

## **P64 – Genetic mapping of phenology-relevant, berry quality and aromatic potential traits from two grapevine bi-parental mapping populations**

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### **Abstract**

Grapevine breeding requires renewed efforts to meet the challenge of the ongoing climate change and the societal demand for low input viticulture. A breeding program supported by Bordeaux wine professional committee (CIVB) aims at generating new cultivars that should meet these two objectives by improving traits such as disease resistance (downy and powdery mildew, black rot), while retaining the typicality of Bordeaux wines.

As part of this program, two *V. vinifera* bi-parental mapping populations were generated by crossing, on the one hand, 'Petit Verdot' (PV) and 'Cabernet Franc' (CF) (n = 202) and, on the other hand, 'Ugni blanc' (UB) and 'Sauvignon blanc' (SB) (n = 214). These two mapping populations were investigated for quantitative trait loci (QTLs) detection of relevant segregating traits such as phenology or aromatic potential with GC-MS and LC-MS analyses.

Genotyping by sequencing (GBS) by Illumina HiSeq 3000 of both mapping populations was performed on GET-plage platform (Toulouse, France). After bioinformatics treatments, the construction of the related genetic maps was achieved using JoinMap 4.1.

High-density genetic maps, based on single nucleotide polymorphism (SNPs), allowed the detection of 25 QTLs related with phenology, berry quality, aroma composition and aroma precursors, as well as the identification of some relevant candidate genes. The QTLs identified typically accounted for 7-27% of the trait variation.

The molecular markers identified in this project will be used for marker-assisted selection in current and future grapevine breeding programs. The project will provide the basis of the genetic architecture of useful traits for the production of red and white wines with emblematic Bordeaux typicality and will thus contribute to the design of new ideotypes.

Acknowledgments: We thank the CIVB for the financial support to the NEWVINE project N° 901 and to the GENOGRAPPE project n°1801053/54

**Keywords:** berry quality, genotyping by sequencing, phenology, QTL detection