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# Genome-Wide Association Studies (GWAS) and Genomic Selection (GS) in grape: Evaluation of phenotypic prediction methods using a large panel of diversity

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## ORAL PRESENTATION

Genome-Wide Association Studies (GWAS) and Genomic Selection (GS) in grape: Evaluation of phenotypic prediction methods using a large panel of diversity.

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The availability of high throughput genotyping tools in grape, allow the development of GWAS and GS approaches in breeding programs. GS allows the obtention of genomic estimated breeding values (GEBV) of breeding candidates based on large sets of markers while GWAS using mlmm R-package, allows the selection of the more pertinent associations (selection of cofactors) to obtain a model explaining the maximum of phenotypic variability. We estimated the efficiency of GWAS and GS, separately or combined, for the marker assisted selection in grape breeding programs using a large diversity panel on four different traits which covariate with the population structure (berry weight, pruning weight, cluster weight and cluster length). Genotypic informations were obtained with a 18000 Illumina SNP genotyping chip ([http://urgj.versailles.inra.fr/Species/Vitis/GrapeReSeq\\_Illumina\\_20K](http://urgj.versailles.inra.fr/Species/Vitis/GrapeReSeq_Illumina_20K)) on two different samples:

- Diversity panel (DP) of 279 individuals divided into three sub-populations used as training population for the phenotype prediction.
- 21 individuals of a Syrah X Grenache progeny used as validation population for phenotype prediction.

GWAS was realized on each sub-population separately and on the entire DP. Associations were only identified in the sub-populations. Best mlmm models, contained cofactors only for berry weight and cluster length. We detected 0 to 9 cofactors according to the tested panel for a total of 24 significant SNPs. The percentage of variance explained varied between 2% and 28% per marker and from 27.5 to 91.7% per model.

Four different phenotype prediction models were performed based on i) effects of cofactors from mlmm analysis ii) Ridge regression iii) Bayesian LASSO and iv) combined model using cofactors effect from mlmm and Ridge regression. These phenotype prediction methods gave  $r^2$  values (correlation between GEBVs and phenotypes) ranging from -0.38 to +0.40. For each studied trait the best phenotype prediction gave  $r^2$  values superior to 0.3. In conclusion, we have thus demonstrated the capacity to predict with a good precision the phenotype of breeding candidates even if no association was found by GWAS.

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