

# Master thesis Bioinformatics

14.06.2019

## Sequencing and assembling the genome of *Beta macrocarpa*

Duration: 6 months

Starting date: 1.9.2019 (earlier or later starting dates possible)

*Beta macrocarpa* is a wild beet endemic to the Mediterranean area. So far, only few sequences from *B. macrocarpa* have been deposited in public databases. The species is fully interbreedable with cultivated beets (sugar beet, fodder beet, chard, table beet) and therefore an extremely valuable breeding resource, because it may be used to improve cultivated beets, e. g. by increasing stress tolerance. In our group, we have performed low-coverage sequencing of 33 different accession of *B. macrocarpa*, obtained from a public seed repository. These data will be the starting point of the Master thesis project. In particular, the project will comprise the following aspects:

- Estimation of the *B. macrocarpa* genome size based on sequencing data
- Identification of a *B. macrocarpa* genotype with minimal heterozygosity among 33 sequenced accessions
- Sequencing of the selected genotype to high coverage (Illumina, Oxford Nanopore), outsourced to a service provider
- Sequencing data quality control and filtering
- Sequencing read correction of nanopore data
- Assembly of the *B. macrocarpa* genome
- Quality assessment of the assembly (contiguity, completeness, accuracy)

The computational work will be carried out on high-performance Linux systems. Ideally, students should have experience with using Linux commands and working on sequencing data, e.g. as covered in the courses “Essentials for bioinformatics data analysis” and “Sequencing data analysis”. Nevertheless, if you are interested in the project please contact us irrespective of your current skills.

The working group “Bioinformatics” is located at the 6<sup>th</sup> floor of building MUG II. For information about the group, visit <http://seq.boku.ac.at>.

Contact: Ass.Prof. Dr. Juliane Dohm ([dohm@boku.ac.at](mailto:dohm@boku.ac.at))

### Literature:

1: Del Río ÁR, Minoche AE, Zwickl NF, Friedrich A, Liedtke S, Schmidt T, Himmelbauer H, Dohm JC. Genomes of the wild beets *Beta patula* and *Beta vulgaris* ssp. *maritima*. Plant J. 2019. [Epub ahead of print].

2: Dohm JC, Minoche AE, Holtgräwe D, Capella-Gutiérrez S, Zakrzewski F, Tafer H, Rupp O, Sörensen TR, Stracke R, Reinhardt R, Goesmann A, Kraft T, Schulz B, Stadler PF, Schmidt T, Gabaldón T, Lehrach H, Weisshaar B, Himmelbauer H. The genome of the recently domesticated crop plant sugar beet (*Beta vulgaris*). Nature. 2014.

