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# Optimization of breeding program for grapevine disease-resistant varieties with genomic and phenomic predictions

**Introduction/ Context -** French viticulture faces the consequences of climate change and the challenge of reducing the use of phytosanitary products. One solution to this scenario is the development of new grapevine disease-resistant varieties with good agronomic and wine quality performances. The INRAE-ResDur[1] breeding program was developed with this objective and has already released eleven grape varieties carrying polygenic resistance against downy and powdery mildews. However, new approaches are needed to reduce the time of the breeding cycle, which is now about 15 years. Understanding the genetic determinism of targeted traits using QTL (Quantitative Trait Locus) analysis or GWAS (Genome-Wide Association Study) is essential for marker-assisted selection (MAS). It can solve the problem of breeding for resistant traits based on only a few genes. However, agronomical traits are mostly quantitative traits, and MAS isn't a solution. The new omic-based predictions, such as genomic and phenomic predictions based on markers and Near Infra-Red spectra (NIRS), have been developed for a few years. This can be a new opportunity to reduce the breeding schemes in grapevines
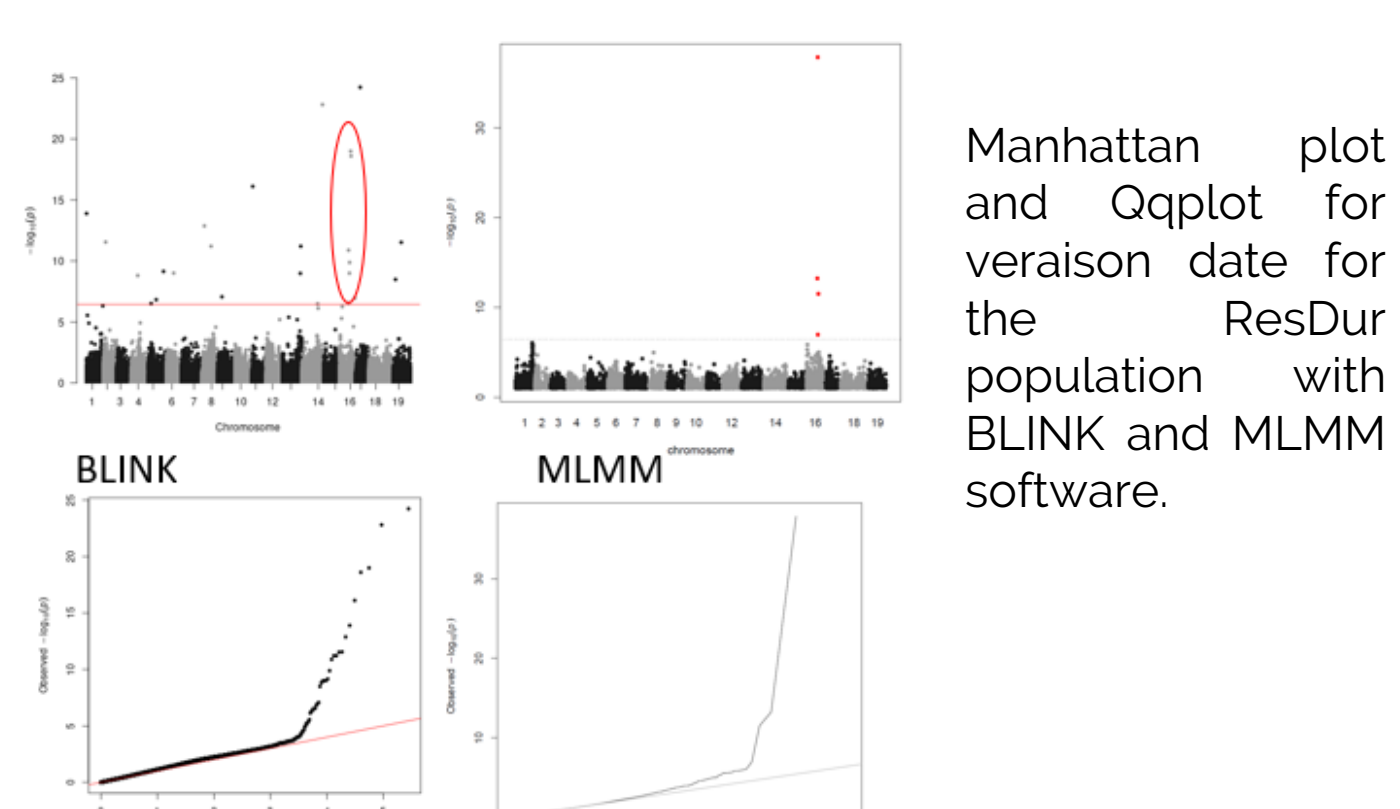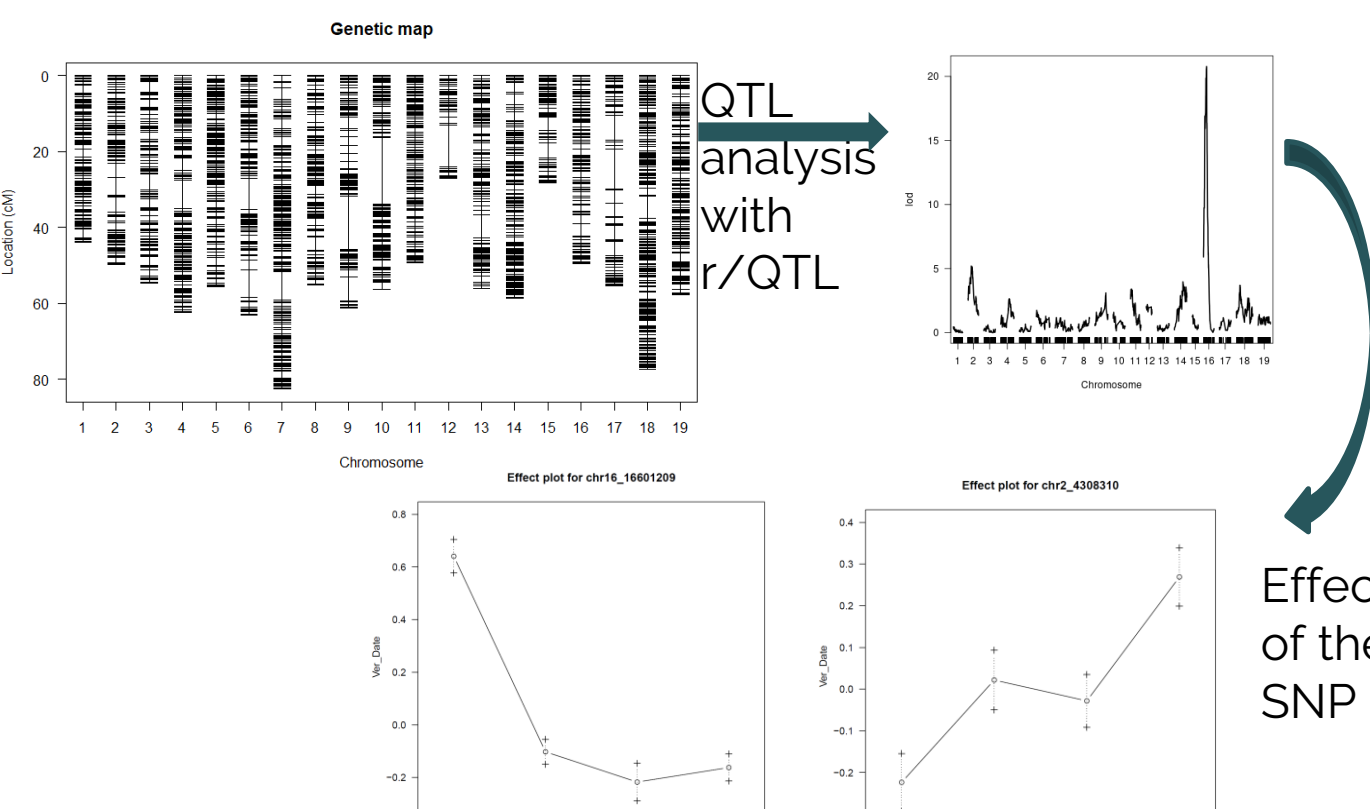
## Objectives

The objectives of this thesis are:
- To evaluate the genetic determinism for agronomicalal traits in grapevine with Genome-Wide Association Study (GWAS) and Quantitative Trait Locus (QTL) analysis in the ResDur material
- To optimize genomic and phenomic prediction models in the ResDur material and compare the results to those of phenotypic selection

## Methods

All individuals from the intermediate selection of the ResDur breeding program are used for the genetic determinism analysis. It means almost 1100 individuals in 95 biparental families. They have been phenotyped for yield traits, berry quality traits, and phenological traits in several locations (at least two) and for several years (at least two). All individuals have been genotyped with GBS (Genotyping-by-Sequencing) and NIRS obtained in 2023 and 2024 on winter woods and leaves at the bud breaks and the flowering.

## Results: Genetic determinism

Statistical analysis of genomic and phenomic analysis to detect loci implicated in a trait and to define its genetic architecture.

| GWAS | QTL analysis in bi-parental population |
|---|---|
| Use all the individual of the ResDur populations | Only in the six biggest bi-parental populations |
| Comparison of two softwares: BLINK[3] (Bayesien-information and Linkage disequilibrium Iteratively Nested Keyway) and MLMM (Multi-Locus Mixed Model) | Genetic map obtained with LepMap3[5] and analysis done with r/QTL[6] |



Manhattan plot and Qqplot for veraison date for the ResDur population with BLINK and MLMM software.

QTL analysis with r/QTL

Effect of the SNP

## Results: Genomic and Phenomic Predictions

A training population is phenotyped, genotyped, and/or NIRS are obtained and used to train statistical models. The test population is only genotyped and/or NIRS, and the statistical models are used to predict the traits.

The NIRS sampling (organs, years, time) and the pretreatment affect the phenomic prediction. Globally, the trait and the statistical methods can affect the genomic and phenomic prediction.
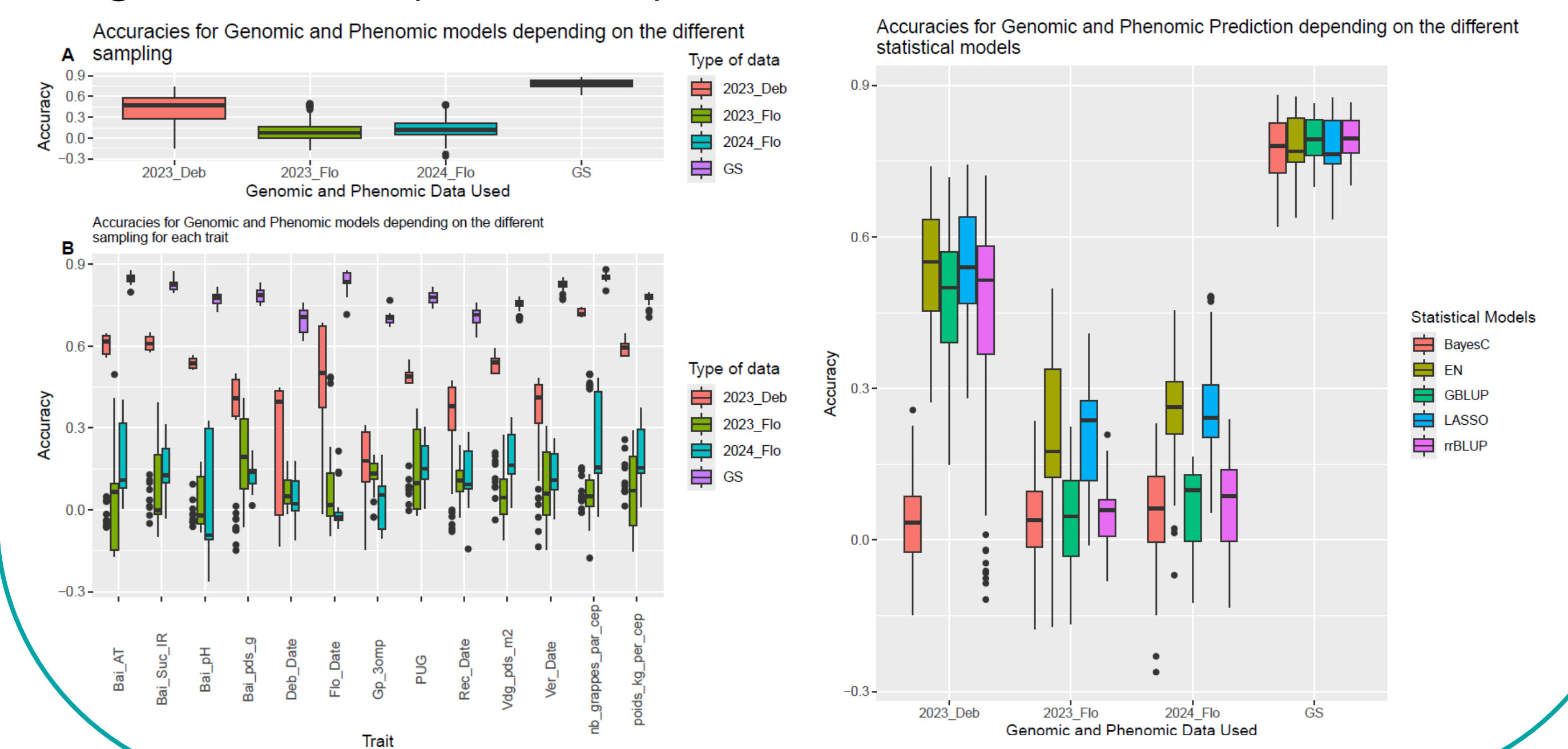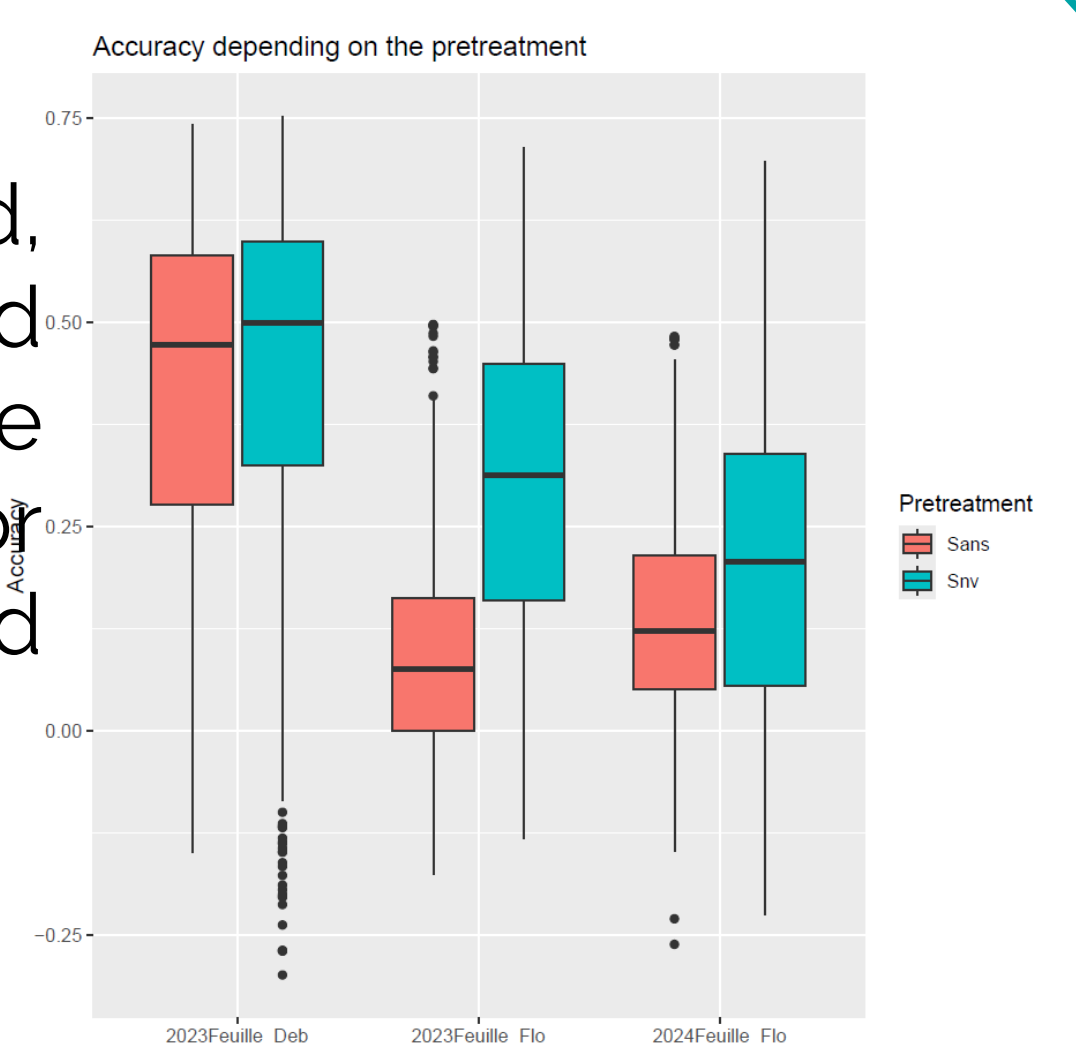


## Conclusion

This work aims to accelerate the breeding cycle of grapevines to create new disease-resistant varieties. Thanks to Marker-Assisted Selection and multi-omics predictions, the intermediate selection of the breeding scheme can be eliminated, decreasing the breeding cycle from 15 years to 9 years.

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