

## Master thesis topics in wheat genetics and genomics

The following topics involve use of genomics tools in wheat, such as the fully annotated wheat genome reference sequence and associated resources to identify the genetic basis of important traits for agriculture. Here are a few examples of different master thesis topics that can be offered in our group. Please drop us an e-mail if you are interested:

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### **Identification of the yellow rust race specific and non-race specific resistance loci in Norwegian wheat breeding germplasm**



Yellow rust, also known as stripe rust, is one of the most yield-reducing wheat diseases globally. In recent years, yellow rust epidemics have re-appeared in Norway and some of the important wheat cultivars are susceptible to the new yellow rust races. We have a Nordic spring wheat association mapping (AM) panel “MASBASIS”, which is genotyped by the wheat 25K SNP chip and consists of current and historically important cultivars grown in Norway. In this project, the master student will use different yellow rust races for greenhouse inoculation on this MASBASIS AM panel and use the disease data for a Genome wide association study (GWAS).

The objectives of this project are to (1) evaluate the seedling resistance of the association panel to different yellow rust races; (2) identify both race-specific and non-race specific resistance loci by GWAS; and (3) compare the resistance loci detected in this GWAS study with previous published rust resistance genes in order to find novel or unique resistance loci in the Norwegian wheat germplasm.

### **Investigations of novel host-pathogen interactions for leaf blotch resistance in wheat**

Leaf blotch caused by *Parastagonospora nodorum* is a severe disease on wheat in Norway leading to grain shrivelling and reduced yield, and is a main cause of fungicide application. Necrotrophic pathogens like *P. nodorum* secrete effector molecules that are recognized by host receptors that trigger cell death in susceptible plants, providing dying tissue for infection by the pathogen. To study host-pathogen interactions, we infiltrate leaves with purified effectors or culture filtrates of the pathogen and evaluate whether plants are sensitive or insensitive to the pathogen effectors:



Left: Infiltration with culture filtrate with a needleless syringe. Right, top: *SnToxA*-insensitive leaf 5 dpi (days past inoculation). Right, bottom: Necrotic tissue developed in the infiltrated area in a *SnToxA*-sensitive leaf 5 dpi. Photos: Anja K. Ruud (left), Min Lin (right).

We have recently found that one of the effectors produced by *P. nodorum*, SnTox3, causes two different reaction types in Nordic spring wheats: either necrosis or chlorosis. It is currently not clear whether these two reaction types are caused by the same or different host sensitivity loci.

For this MSc thesis topic, we have developed a new mapping population segregating for the two reaction types, which needs to be screened for sensitivity to SnTox3 and evaluated for adult plant resistance in the field. The student will also be analyzing 25K SNP marker data in order to develop linkage maps and identify the genetic loci responsible for the different reaction types and disease scores to this important wheat disease.

### ***Fine-mapping and functional characterization of an important Fusarium head blight resistance gene in wheat***

Fusarium head blight (FHB) is an important wheat disease, as it not only reduces grain yield, but also leads to the contamination of the grains with harmful mycotoxins.

Based on field experiments, we have mapped one major FHB resistance QTL on the long arm of wheat chromosome 2D. In addition, we have also developed near-isogenic lines (NILs) and large fine-mapping populations to fine-map this FHB 2D QTL. The master student will do bioinformatic studies to narrow down the QTL interval based on mapping population data and the wheat reference genome sequence, followed by SNP marker genotyping and identifying recombinants for phenotyping. Once the candidate recombinants are selected, greenhouse inoculation with *Fusarium graminearum* will be done to more precisely locate the QTL and search for candidate genes. The final goal is to identify the mechanisms behind this important FHB resistance QTL on chromosome 2D.



### ***Functional characterization of an important waterlogging QTL in wheat.***

Through genome-wide association mapping (GWAS) we have recently identified an important QTL for waterlogging tolerance on chromosome 6A in Norwegian spring wheat. Here, we are looking for a student to do follow-up waterlogging experiments with selected cultivars and breeding lines both in the field and under controlled greenhouse conditions. The work will also involve some SNP marker genotyping and sequencing of candidate genes in the QTL region.