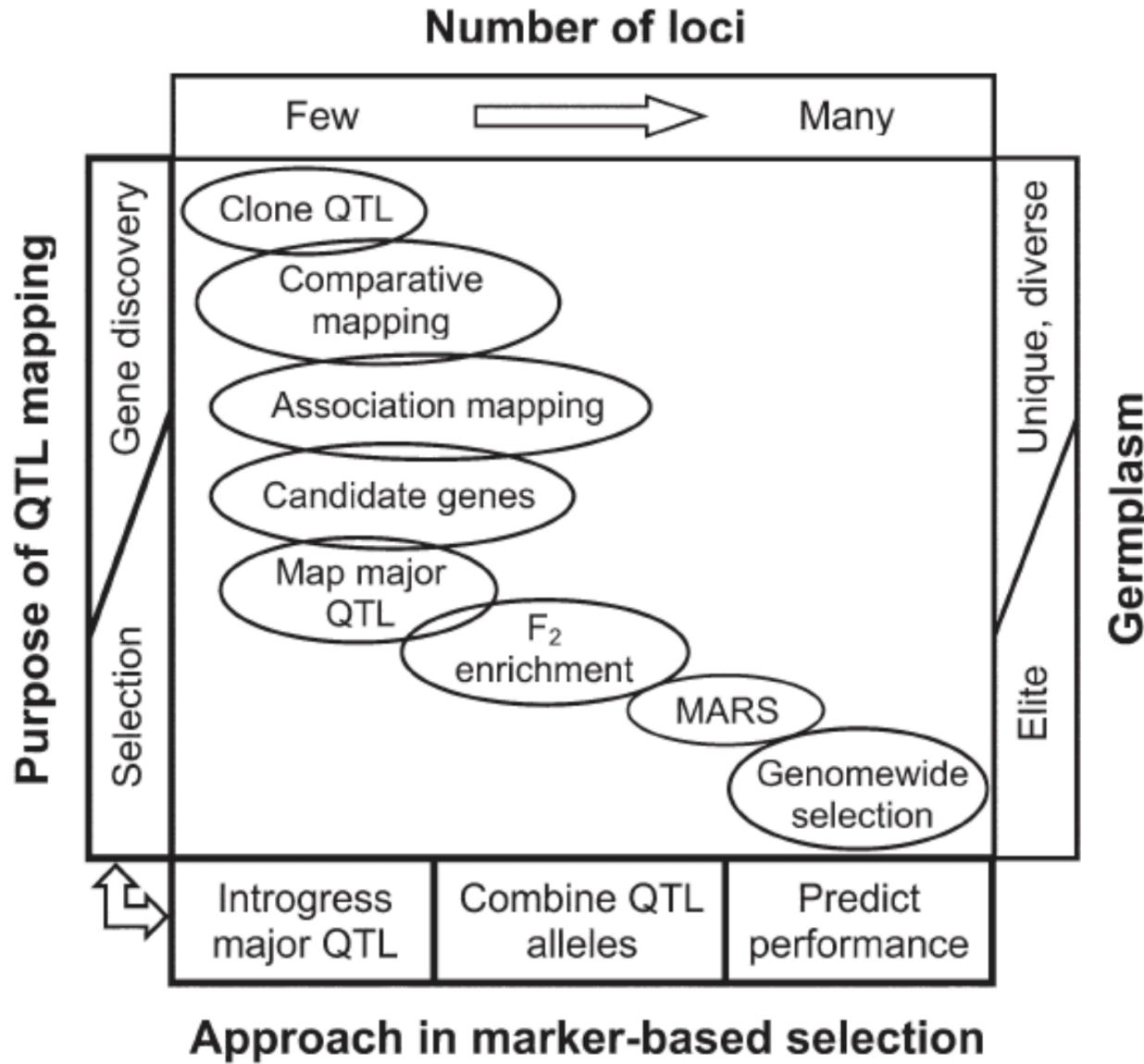
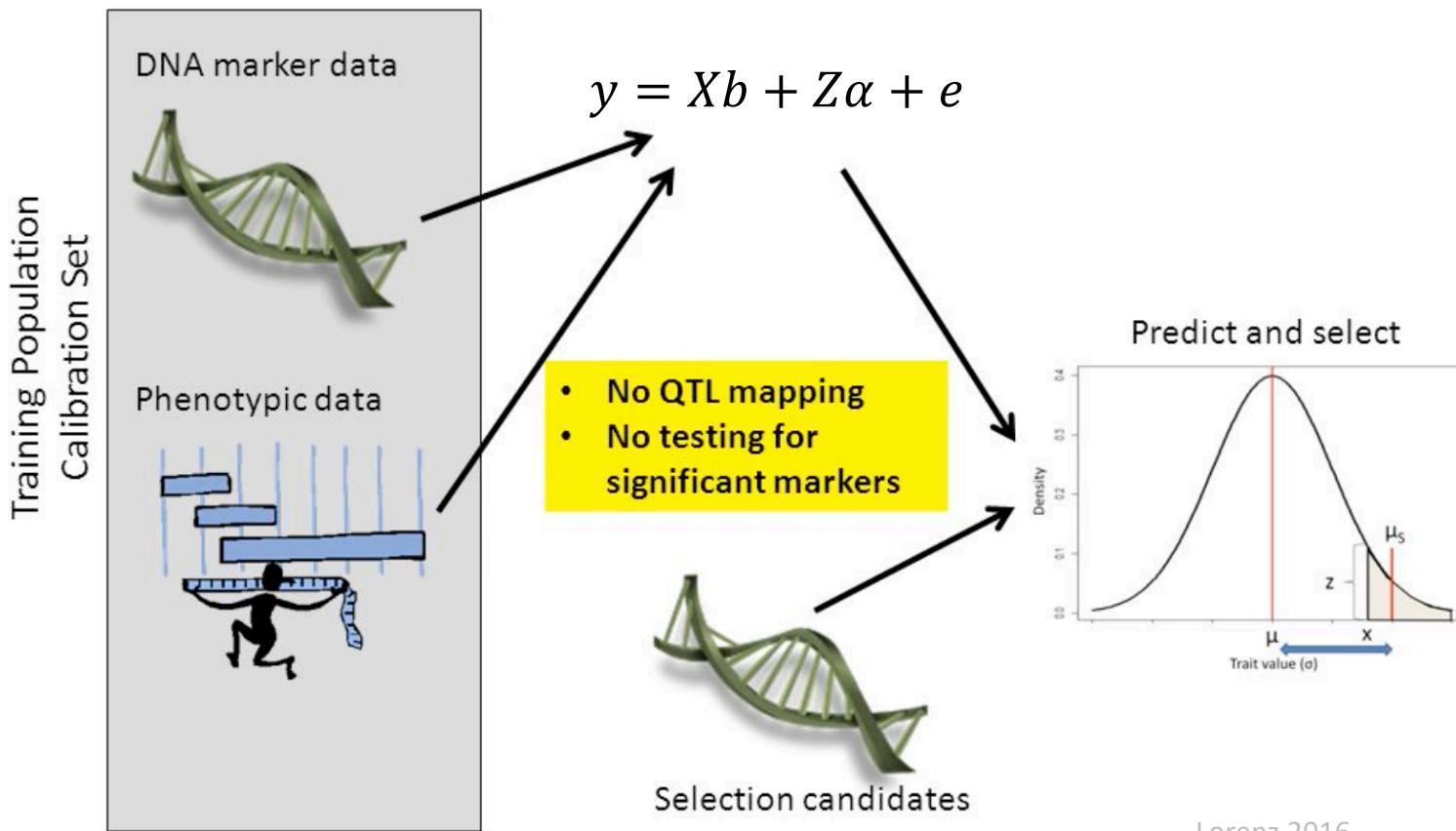


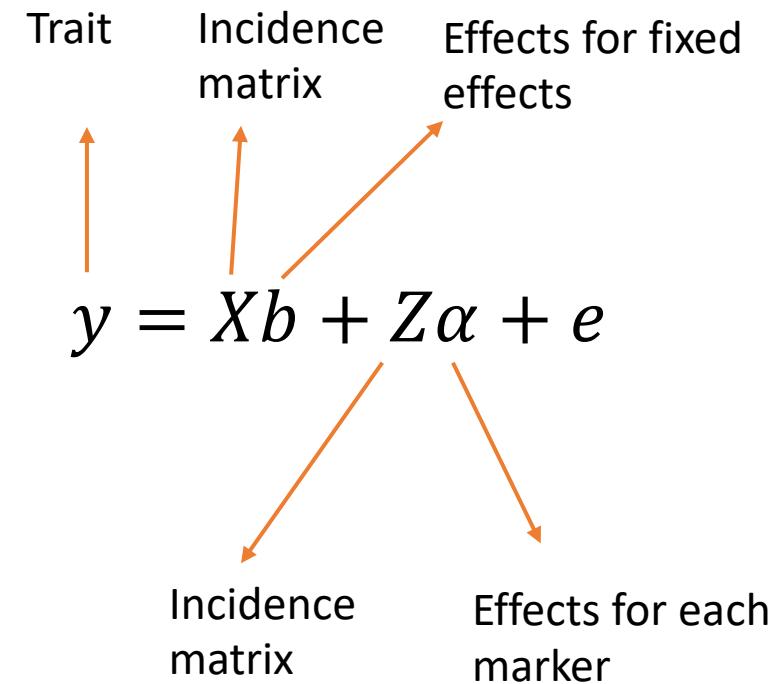
Gomomic selection
or
Genomewide selection



Genomic selection



Lorenz 2016

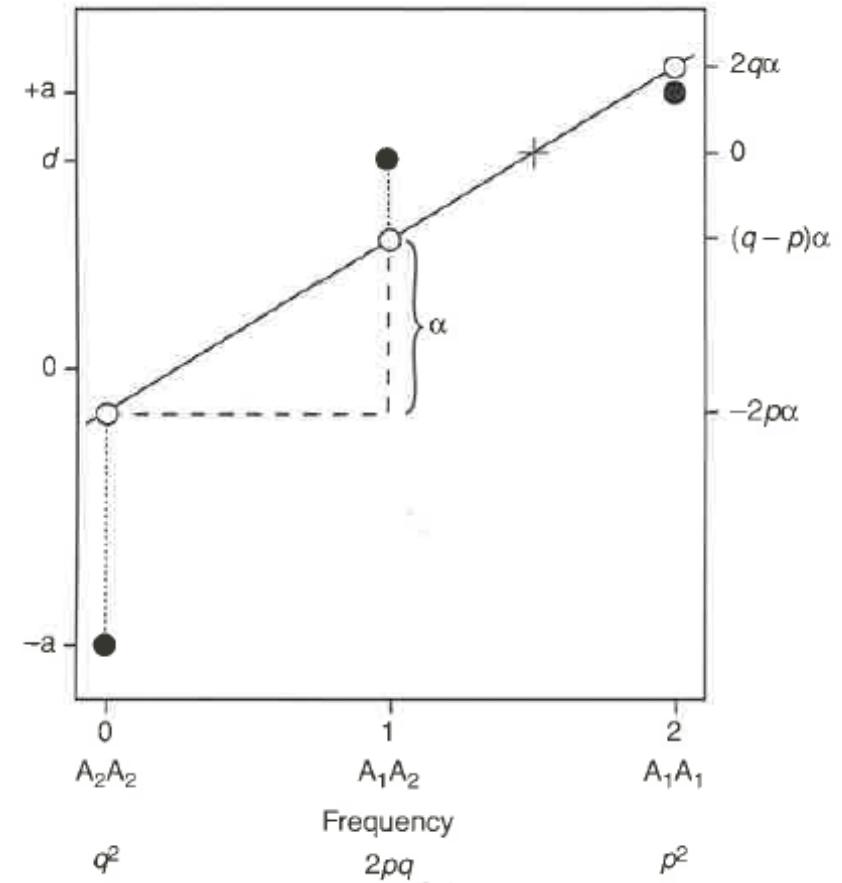


Genomic selection

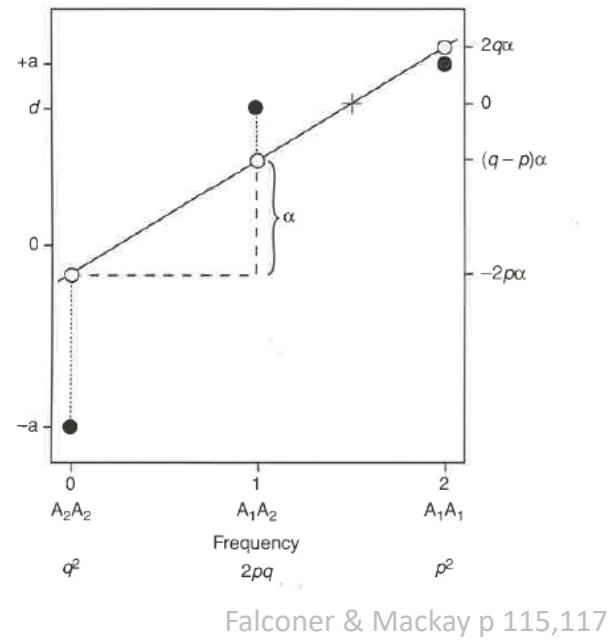
- GS uses all molecular markers to predict genomic estimated breeding values (**GEBV**).

Genotype	Breeding value
A ₁ A ₁	2α ₁ = 2qα
A ₁ A ₂	α ₁ + α ₂ = (q - p)α
A ₂ A ₂	2α ₂ = -2pα

$$GEBV = \sum_i^p Z_i \alpha_i$$



Genomic selection



Average effects of the alleles:

$$\alpha_1 = q[a + d(q - p)] \quad \alpha_2 = -p[a + d(q - p)]$$

Average effects of gene substitution:

$$\alpha = \alpha_1 - \alpha_2 = a + d(q - p)$$

$$GEBV = \sum_i^p Z_i \alpha_i$$

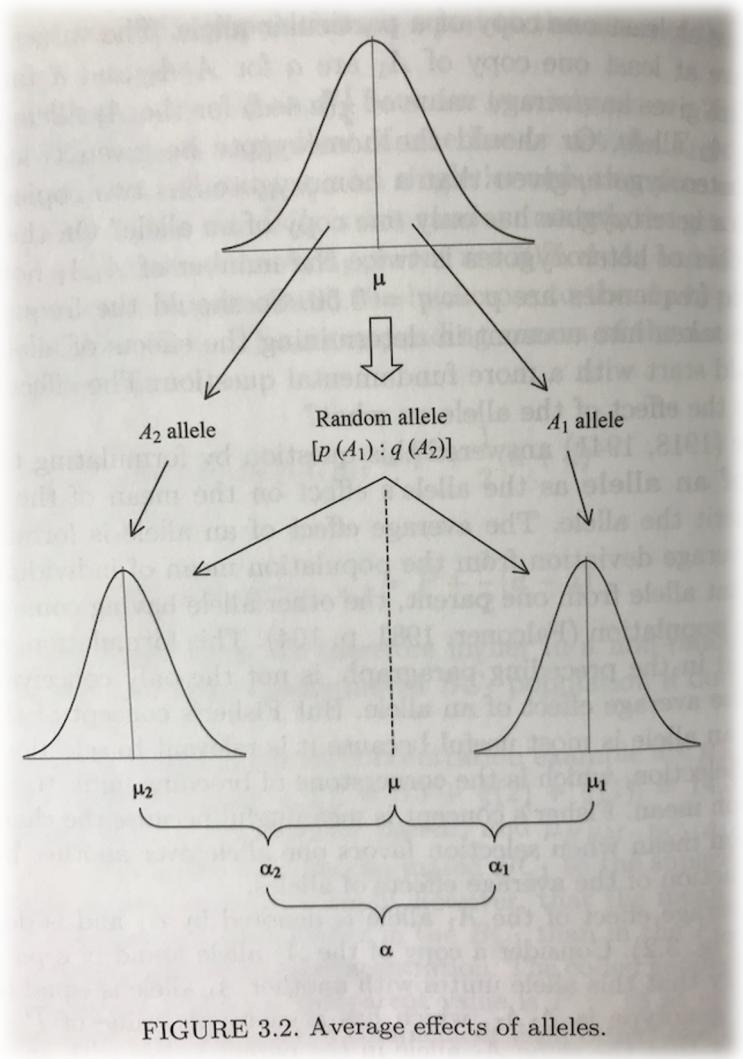
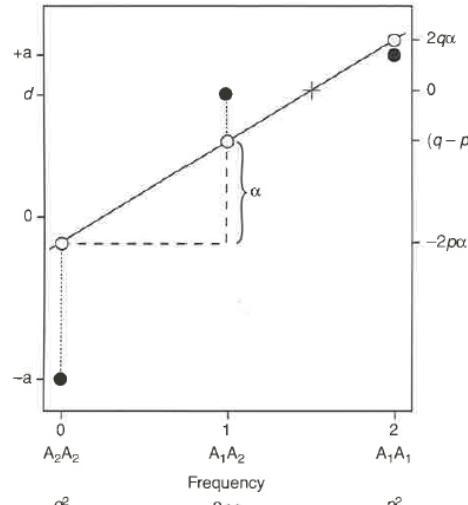


FIGURE 3.2. Average effects of alleles.

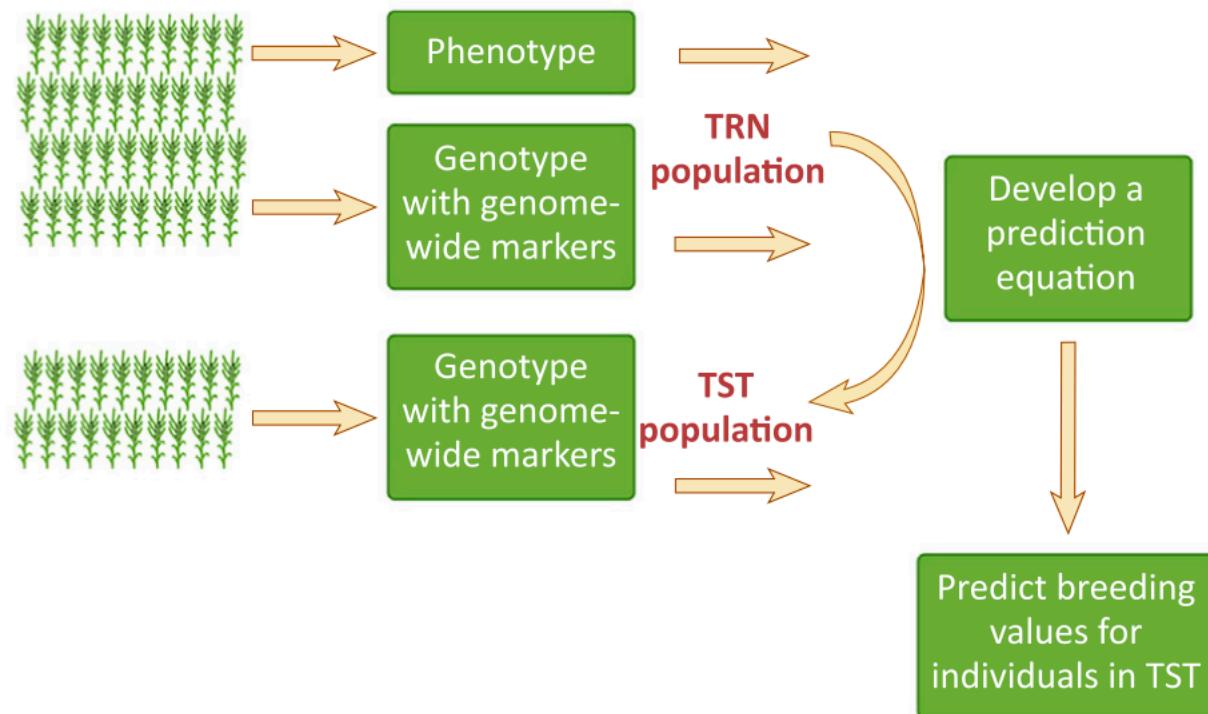
Bernardo 2020

Genomic selection

- GS uses all molecular markers to predict genomic estimated breeding values (**GEBV**).
- GS combines molecular and phenotypic data in a training population to obtain the GEBV of individuals in a testing population that have been genotyped but not phenotyped.



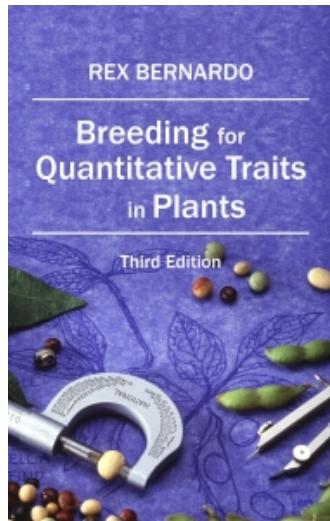
$$GEBV = \sum_i^p Z_i \alpha_i$$



Genomic selection

- Are interested in go deeper in GS basic model?

$$GEBV = \sum_i^p Z_i \alpha_i$$



University of Minnesota



<https://www.youtube.com/watch?v=O7KYISOZhZo&t=1939s>

MAS vs GS

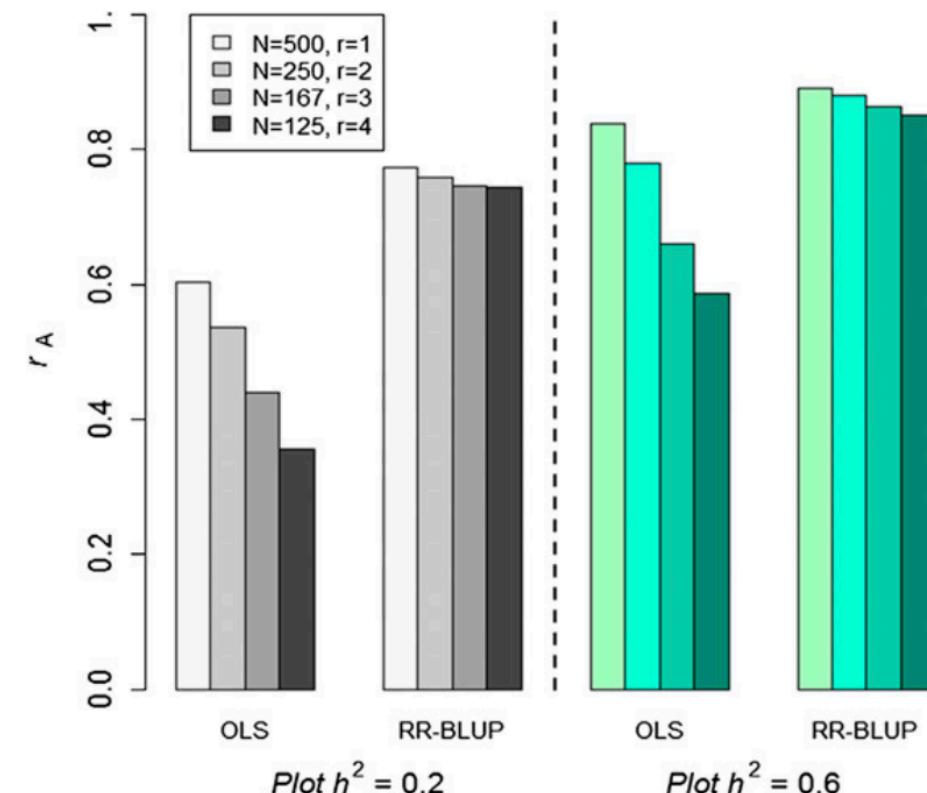
A multiple regression model in which marker effects were estimated with ordinary least squares (OLS)

Ridge regression best linear unbiased prediction (RR-BLUP)

markers > population size

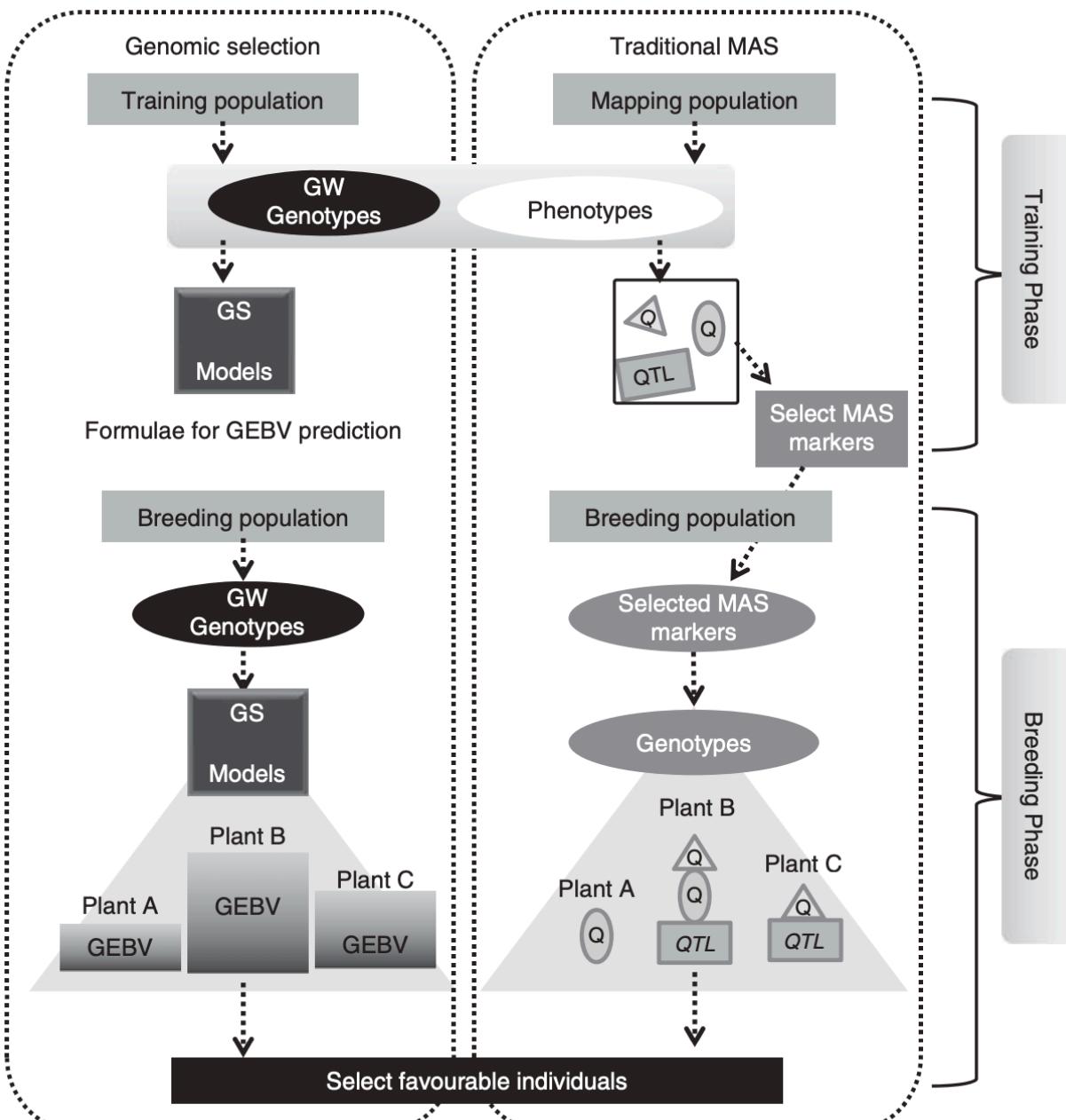
h^2 and number of molecular markers to set the phenotypic variance that can be explained in the model

1. MAS VS GS
2. Population size
3. h^2



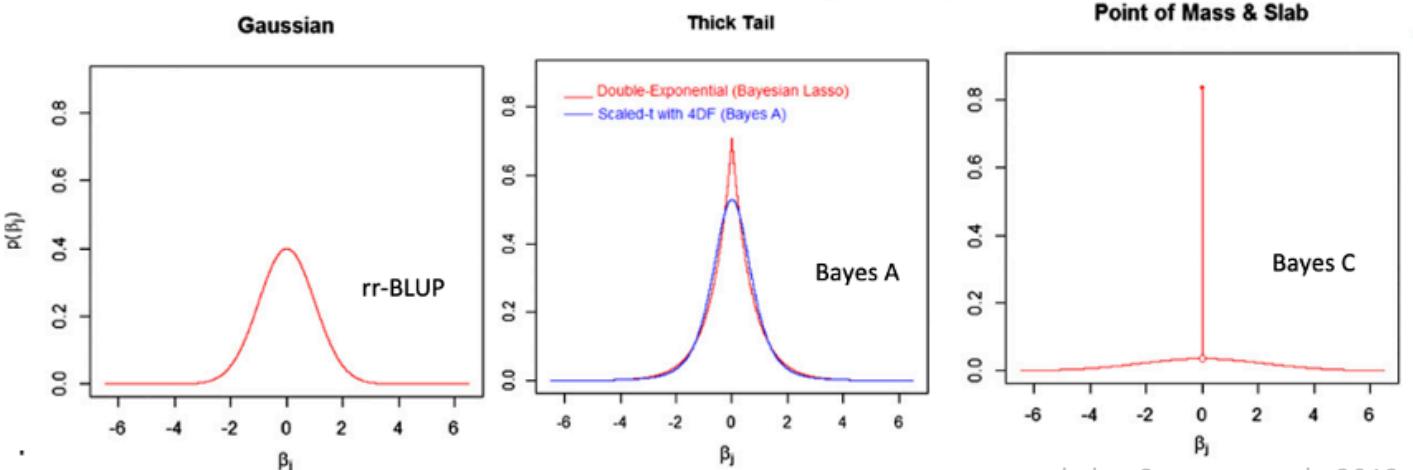
MAS vs GS

Schemes of GS and traditional MAS for the selection of quantitative traits (right).



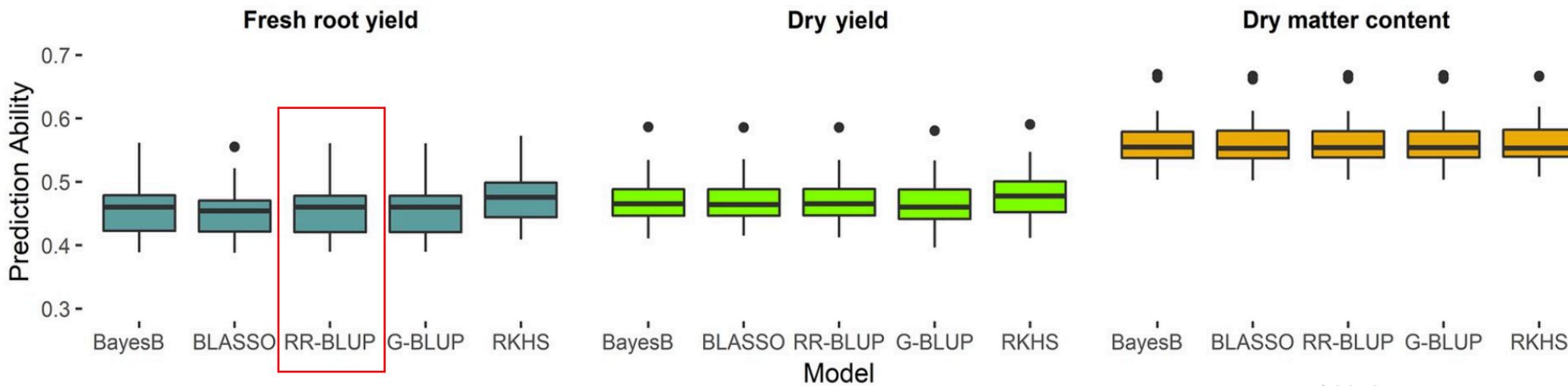
GS Models

In general, genomic selection tend to have similar predictive ability.

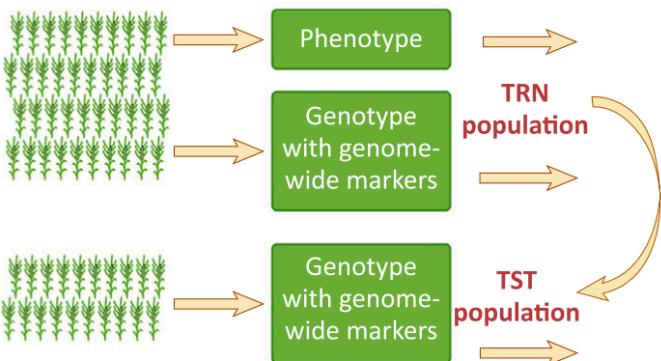


BayesC : Small number QTL
 BayesA: Moderate number of QTL
 RR-BLUP: Extreme number of QTL

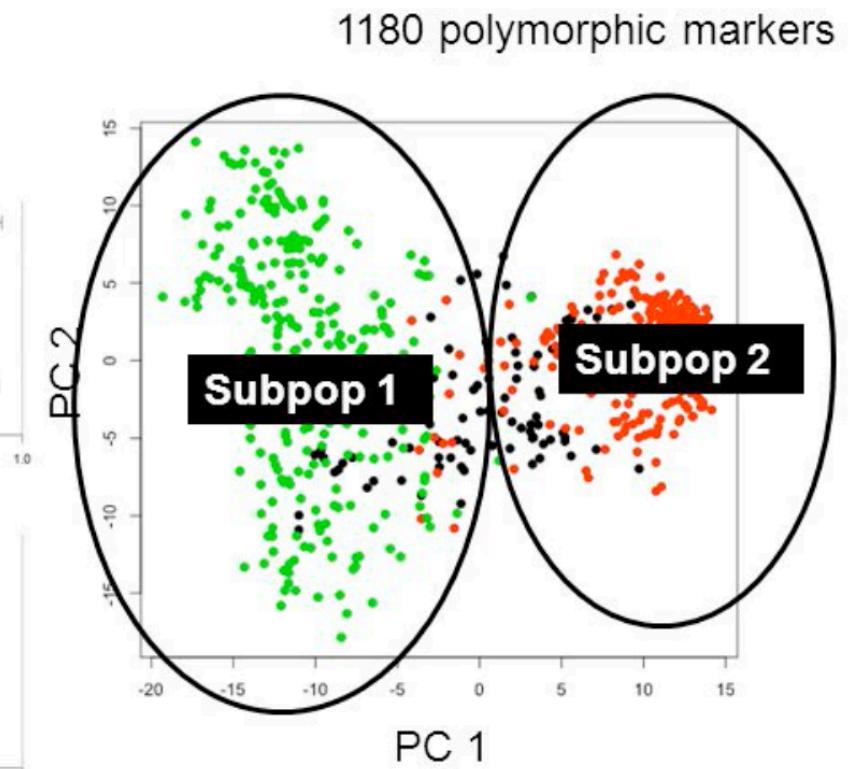
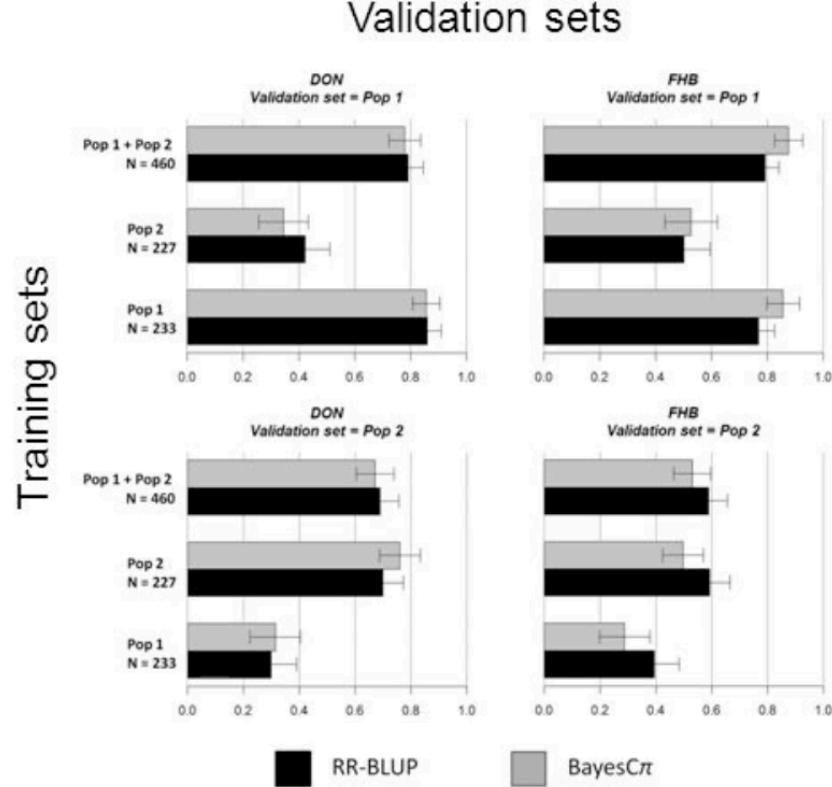
Wang et al., 2015



Population structure

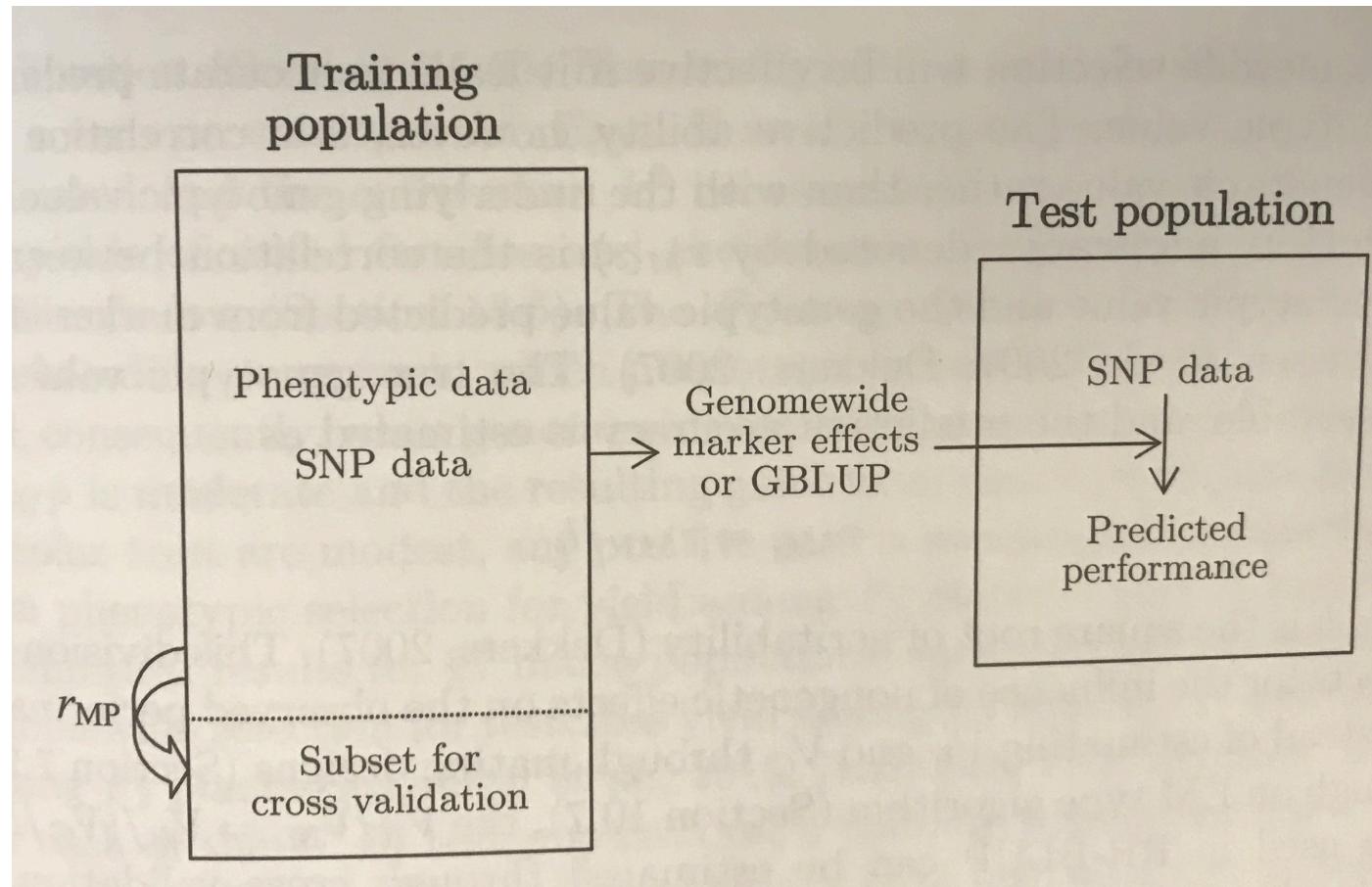


Crossa et al 2017

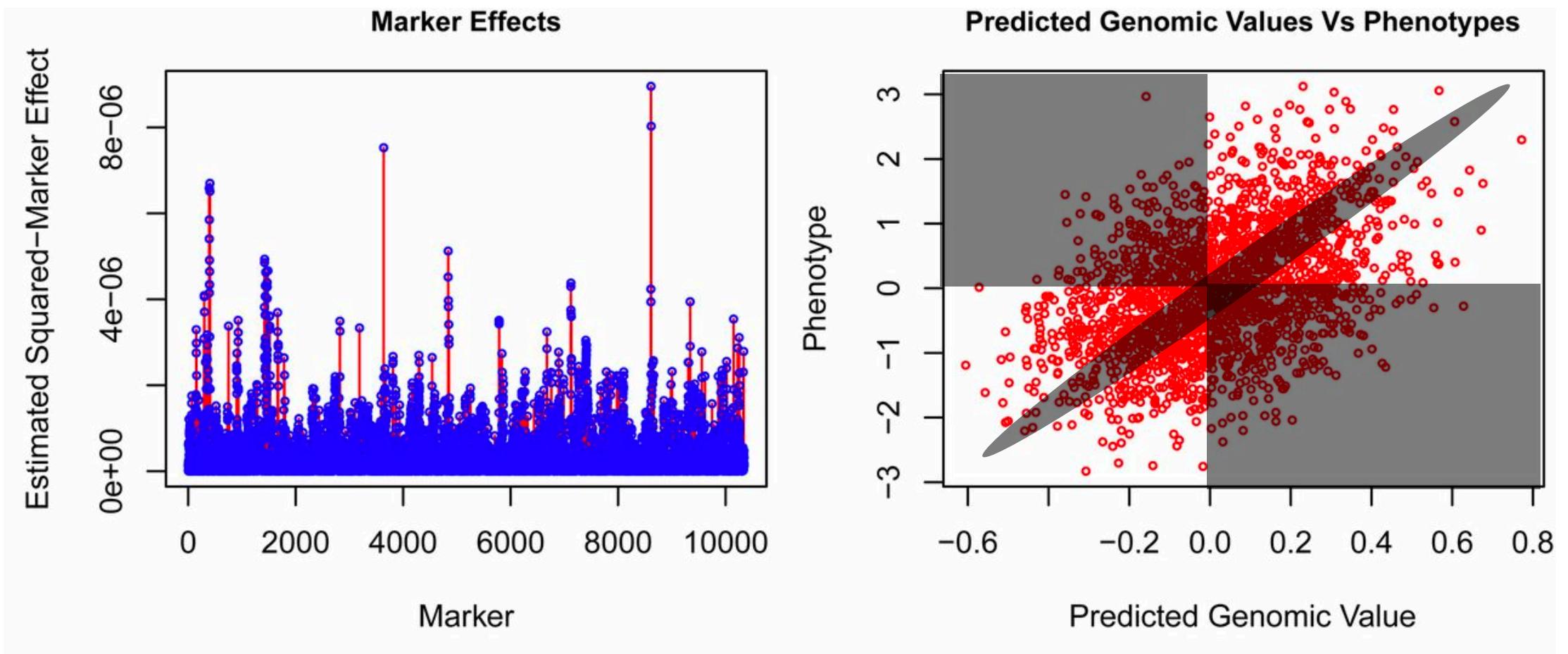


Lorenz 2016

Framework for GS

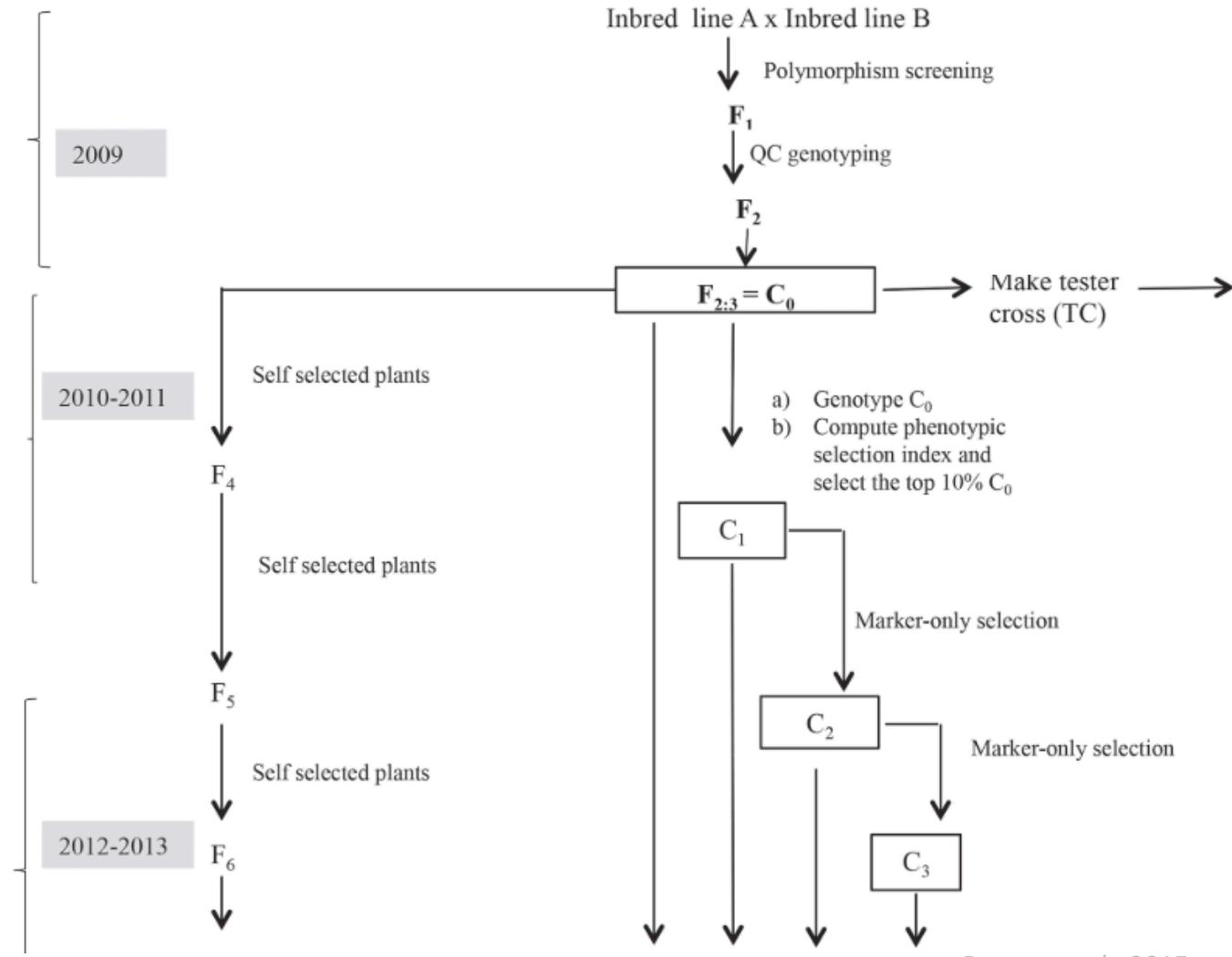


Framework for GS



GS vs traditional breeding

Entries	Across eight populations			Five WEMA populations [†]		
	GY Mg ha ⁻¹	AD days	PH cm	GY Mg ha ⁻¹	AD days	PH cm
C ₀	2.286	63.910	179.900	2.212	64.060	174.300
C ₁	2.420	64.080	181.900	2.482	64.160	178.100
C ₂	2.438	64.410	184.600	2.474	64.160	179.400
C ₃	2.593	64.100	182.200	2.581	63.730	175.600
Pedigree	2.417	64.400	181.700	2.417	64.400	181.700
F ₁	2.394	63.930	175.600	2.394	63.930	175.600
Parents	2.361	64.000	178.400	2.431	63.950	176.600



Beyene et al., 2015

GS is not the solution of all our problems

...but it is helpful

- Reduce breeding cycle
- Increase selection intensity
- Increase genetic variance
- Reduce costs

$$\Delta G_{\text{year}} = \frac{i r_{\text{AI}} \sigma_A}{L}$$

i = Selection intensity

r_{AI} = Accuracy

σ_A = Genetic standard deviation

L = Generation interval

In the next presentation we are going to talk about it!