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GENETIC DISSECTION OF PHENOLOGY IN VITIS VINIFERA THROUGH MULTI-POPULATION QTL ANALYSIS

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Understanding the genetic determinants and regulatory mechanisms underlying phenological development in *Vitis vinifera* is a central objective of current breeding efforts. These initiatives aim to develop cultivars better adapted to ongoing climate change, while maintaining distinctive regional characteristics of both grape production and resulting wines. In grapevine, phenological traits display complex patterns of quantitative inheritance, typically governed by the additive and/or dominance effects of multiple genes. Quantitative Trait Loci (QTL) analysis offers a powerful approach to identify genomic regions associated with phenotypic variation, potentially including candidate genes involved in the regulation of these traits.

In this study, we report the results of a QTL mapping experiment conducted on three segregating populations derived from crosses between "Cabernet Sauvignon" and "Corvina" (CSxC), "Corvina" and "Solaris" (CxS), and "Rhine Riesling" and "Cabernet Sauvignon" (RRxCS). Six parental linkage maps were generated using genotypic data obtained by hybridizing DNA from 144, 129, and 139 individuals, respectively, with the Illumina Vitis18KSNP chip. Overall, these maps included 6,316 markers, 3,497 of which were shared in at least two maps, allowing integrated analyses and direct comparisons of QTL results. From 2018 onwards, the three progenies were phenotypically evaluated under field conditions over four to five growing seasons and phenological traits such as budbreak, flowering, and veraison were recorded. Best Linear Unbiased Predictor (BLUP) values were extracted to estimate the genetic contribution of each genotype to the different phenotypes, eliminating or reducing environmental effects. QTL analysis with all datasets yielded 183 QTLs associated with phenological development. Concerning budbreak, among the 37 genomic regions highlighted, some were consistently found in more years (chr 1, 6, 7, 9 and 13). For flowering, among the 49 genomic regions identified, those reproducible in more years were located on chr 1, 2, 5 and 18. Finally, for veraison, among the 57 genomic regions identified we found 6 confirmed across more years (chr 1, 3, 11, 13, 16 and 17). This analysis also highlighted the existence of several shared regions across traits at the level of the same map and/or among multiple parental maps. The results underline the highly polygenic nature of grapevine phenological traits, characterized by the involvement of numerous loci with relatively small individual effects. Select candidate genes at the QTL locations are discussed.