Pre-breeding strategies for obtaining new resilient and added value berries

Workshop

Advancing Berry Breeding: From Phenotyping to Genomic Innovation

The benefits of GS in a cultivated strawberry breeding programme: an example of powdery mildew resistance

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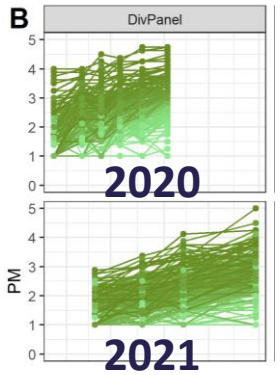
Powdery mildew (PM) in Strawberry

- Pathogen agent: *Podosphaera aphanis*
- Major threat for strawberry production in France and the world
- Affects all aerial parts
  Vegetative parts = diminution of photosynthesis and yield
  Fruits = non commerciable yield
- **Resistant varieties** = practical and efficient control strategy

Powdery mildew symptoms

2 years of phenotyping



Scale
0 (resistant) **to**
5 (highly susceptible)

Diversity panel

223 genotypes

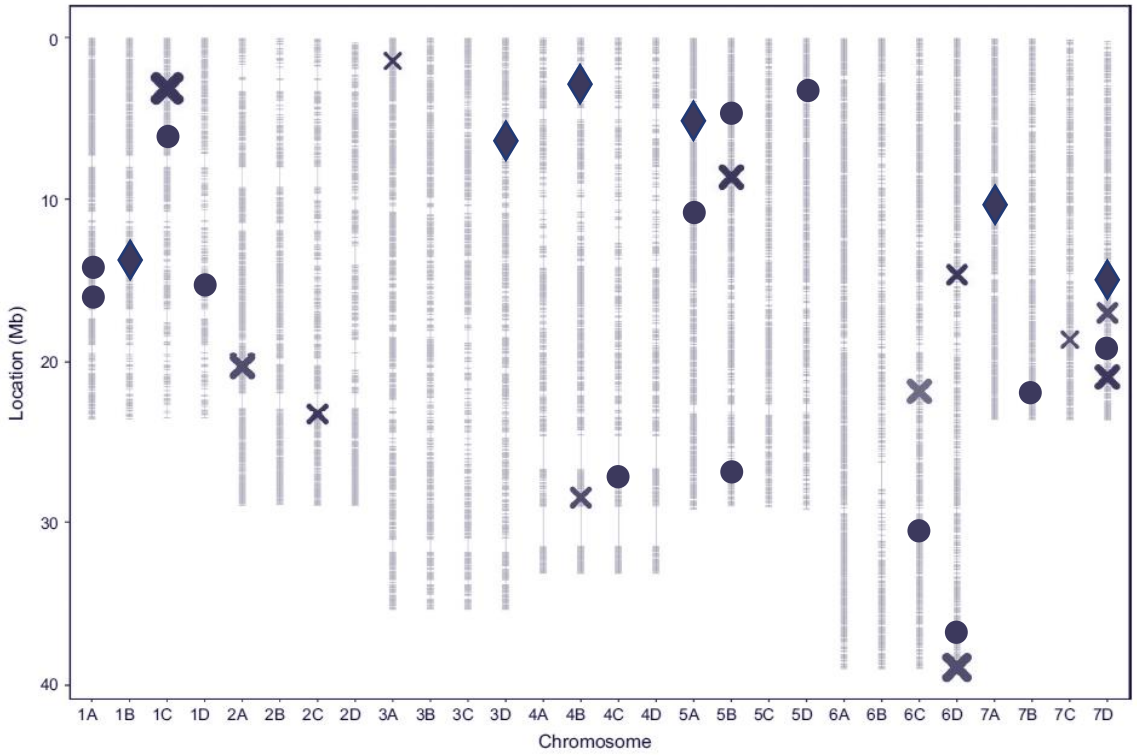
GWAS on AUDPC

Prohaska, Rey-Serra, Bénéjam et al., *in prep*

QTLs/SNPs linked to PM resistances in Strawberry

Genetic map of some QTLs/SNPs-associated to PM (approximative positions)

- × Cockerton et al., 2018
- ♦ Lynn et al., 2024
- O Prohaska, Rey-Serra, Bénéjam et al., *in prep*



PM resistances are :

- Highly polygenic
- Unstable between environments
- Mainly additive

Breeding strategies adapted to powdery mildew

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Screening based on phenotypes

Advantages	Limits
Conventionally used Easy to use	Time-consuming Subjective Depends on the trial

Breeding strategies adapted to powdery mildew

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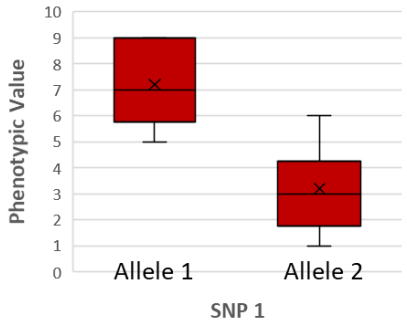
Marker-assisted selection



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Objective (based on genetic information) Efficient for additivity	Polygenic traits

Breeding strategies adapted to powdery mildew

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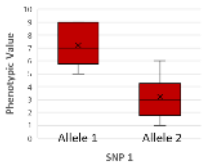
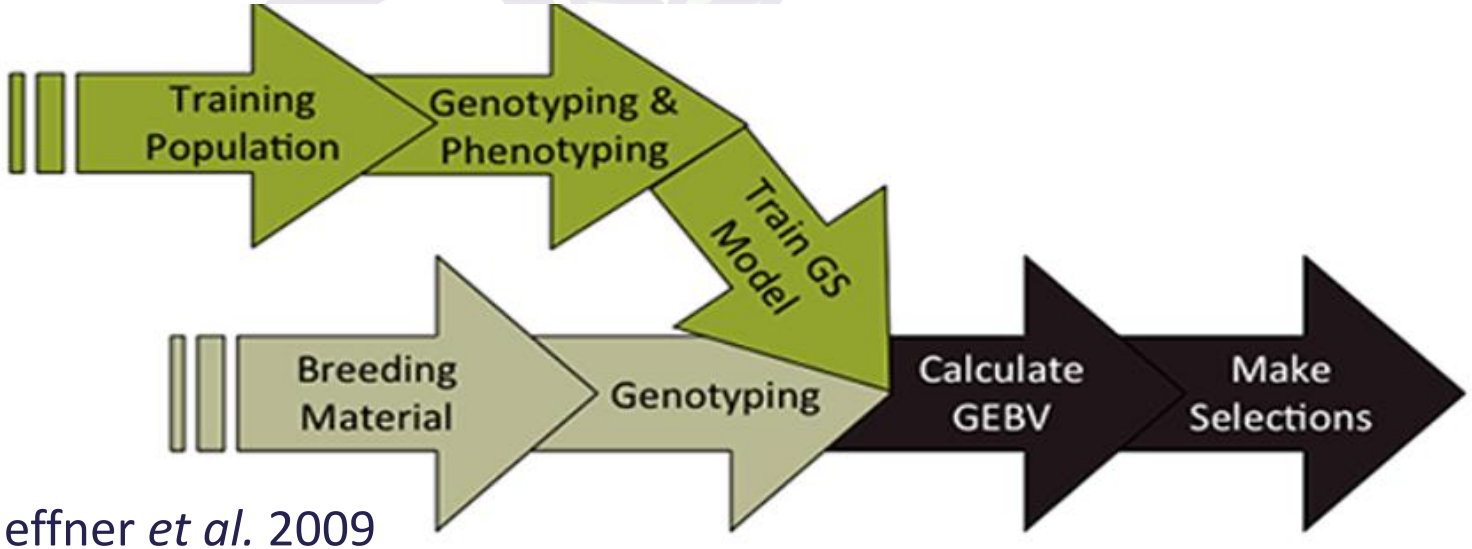
Marker-assisted selection		Objective (based on genetic information) Efficient for additivity	Polygenic traits
Genomic selection			

New breeding strategy for PM?

Objective
Additive and polygenic traits
Environment can be considered
Multiple trait selection

Principle of genomic selection

1- Design of the prediction model using a training population



Heffner *et al.* 2009

2- Model application

Principle of genomic selection

Prediction model:
Whittaker *et al.* 2000

Y= a*x + b

$$y_i = \mu + \sum_k w_{ik}\beta_k + e_i$$

e_i residual vector

$$e_i \tilde{N}(0, \sigma_e^2)$$

Y= vector of phenotypes
y_i for individual i

μ overall mean

w_{ik} is the genotype at locus k {0, 1, 2}
β_k the effect of this allele

Allele SNP1 (genotypeA) * SNP1 effect + Allele SNP2 (genotypeA) * SNP2 effect + …..

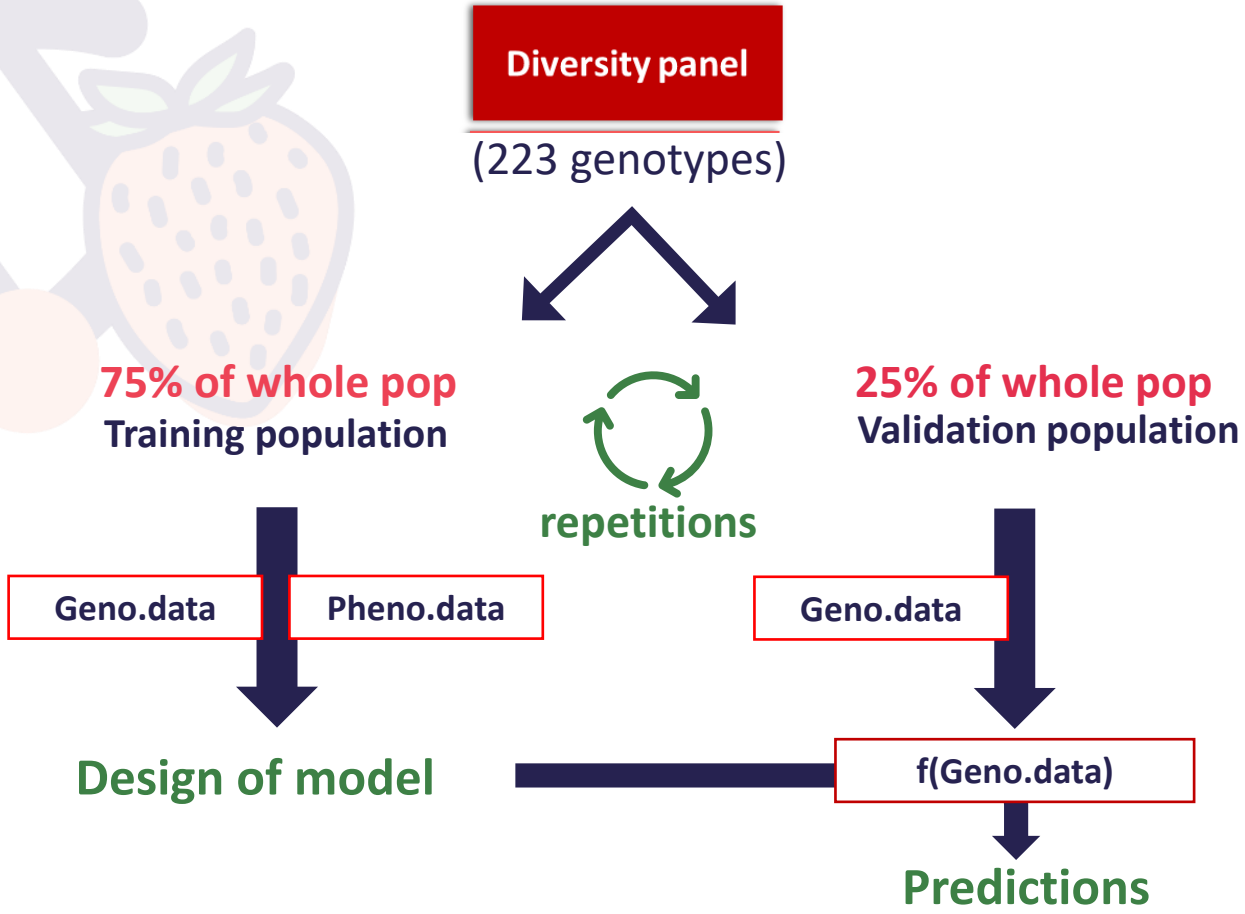
Genomic Best Linear Unbiased Prediction (GBLUP)

Predictive ability of powdery mildew

Evaluation of the performance of genomic prediction for powdery mildew resistance

Cross-validation

For testing the efficency of genomic prediction



Prediction ability = cor(**predicted** pheno , **observed** pheno)

Predictive ability of powdery mildew

75% of whole pop -> Training population =
collection of 165 genotypes

↓

Y = vector of susceptibility values
X = matrix with 33K SNPs

↓

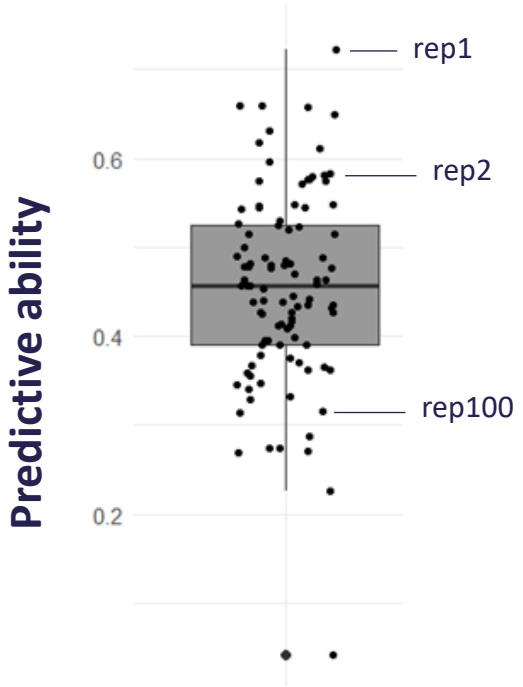
Model : RRBLUP (x100 repetitions)

25% of whole pop -> Validation population =
55 genotypes

↓

Calculation of **predictive ability**
~ Model efficiency / accuracy

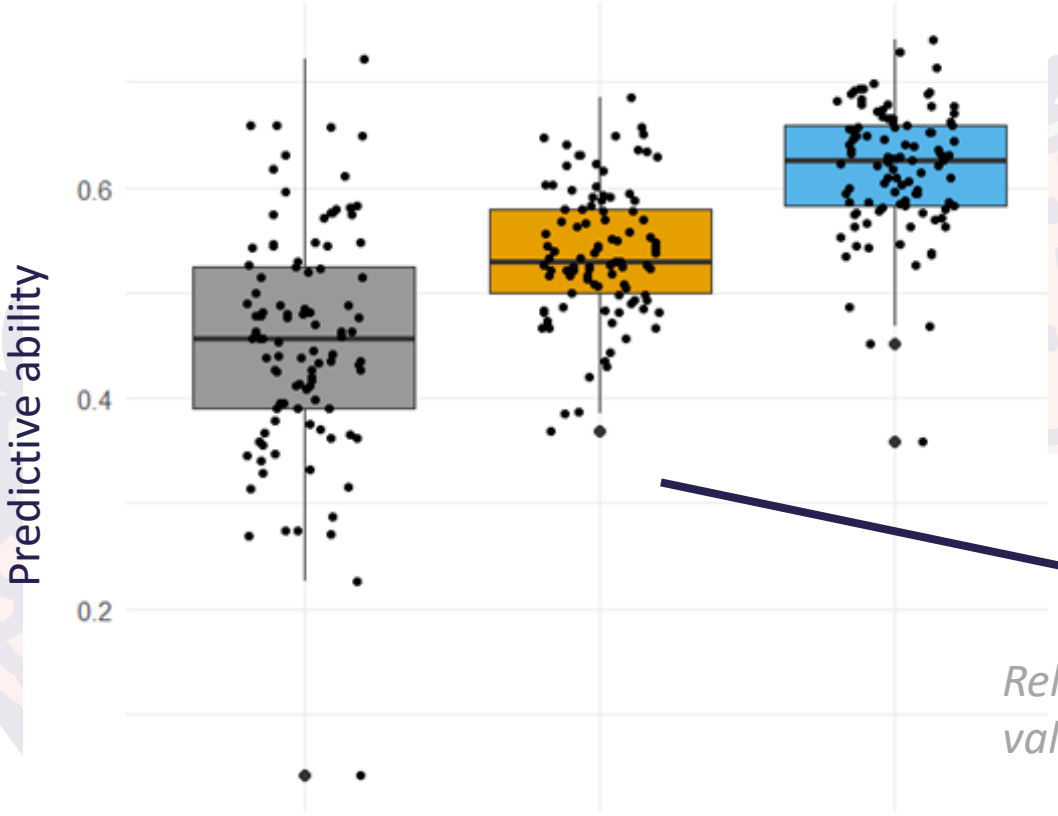
Boxplot of result



Perfomance:
Predicitve ability ~ 0.45

Predictive ability of powdery mildew

2 examples of ways to improve predictive ability



Equation optimization

Adding **cofactors** as fixed effects in the model

Environmental effect, QTL, other influencing factors…

Training population optimization

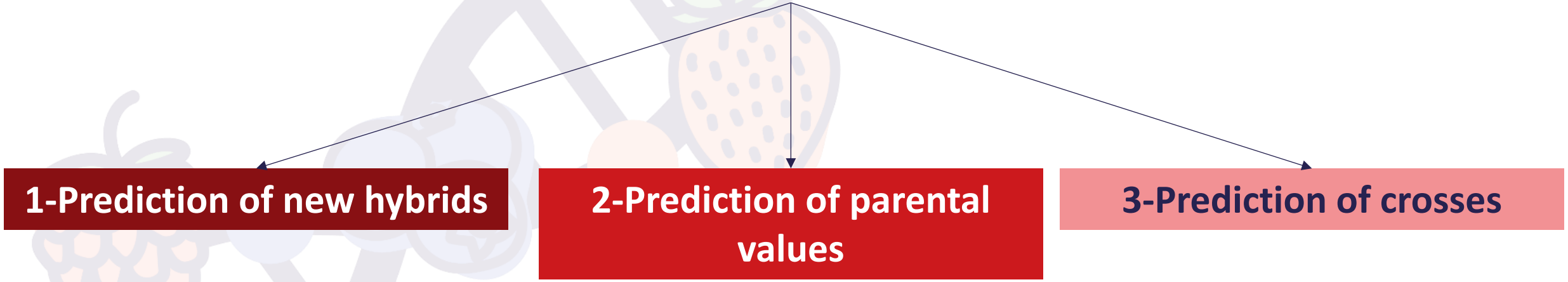
Relationship between training and validation population, size of validation population, intra- / inter- population prediction…

Perfomance after optimization:

Predicitve ability ~ 0.65

Predictive ability of powdery mildew

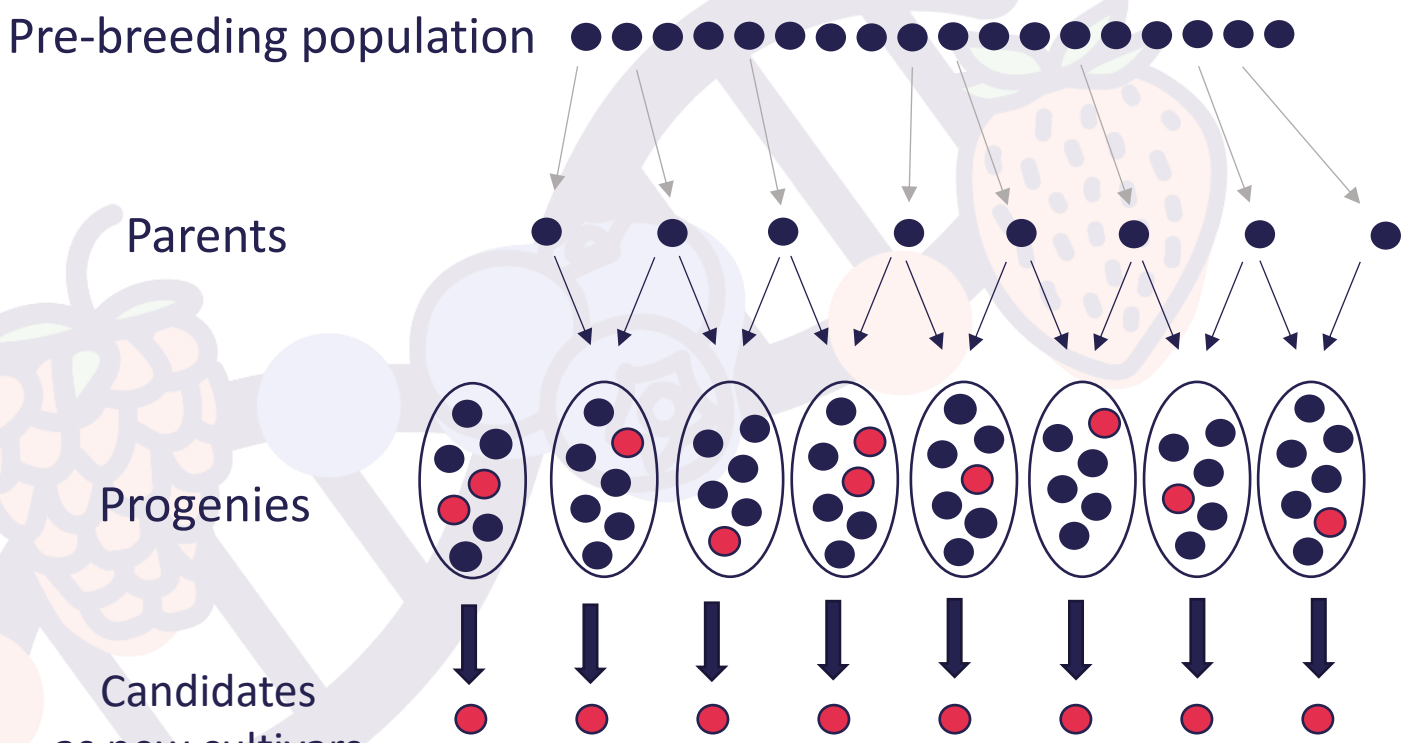
Application of genomic selection
in breeding programme



Predictive ability of powdery mildew

1- Prediction of phenotypic values of new hybrids

Breeding programme



→ *Genotyping*
→ *Phenotyping*

→Model design

For high efficiency: adapt the training population to the breeder programme

→ *Genotyping*

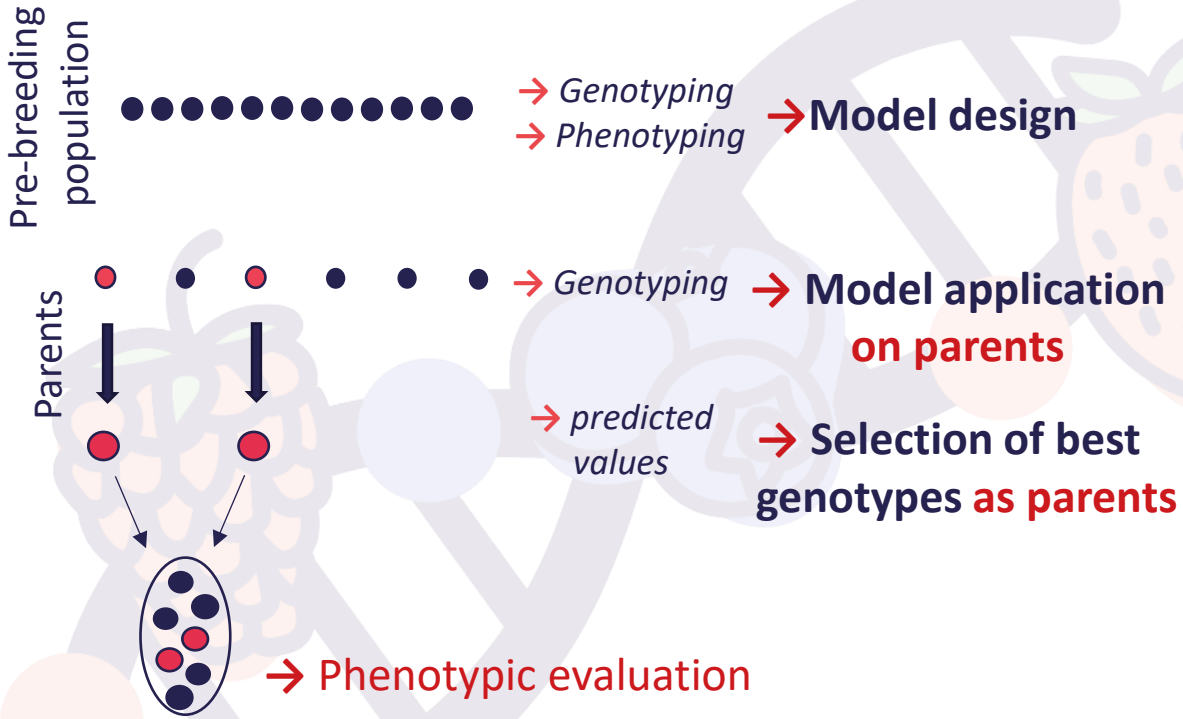
→ Model application on progenies

→ *predicted values*

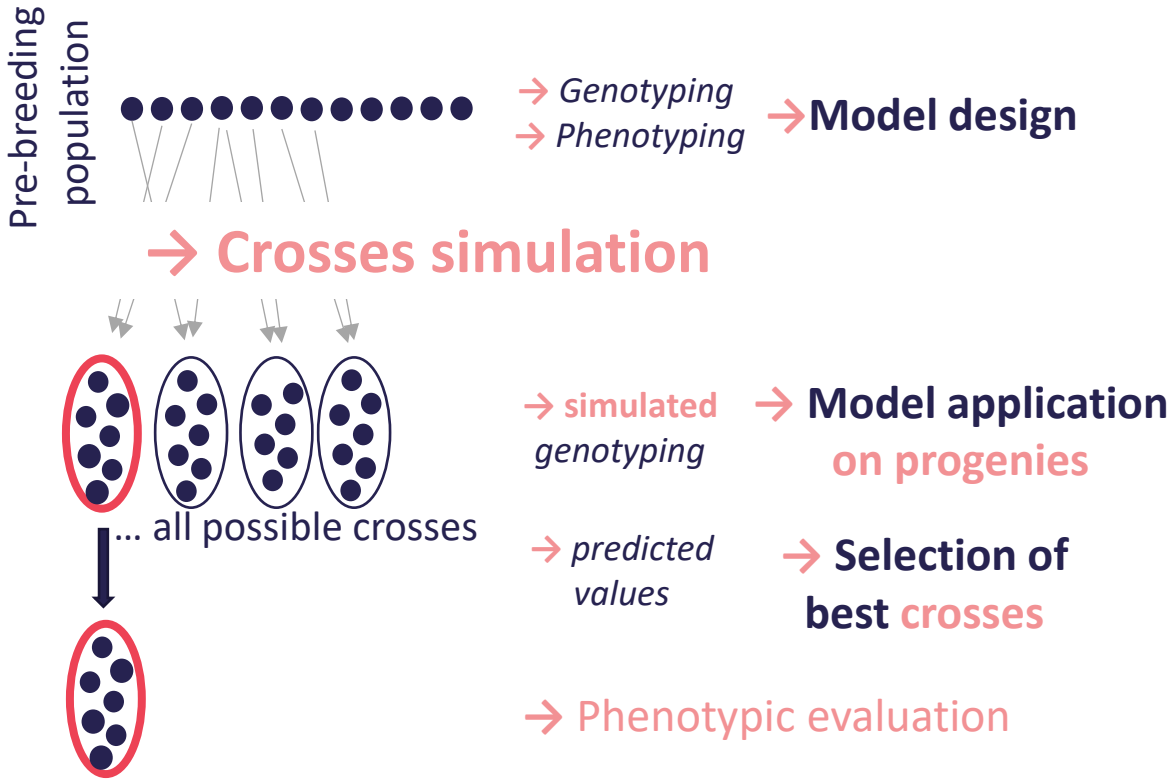
→ Selection of best genotypes

Predictive ability of powdery mildew

2-Prediction of parental values



3-Prediction of crosses



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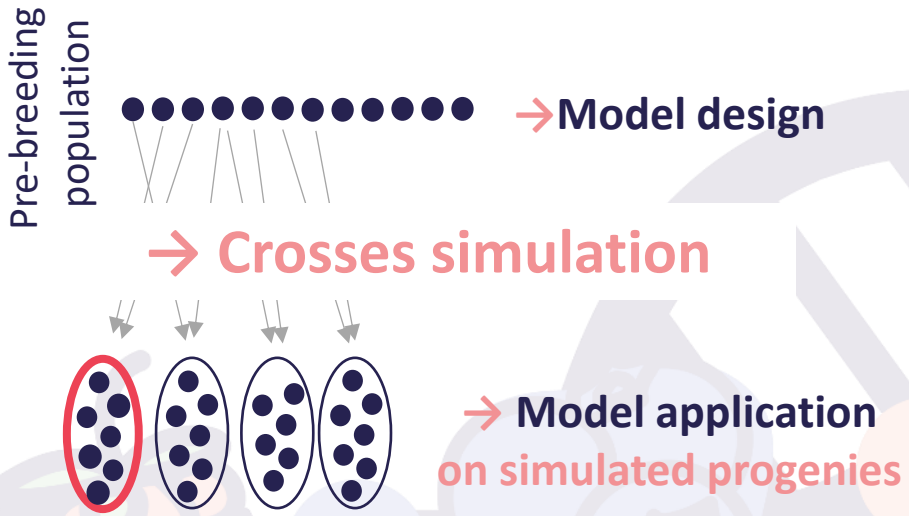
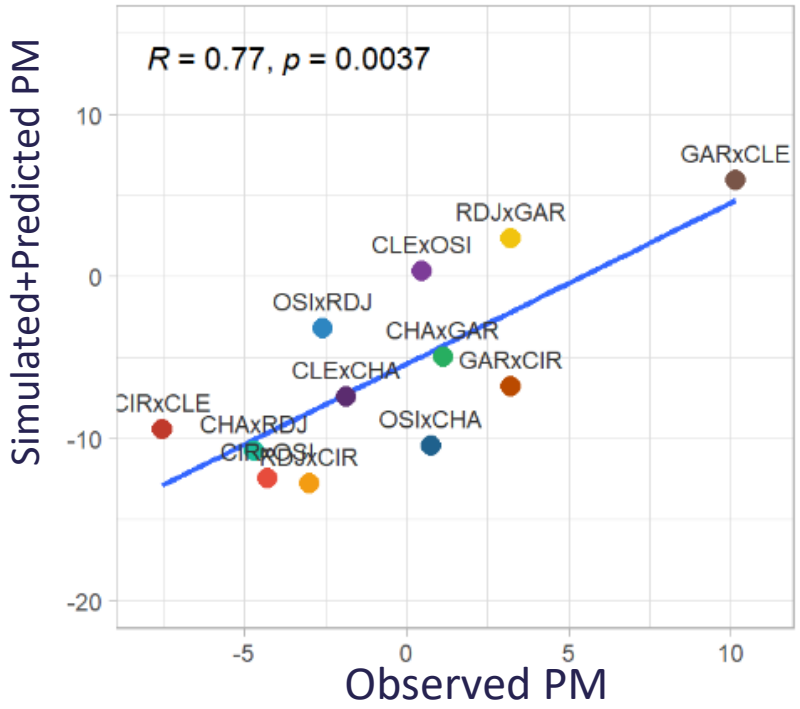


Means and variances are predicted for each simulated cross

Results: High correlation between observed and simulated+predicted PM means in 12 progenies



Simulation coupled with prediction of the values of new crosses is promising

-> easy way to transfer to breeding programmes?

Perspectives

Genomic prediction:

Very promising (optimization in progress)

Efficient for complex and integrated traits

For powdery mildew resistance:

Genomic prediction = efficient alternative (highly polygenic and additive trait).

Crosses simulation:

Prediction of crosses -> **sort out promising crosses**

First step towards implementing GS in the breeding programme

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first step towards implementing GS in the breeding programme

THANK YOU !

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