

Genetic structure exploration and association mapping for root related traits in *V. berlandieri*

Blois, Louis^{1,2*}; Rubio, Bernadette¹; Bert, Pierre-François¹; Girollet, Nabil¹; De Miguel, Marina¹; Voss-Fels, Kai²; Ollat, Nathalie¹; Schmid, Joachim²; Marguerit, Elisa¹

¹EGFV, Univ. Bordeaux, Bordeaux Sciences Agro, INRAE, ISVV, Villenave d'Ornon, France

²Hochschule Geisenheim University, Institut für Rebenzüchtung, Geisenheim, Germany

*louis.blois@inrae.fr

Abstract

In grafted plants like grapevine, increasing the choice of rootstocks available to growers is an ideal strategy to adapt plants to climate change whilst maintaining the wine typicity. In grapevine, the scion is *Vitis vinifera* and the rootstock is generally a hybrid between various American *Vitis* species. *Vitis vinifera* has been domesticated and bred for centuries, but the use of American species is more recent and these genotypes remain poorly characterised. A few traits such as root architecture, water deficit responses, and traits related to biotic and abiotic stresses have been studied on American rootstocks; these studies have described genetic variability, but have rarely characterised the genetic architecture of traits of interest. Among the three main species used for breeding rootstocks, *V. riparia*, *V. rupestris* and *V. berlandieri*, *V. berlandieri* hybrids generally show high performances for chlorosis and water deficit tolerance. One hundred years ago when most rootstocks used today were created only few individuals were available as parents. In this project, seeds of 78 wild *V. berlandieri* were collected in Texas after open fertilization. A total of 286 genotypes were genotyped to describe the population genetic structure, and phenotyped for root related traits in order to perform genome wide association analysis (GWAS). De novo *V. berlandieri* long read whole genome sequencing allowed us to identify and filter 104378 SNPs. STRUCTURE analysis identified two gene-pools that were associated with differences in altitude. Root phenotyping revealed diverse root system architectures and GWAS allowed detecting 8 QTLs associated with root traits with medium to high heritability (from 0.36 to 0.82) on chromosomes 1, 5, 9, 10, 13, 14 and 17. This original work is the first GWAS study done with a population of grapevines sampled in natural conditions and phenotyped as grafted plants. Our results offer new insights into rootstock genetics and could offer the potential to use marker assisted selection in grapevine rootstocks improvement programs.

Keywords: Grapevine, Population genetics, Genome-wide association, Genotyping by sequencing, Root architecture