

Master thesis Bioinformatics

14.6.2019



Universität für Bodenkultur Wien
Department für Biotechnologie

Generation and characterisation of a new sugar beet genome assembly

Duration: 6 months

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

Today, a single reference genome per taxon is no longer considered as sufficient for obtaining a comprehensive understanding of a species' biology. In order to facilitate comparative genomics approaches, several genome assemblies of high quality are required from each species. For the genome of sugar beet (*Beta vulgaris*), a well-annotated reference genome is available. We have also calculated a genome assembly from another sugar beet genotype, dubbed KDH, based on Illumina sequencing data. Goal of this master thesis is to improve the KDH genome assembly by two different strategies: First, reference-assisted improvement and, second, improvement by using long-read Nanopore sequencing data. Specifically, this thesis project will comprise the following aspects:

- Assessing assembly metrics of the existing genome assembly of sugar beet (KDH)
- Reference-assisted re-assembly of the KDH genome based on the published high-quality reference assembly of sugar beet
- Quality control and correction of KDH nanopore sequencing data
- Use of corrected nanopore sequencing data for KDH assembly improvement
- Comparison and evaluation of the assembly improvement strategies

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 6th floor of building MUG II. For information about the group, visit <http://seq.boku.ac.at>.

Contact: Prof. Heinz Himmelbauer (heinz.himmelbauer@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.