

## **P69 – Genome wide association mapping of flowering-veraison interval in *Vitis vinifera* L.**

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### **Abstract**

Grapevine cultivation is being afflicted, as for many other crops, by environmental changes. Indeed, high temperatures occurring during growth may advance the date of phenological stages changing climate conditions over ripening and thus negatively affecting grape and wine quality. In particular, starting of veraison, that is the onset of the berry ripening process, and its laps of time from flowering are variable among the different varieties. Therefore, dissection of genetic determinants driving the phenological stages of flowering, veraison, as well as the interval among these, represents an interesting target in the contest of adapting grape varieties to changing environmental conditions. This has been previously enquired by QTL studies conducted in bi-parental populations. By using large diversity panels, Genome Wide Association Study (GWAS) provides a further promising approach for mapping of these traits and associated variants.

To this aim, starting from a panel of more than 600 cultivars grown in the large germplasm collection of CREA-VE in Susegana (Treviso, Italy) a core of 132 genotypes representative of the genetic diversity of the whole panel was pulled out, based on genotypic data at 45 SSR markers. Using this core we have conducted a GWAS to identify loci linked to the extension of the interval between flowering and veraison times. Phenotypic data, collected over a period of 11 years, were managed together with GrapeReSeq *Vitis* 18K SNPChip genotyping data and bioinformatic analysis was conducted, with 3 different softwares. We identified a list of SNPs significantly associated to the phenotype by at least one of these softwares among which some were confirmed by more softwares. Alternative strategies for SNP validation were implemented, either based on further available SNP data in public repositories or on direct Sanger sequencing of some of the associated SNPs in genotypes with extreme behaviors (48 selected samples with long and 48 selected samples with short flowering-veraison interval). Potential candidate genes in the associated regions were also identified.

All together these results provide useful clues for the flowering-veraison interval genetic regulation and for the molecular breeding in *Vitis vinifera*.

**Keywords:** grapevine, climate change, GWAS, QTL