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Genome wide association mapping of phenology related traits in *Vitis vinifera* L

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Abstract

Climate change, with rise in temperatures, is leading to an advance in the dates of phenological stages, with a loss in quality of the grape final product. Therefore, the understanding of the genetic determinants driving the phenological stages of flowering, veraison and the interval between them, represents a target for the development of grapevine's cultivar adapted to the changing environment. Here we conducted a GWA study to identify SNPs significantly associated to flowering time, veraison time and to the interval among them. A germplasm collection (CREA-VE in Susegana, Treviso, Italy) including 649 grapevine's cultivar representing 365 unique genotypes was considered. Cultivars were phenotyped for flowering time and veraison time along 11 years. Flowering-veraison intervals were also derived and distribution for all traits was inspected and eventually corrected. For this analysis we have built a genetic dataset including 6679 SNPs. SNPs were either recovered from litterature or integrated by genotyping through grapevine Illumina SNPChip 18K and used for evaluating the genetic structure. MLM analysis conducted independently for the three different phenological traits identified a list of few significantly associated SNPs. Among the three traits flowering time yielded the highest number of associated SNPs. For each trait SNPs consistently associated across more years were found. Moreover partially overlapping SNPs associated both to veraison time and flowering-veraison time interval were found. Interestingly most of the associated SNPs co-localized with QTL regions already known either for flowering or veraison traits in grapevine. Putative candidate genes underlying such regions are discussed.

Keywords: Climate change, GWAS, phenology, candidate genes.