

## **IDENTIFICATION AND VALIDATION OF SNPS ASSOCIATED TO THE VERAISON TIME/FLOWERING-VERAISON TIME INTERVAL IN GRAPEVINE**

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Grapevine (*Vitis vinifera* ssp. *vinifera*) is a perennial fruit crop cultivated all over the world. It is one of the most important fruit crops and has a relevant role in the economy especially because of wine production.

As for many other crops, also grapevine cultivation is afflicted by environmental changes. Indeed, high temperatures occurring during early growth season may advance the date of main phenological stages changing conditions over ripening and finally negatively impacting on grape and wine quality. Therefore, dissection of genetic determinants driving main phenological stages affecting conditions over ripening, like flowering, veraison time and the interval among these, has become a challenge to adapt local grape varieties to environmental conditions.

In grapevine, as in many other crops, phenotypic traits show mainly a complex quantitative inheritance. By using a large diversity panel, Genome Wide Association Study (GWAS) provides a promising tool for mapping of trait-associated variants.

We developed a project aiming to identify QTLs and candidate genes linked to the veraison time in *V. vinifera*, with the practical purpose to use this information in the development of improved cultivars. To this aim, starting from a panel of more than 600 cultivars grown in the germplasm collection of CREA-VE in Susegana (Treviso, Italy), a core collection of 132 unique genotypes was pulled out, based on data at 45 SSR markers, representing the minimum number of cultivars covering all the alleles and reaching the genetic diversity of the initial panel. Then, SNPs genetic data obtained through hybridization to the GrapeReSeq 18KVitis SNP Chip were retrieved for the whole core collection. Altogether, 9536 SNP markers were selected and managed with phenotypic data, i.e. flowering time, veraison time and interval flowering-veraison collected over 13 years, to perform GWAS. Bioinformatic analysis was conducted with 3 different software applying different corrections to check the association of SNP markers with phenotypes. Fifteen SNPs significantly associated were found. More in detail 5 SNPs associated to veraison time and 13 SNPs associated with the interval flowering-veraison were identified by at least one of the 3 software. Among these, three SNPs, located on chromosomes 12, 16 and 18, were detected as significantly associated to both phenotypic traits and chosen to further enquire and validate the associations. Interestingly, SNPs annotation showed that the SNP located on chromosome 18 falls in a region found to be associated to grapevine veraison time also according to previous QTL studies performed in biparental populations. Potential candidate genes in all the identified regions are discussed. From the initial panel of 600 cultivars, a subset of 94 individuals, showing extreme phenotypes in flowering-veraison interval, was then Sanger-sequenced to

confirm the associations.