# Mining data from sweet cherry resequencing

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Relatively cheap sequencing produces huge amount of sequencing data. Simultaneously, the available scripts, tools and programmes allow processing gained data sets in simple ways and obtain interesting results supporting fundamental and applied research as well as breeding. Thus, genome resequencing could be valuable resource for multiple analysis. However, the data processing is labouring and time consuming, extracting all available information is not possible.

In our study, we sequenced 235 genotypes from *Prunus avium* with minimal genome coverage 20X and called SNP markers. The main goal was to associate SNPs with phenotypes scored through five years and design markers that will be used for marker-assisted selection in breeding. Besides, both the resequencing and the first basic analysis open the door for other research goals. With a basic tools we was able to detected genes responsible for particular phenotypes, find the mis-assembly in the reference genome, defined the deletion which take out MYB genes responsible for red colour of fruit, detected duplicated accessions on the basis of DNA fingerprint, designed the SSR and SNP markers for genotyping. How can this data be used more?

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