

Identifying genes affecting individual metabolites in barley

Department and supervisor

Quantitative Genetics and Genomics

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Physical location of the project and students work

QGG-AU Aarhus

Project start

Flexible

Main subject area

Genes affecting individual metabolites in barley

Short project description

Individual metabolites in samples of barley have been measured by high quality LC-MS-MS methods. This method allow almost all metabolites in a sample to be measured. Individual metabolites are usually thought to be under the control of few genes related to the pathway(s) where the individual metabolite is involved.

The goal of the project is to identify individual genes or gene complexes that affect individual metabolites. The goal of the project is to gain a better understanding of the genetic control of metabolic pathway in barley.

The lines under study includes a sample of lines from the breeding program for spring barley at Nordic Seed. In addition to the metabolomic information each line also are genotyped with dense genotypic markers.

The project will provide the student with hands-on experience in identifying genes affecting a large set of traits (metabolites) in barley. This will include a good understanding of methods to identify genes as well as hands-on experience with large scale computing.

The dataset have not been analysed before and can form the basis for a M.Sc thesis and potentially also a paper in an international scientific journal.

Extent and type of project

60 ECTS: Experimental theses in which the student is responsible for planning, trial design and collection and analysis of his/her own original data

Additional information

Good understanding of basic quantitative genetics and an interest for conducting large scale computations.