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SNP signatures of selection and their association with flowering time in a core collection of grapevine

Corresponding author: lukasz.grzeskowiak@fmach.it

Authors: Grzeskowiak L.; Lorenzi S, Grando M.S.

Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all'Adige (Italy)

Abstract: Flowering time is a target trait of choice in the breeding for crop improvement. A QTL related to the dates of flowering was detected in different grapevine crosses, accounting for 8.3-22.6% of the trait variation. To determine if polymorphism in that QTL could be a cause of different flowering phenotypes in a species wide sample, we took a candidate gene approach and tested for outlier SNP loci. We measured flowering time over several years in a collection of cultivated grapes sampled from their countries of origin and grown in the field at Fondazione Edmund Mach. Next, we sequenced six positional candidate genes, which cooperate to regulate meristem formation and floral induction. Two of the candidates, FT and SVP, physically interact and play key roles in the early stages of transition to bloom phase. We found that the phenotypic variation observed in grapevine was associated with polymorphism in the gene SVP, and that the genes from this QTL region might have experienced directional selection, which could lead to differences in their expression. The results may help us to develop SNP markers for marker-assisted breeding of this complex trait.

Keywords: flowering time, crop improvement, selection, core collection, *Vitis vinifera*