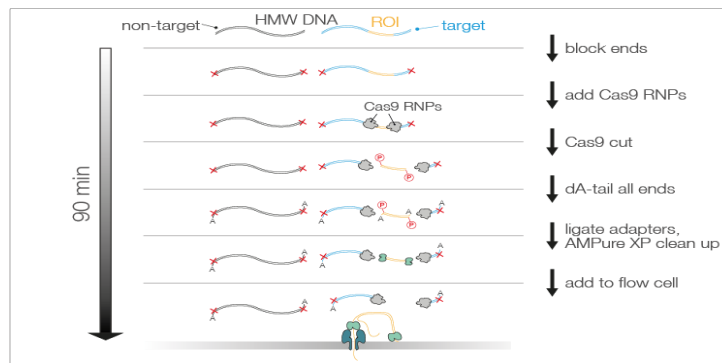


Topic/Title (English) Detecting haplotype-resolved single-nucleotide variants and structural variation in the targeted genes/alleles for freezing and drought genes using Cas9 targeted sequencing in *Lolium perenne*.



Summary

The climate change may provide the opportunity to expand the growing area of perennial ryegrass (*Lolium perenne* L.) in Baltic and Nordic countries. However, more use of perennial ryegrass during milder winters may paradoxically be compromised by the reduced winter survival due to lack of sufficient cold acclimation, accompanied by deacclimation. The predicted variability in rainfall, resulting in mild summer drought is another challenge. Thus, it is of vital importance to develop crops with high and stable good quality yields. Here in this study, we will be using 350 perennial ryegrass genotypes. Five candidate genes involved in freezing tolerance, and five genes, responsible for leaf growth under water deficit conditions will be used to characterize for haplotype-resolved single-nucleotide variants and structural variation in the targeted genes/alleles for freezing and drought genes. We will use Cas9 targeted sequence method using oxford nanopore minION sequencing, which generates long reads, enables rapid assembly of contigs, analysis of sequence diversity and identification of haplotypes. The functional SNPs identified will be used as key information for identification of the targets for CRISPR

You will be supervised and trained at the CIGENE lab, for DNA extractions, library preparation and sequencing. Further, you will also be trained in bioinformatics analysis regarding sequence data analysis. After this project, you would expect to be familiar with several bioinformatics methods in handling sequencing data, identifying SNPs.

Type of thesis work: laboratory work, literature study

Subject area Plant Science, Genome Science, Biology

Language thesis English

Master thesis & Credits 60 ETC

Project/company Dept. of plant Science, BIOVIT, NMBU

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