

Genotyping columnar apples by rtGBS

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Columnar growth in apples is a natural mutation altering the growth to a compact, column-like phenotype, making them well-suited for cultivation in high-density orchards. Major working parts can be mechanized, like thinning and harvesting. The growth habit is caused by an 8.2 kb insertion on chromosome 10 by a not yet fully understood mechanism. Due to being a stable and dominant mutation it is readily available for breeding and half of the progeny have the insertion. However, the phenotype is quite variable suggesting that the columnar growth habit can be modulated by other factors.

In this project, we want to elucidate these interactions by the identification of QTLs correlating with phenotype variations. Ultimately molecular markers will be developed for these QTLs to accelerate the breeding of columnar cultivars via marker-assisted selection. This is especially advantageous in apple, as classical breeding is obstructed due to their long juvenile phase, their highly heterozygous genomes and their self-incompatibility. For the identification of such QTLs we will perform a genome wide association study (GWAS) correlating genotype data with growth habit phenotype data. Currently we are in the process of genotyping our progenies (two progenies with 300 individuals each) by random tagging Genotyping-by-Sequencing (rtGBS, Hilario et al., 2015). The method is based on reducing the genome complexity by restriction enzymes, sequencing these subsets, and thereby identifying single nucleotide polymorphisms (SNPs). In the upcoming winter the phenotypes will be evaluated. The correlation of both datasets is set for early 2018, followed by the development of markers for the identified QTLs. The final step will be the verification of the markers with a third, independent progeny.