Comparative studies of bunch architecture in grapevine varieties and 'Pinot Noir' clones

Robert Richter[1], Susanne Rossmann[2], Reinhard Töpfer[1], Klaus Theres[2], Eva Zyprian[1]

[1] Julius Kühn-Institut, Institute for Grapevine Breeding, Siebeldingen
[2] Max Planck Institute for Plant Breeding, Research Dept. of Plant Breeding and Genetics, Köln
Email of corresponding author: eva.zyprian@julius-kuehn.de

A loose grape cluster is a desirable trait in grapevine breeding, since it reduces the abundance and severity of fungal infections. This is due to an efficient air exchange within the grape cluster. The reduced exposure to high humidity or water acts as a physical barrier against pathogens which are in need of high moisture to infect and proliferate, e.g. *Botryotinia fuckeliana*, teleomorph of *Botrytis cinerea*.

The aim of this study is to identify loci of genes influencing bunch architecture and the development of molecular markers linked to loose cluster architecture to accelerate the selection process in grapevine breeding.

The plant material under study is a segregating population (GF.GA-47-42 x 'Villard blanc'), a set of 'Pinot Noir' clones with loose as well as compact clusters and extremely loose clustered table grapes of the 'Cardinal' family.

Phenotypic characterization uses 150 F1 individuals of the segregating population for QTL analysis. The assessments of eleven sub traits for loose cluster architecture revealed that seven of the sub traits show 22 QTLs during two years. Deduced from QTL calculation performed in 2013 and 2014 the peduncle length and the length of the pedicel exhibit five stable QTLs over three consecutive years. However the QTLs discovered so far extend over wide genomic regions and candidate gene suggestion is therefore hampered. Gene ontology enrichment studies within the confidence interval of the QTL regions on the reference genome may be helpful for the identification of candidate genes.

In a transcriptional profiling approach 'Pinot Noir' clones with loose and compact clusters 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. RNA sequencing was performed at the Max-Planck-Institute for Plant Breeding. First candidate genes could be validated with quantitative PCR. In a second step RNA of inflorescences was sampled at time points when loose clustered clones grow faster than the compact clones. With the repeated experiment during two consecutive growing seasons the kinetics of candidate genes could be tracked and further candidate genes should be revealed.

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 has a great impact on the inflorescence and bunch architecture. Based on the grapevine reference genome (PN40024) orthologues of these genes should be detected.