetic relationship.

$$\textit{Trait} \sim \textit{Genetic} + \textit{Environment} + \textit{Residual}$$

Model genetic relationship with spectral data



Rincent et al (2017)

Short term plans

Improving genetic introgression strategy

- Multi-parents
- Multi-traits
- Population types
- Species
- Models

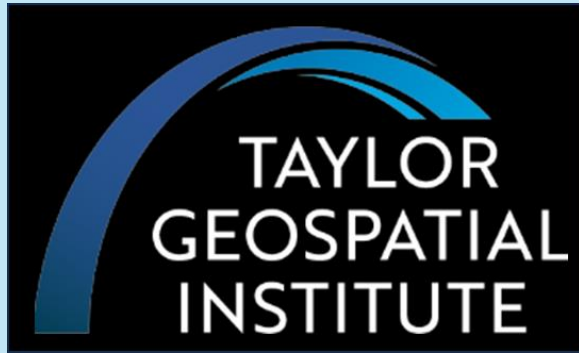
Simulation and build on previous work

Optimizing phenomic selection method

- Phenomic data types
- Developmental stages
- Traits
- Population types
- Species
- Models

Submit proposals for grant funding

Research with TGI & SLU Biology



Infrastructure
Geospatial data
Expertise



E.g. hyperspectral, satellite, LiDAR

SLU Biology

Collaboration



- Genetic-environment interaction
- Perennial genetics
- Soil microbiome
- Photosynthesis
- Epigenetics



Our research group >>> New knowledge & applications in plant breeding and genetics

Summary

- Plant breeding, complex traits and genetic gain.
- Research experience.
 - QG-perspective on maize domestication.
 - Genetic introgression in pre-breeding.
- Interest in QG, RUE and GEM.



- Breeding efficiency
- Sustainability
- Climate resilience

Acknowledgement

Many thanks for the opportunity to present today!

Wisconsin + Others

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M Cinta Romay
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Rodney Edmondson
Hans-Peter Piepho
Joanne Russell
Luke Ramsay
Bill Thomas
Funmi Ladejobi
Richard Mott



<https://cjyang-work.github.io/>



XXX



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