P78 – Uncovering genetic and epigenetic factors as a source for trait variation in ‘Riesling’

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Abstract

The Department of Grapevine Breeding has a collection of almost 1200 ‘Riesling’ clones that encompass a broad range of trait characteristics, e.g. growth types or cluster architecture. While the phenotypic variation in this collection is well described the underlying genetic and epigenetic mechanisms remain largely unknown. Therefore, we are applying state-of-the-art sequencing technologies like Oxford Nanopore Sequencing to generate long DNA sequences that enable simultaneous scoring of genome-wide methylation patterns. This type of data is especially suited to detect differences between the two haplotypes of the diploid ‘Riesling’ genome so that a reference assembly can be generated that contains both haplotypes of all 19 chromosomes. The new ‘Riesling’ reference genome assembly will enable to study the variation between the two haplotypes within clones while also being able to assess the degree of differential mutation and methylation between clones. This information is then analysed with comprehensive phenotypic data collected from over more than a decade to unravel underlying causal polymorphisms and determine the relative importance of genetics vs. epigenetic for trait variation in ‘Riesling’. This information can then be used to facilitate the identification and selection of clones that are better adapted to certain vineyards, which is especially important in the light of rapidly changing environments due to climate change.

Keywords: genomics, epigenetics, ‘Riesling’, clonal variation, genome sequencing, genome assembly