

Genetic loci determining the flowering time phenotype in grapevine

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In contrast to genetic studies on resistance, studies addressing phenological traits of grapevine such as bud break, flowering and ripening are still in their infancy. The fact, that these traits are highly affected by environmental determinants like light intensity and temperature makes it difficult to investigate their genetic background and respective knowledge is still limited. Therefore, we are interested in detecting loci and underlying genes that are relevant for control of flowering time in grapevine.

Phenotyping of flowering time and subsequent QTL analysis were carried out for several years using a mapping population derived from a cross of the early-flowering breeding line GF.GA-47-42 and the late-flowering cultivar 'Villard Blanc' consisting of 151 F1 individuals. Results show QTLs for time of full bloom on seven chromosomes with a major QTL on chromosome 14. For the purpose of refinement and verification of the QTL regions the mapping population was expanded to about 1000 F1 individuals and first QTL analyses were conducted.

In a previous work putative flowering time candidate genes were identified by

a global approach using sequence information of model organisms and the grapevine reference genome sequence, resulting in a list of about 400 candidate genes spread over the whole grapevine genome.

Yet for a detailed investigation the major QTL region on chromosome 14 was screened for candidate genes combining knowledge about the physical QTL position, known conserved domains and RNA-Seq data from time series covering inflorescence development. This strategy led to promising candidate genes with potential roles in the flowering time control network of grapevine, which needs to be verified in the future.

Additionally, time of bud break was phenotyped in the same mapping population to check whether early or late flowering time is dependent on the time of bud break. However, QTL analysis with data from three years detected a single locus on chromosome 7 that does not overlap with any QTL for flowering time. Next steps will be fine mapping of the QTL region on this chromosome and screening for candidate genes that control the time of bud break.