

## **P59 – In-depth genotyping-by-sequencing of a grapevine F1 mapping population towards the prediction of wine quality potential**

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### **Abstract**

The molecular and genetic characterization of grapevine is a basic requirement to increase grapevine breeding efficiency. The introduction of marker-assisted selection (MAS) increased the efficiency of grapevine breeding programs and paved the way from empirical to predictive design of crosses. Resource optimization is achieved by early seedling removal as well as the selection of parental plants with favourable alleles. MAS is particularly important for perennial crop breeding, where solely the period from planting to first fruit set lasts years, in grapevine usually three years. For the subsequent in-depth evaluation during the breeding process, in particular to assess the quality potential of breeding lines, at least two more decades have currently to be scheduled.

An improved high-density genetic map of the cross population ‘Calardis Musqué’ and ‘Villard Blanc’ (150 genotypes) was developed based on genotyping by sequencing (GBS) data. Our GBS and computational pipelines are designed to maximize the gain of information from DNA sequencing data. To improve the amount of initial loci, our computational pipeline is based on de novo clustering and alignment on the read length level. By choosing this procedure we were able to identify not only SNPs, but also InDels which might represent valuable candidates for marker development followed by application using selective PCR. All in all, our modular de novo approach is taxon independent, does not necessarily rely on a reference genome, and allows for the incorporation of different marker types (SNPs, SSRs, InDels). Consequently it is highly versatile and expandable to future application platforms. Therefore, we minimized early filtering steps at different levels of the approach, resulting in a large dataset of ~500,000 loci. Adjacent biallelic SNPs from individual reads were translated into 20.410 haplotype-based markers with informative segregation patterns. The map was validated and used in QTL analyses on quality related traits like véraison (onset of berry ripening) and linalool content. Thus, the genetic map derived from our GBS data was proven to be suitable for the identification of trait-linked markers to give MAS access to wine quality potential. Additionally, our highly efficient GBS strategy was applied to selected genotypes of the extended crossing population (850 genotypes). (style Standard)

**Keywords:** GBS, haplotype-based markers, high-density genetic map, wine quality potential (style Standard)