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Studies on flowering time control in grapevine

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Viticulture is impaired by effects of biotic and abiotic stress at the same time. Apart from resistance research, studies of phenological traits such as flowering and ripening are becoming increasingly important due to climatic change. Especially high light intensities and temperature promote an early development and hence negative effects like e.g. late frost danger during spring time. To counteract this problem breeding programs aim at selecting genetically determined late flowering within new breeding lines. However, knowledge about which genetic loci are involved in the complex flowering time control network of grapevine is still limited.

Phenotyping of flowering time was carried out during 10 years on a mapping population derived from a cross of the early-flowering breeding line GF.GA-47-42 and late-flowering cultivar 'Villard Blanc' consisting of 151 F1 individuals ("basic population"). Subsequent QTL analysis showed QTLs for time of full bloom on seven chromosomes, yet some of them span rather large chromosomal regions. Limitation and verification of the detected QTL regions is intended by the refinement of the underlying genetic map and QTL analysis in further populations. For this purpose the "basic population" was expanded to about 1000 F1 individuals ("extended population") and a half-sib population was included in the experiments.

Identification of candidate genes so far was realised by a global approach using sequence information of model organisms, which led to various candidate genes spread over the whole grapevine reference genome. However, for a detailed investigation of the detected QTL regions screening for conserved domains known to be associated with flowering time is in progress.

The analysis for correlation of the allelic constitution in the QTLs with the flowering time phenotype will lead to the identification of genetic markers to be used in marker assisted selection (MAS). This will accelerate the selection process for late flowering breeding lines. First investigations within the basic and extended population led to several potentially suitable markers. Their analysis in a set of related and unrelated cultivars will clarify their general usefulness for the prediction of flowering time phenotype and therefore in MAS.