P-005: Genetic mapping of wine quality traits in grapevine

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Determining wine quality potential of an individual seedling is the most time consuming step in grapevine breeding. Young plants have to be cultivated at least three to four years to yield the first time sufficient grapes for a small-scale winemaking (micro-vinification). Product variation based on annual climate variability and several propagation stages additionally result in several years of wine quality assessments prior variety release.

One promising strategy to increase breeding efficiency tremendously is the early elimination of seedlings with expectable deficiency in wine quality potential by trait-linked molecular markers. Marker assisted selection (MAS) is already established in the breeding process to identify and stack resistances against major grapevine pathogens. Promising resistant plants at seedling stage meanwhile exceed the capacities for handling and vineyard space. New early applicable selection criteria, especially for the important but rather complex trait of wine quality, are required.

Genetic mapping of F1 populations with variance in quantitative traits of interests is a well-established method and has proven to be highly efficient in supplying the breeder with molecular markers suitable for MAS. QTL analysis (quantitative trait loci) is an efficient tool to identify genetic loci linked to quantitative traits by combining precise phenotypical data of the individuals with the genotypic structure.

Important quality traits in grapevines for wine production are a balanced acidity structure, an adequate must weight, body and mouthfeel, desired aroma profiles and the absence of off-flavors.

FTIR (Fourier-transform infrared)-spectroscopy is a well established and official accepted method to acquire a wide range of important parameters in wine and grape juice. Included are total acidity, tartaric acid, malic acid, pH value, total soluble solids, fructose, glucose, alpha amino nitrogen and others. High degree of automation and analysis time of about 1 minute per sample for all parameters enable high throughput for a wide range of relevant metabolomic traits with multiple sampling per season.

QTL-analysis captured in the growing seasons of eight successive years in the F1 population 'Calardis musqué' x 'Villard blanc' resulted in genetic loci found to be highly relevant and stable over the years. Especially, as the contents of acids and sugars in grapes are expected to be within a specific range under the local climatic conditions at harvest time, their genetic potential can be used as effective early selection criteria in marker-assisted selection (MAS) as soon as fully validated.