

## An independant haplotype responsible for white berry phenotype in *Vitis vinifera* arose from a large deletion at the berry color locus

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### Abstract

Since the seminal work of Gregor Mendel in the middle of the XIX century, the inheritance and genetic bases of color variation in plants have attracted significant scientific interest. For Eurasian grapevine (*Vitis vinifera*), the thousand different cultivars can be grouped into two main categories, based on the presence/absence of anthocyanins in the berry skin. One locus on chromosome 2 has been shown to be the major genetic determinant of berry skin coloration. This berry color locus contains a cluster of Myb transcriptional factors (*e.g.*, MybA1 and MybA2). In this study, we investigated a particular allele of MybA1 gene, MybA1\_SUB (from haplotype F), originally described in the Sultanine cultivar. We analysed 528 cultivars originating from diverse countries and found 78 cultivars possessing the MybA1\_SUB allele, but displaying both phenotypes: colored and non-colored berry skins. This allele is rare in western European cultivars. However, we identified this allele in 9 black-skinned autochthonous cultivars from the Alpine region. These cultivars are cultivated on both sides of the border in the Valais canton (Switzerland) and Aosta Valley (Italy). To gain a better understanding of the genetic mechanisms underlying the presence/absence of anthocyanin in berry skins, we characterized the berry locus region from several black and white-skinned berries cultivars possessing the MybA1\_SUB allele. To facilitate genetic analyses, homozygous genotypes were created using selfing and investigated using long-read genome sequencing to reconstruct a large portion of chromosome 2. Our finding showed that the structural organization of the berry color locus for black-skinned variety with SUB allele is different from what has been described for the canonical haplotype of Pinot noir (PN40024). Examining the berry color locus for white-skinned berries SUB cultivars, we identified a large deletion (ca. 77kb). Furthermore, using RNAseq on berry skins tissues during ripening, we examined gene expression profiles for four cultivars carrying the MybA1\_SUB allele. Our findings indicate that haplotype F can be divided into two subhaplotypes: one functional that can trigger anthocyanin production and one complete or partial loss-of-function allele due to the deletion. The non-functional haplotype F was identified only in table grape cultivars. In conclusion, contrary to what it has been previously proposed, our results suggest that not all white cultivars share a common origin, but rather that during the domestication process, at least two independent haplotypes were selected for white-skinned berries phenotype.

**Keywords:** *Vitis vinifera*, berry color, Myb genes, structural variation