

Genetics of flowering time in grapevine

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Due to climatic change, phenology traits are becoming increasingly important in grapevine breeding, since a premature flowering and ripening time could be observed for grapevine in the last decades. However, knowledge about these traits is still limited as they are genetically very complex and highly influenced by environmental factors. The analysis of the genetic basis of flowering time therefore will enable the development of tightly linked molecular markers useful for marker-assisted selection of especially late flowering breeding lines.

A QTL analysis approach was followed to detect major genetic factors within a biparental mapping population derived from a cross of the early-flowering breeding line GF.GA-47-42 and late-flowering cultivar 'Villard blanc'. Phenotyping of flowering time was carried out for the 150 F1 individuals in seven years. First investigations indicate QTLs on six chromosomes, some of which could also be confirmed in a second unrelated mapping population. Analysis of the QTLs indicates that certain combinations of marker alleles from the

different QTL regions lead to a very early, medium or late flowering phenotype, respectively, and suggests a dominant effect for early flowering. However, the revealed QTLs still cover large regions of the respective chromosome which hampers the detection of credible candidate genes.

Future aims of the project are: (1) Fine mapping of the QTL regions by developing new SSR markers and also with genotyping-by-sequencing (GBS) of a subset of F1 individuals. Additionally, an extended mapping population of approximately 900 F1 plants is available for phenotyping, in order to refine the QTL regions, hence limit the number of candidate genes and determine more reliable ones. (2) A deeper investigation of allelic variation at the QTL regions and the impact of their combination on the flowering time phenotype. (3) Flowering time homologues described in model plants and located within a QTL are examined for their expression at various developmental time points in both parents to find differences between the early and late genotype.