

Analysis of bunch architecture in grapevine

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A loose grape cluster is a desirable trait in grapevine breeding, since it reduces the abundance and severity of fungal infections. This is partly due to a better coverage of the grape bunch with anti-fungal spraying agents but nonetheless due to a higher air exchange within the grape cluster. The reduced exposure to high humidity acts as a physical barrier against pathogens which are in need of high moisture to proliferate, e.g. *Botrytis cinerea*. The aim of this study is to identify bunch architecture influencing genes and to introduce molecular markers to accelerate the selection process in grapevine breeding.

To calculate the compactness factor for the bunch architecture a phenotyping procedure was established. The experimental trials are spread over three wine growing regions in Germany and located in the climate areas A and B. The plant range contains a mapping population (GF.GA-47-42 x 'Villard blanc'), a set of 'Pinot Noir' clones with loose as well as compact clusters and additionally extremely loose clustered table grapes of the 'Cardinal' family.

A phenotype-DNA based approach uses the 150 F1 individuals of the mapping population for QTL analysis. The F1 progeny segregates in terms of cluster size and compactness. QTL calculations performed in 2012 suggest QTLs on one chromosome related to rachis length. The calculation of two consecutive

years (2012, 2013) confirmed a QTL related to pedicel length. However the QTLs still cover wide genomic regions and candidate gene suggestion is therefore hampered. Using the phenological data of the upcoming two years in association experiments should result in verification and definition, as well as revelation of QTLs.

For model plants, the literature provides information about genes involved in the regulation of floral meristem formation. The expression of these genes is conserved over genetic distances and displays a great impact on the inflorescence and bunch architecture. Based on the grapevine reference genome (PN40024) orthologues of these genes should be detected. Furthermore molecular markers linked to these traits need to be established.

In a transcriptional profiling approach two loose and three compactly clustered clones of 'Pinot Noir' were compared. In a first step RNA from dormant winter buds and compound buds harvested during the growing period were used in a differential gene expression experiment. The RNA sequencing was performed at the Max-Planck-Institute for Plant Breeding. First candidate genes have to be verified with chip-based micro fluidic PCR (Fluidigm) and quantitative PCR.