

Popular science summary

Oats is an important crop used to feed both humans and animals. Many people eat oat products daily, and regular consumption of oat beta-glucans is known to lower the risk of heart disease. In spite of this, the full genetic sequence of oats has been unknown until recently, and a comprehensive overview of oat genes has been missing. This has made life harder for both researchers and plant breeders. In order to ensure that people have food to eat, we need to be able to improve our crops and make them more resilient to a changing climate while minimizing their climate impacts.

The first part of this thesis focuses on the creation of a comprehensive list of oat genes and how we identified where in the oat genetic sequence they are located. Not only does this list identify the location of these genes, but it also provides an idea about gene function, and a way of relating oat genes to similar genes in other species. This will help researchers use what is known about other plants when doing research on oats going forward. We used this connection to genes in other species, along with a barley gene known to be involved in resistance against *Fusarium* infections, to identify oat genes with similar function.

Another part of the thesis focuses on so-called 'genetic markers', short pieces of genetic sequence with some known properties. When studying large populations, or when the full genetic sequence is not known, we can get the relative position of markers, and this may help us identify approximate locations of genetic regions controlling different plant traits. This thesis looks at different ways of connecting existing markers to the oat genetic sequence, how they may be visualized, and how we can combine them with information about oat genes. The combination of previous research identifying genetic regions controlling traits, and new lists of oat genes open doors for researchers and plant breeders to understand which gene variants cause different traits, study the exact function of these variants further, or select for variants that are beneficial.

Not only does this research allow us to connect to what has already been studied, but it also lets us study the genes underlying traits seen in mutant oats. By crossing mutants with non-mutant oats and looking at which parts of the genetic sequence are identical among siblings that share a trait, we were able to identify the function of two genes in oats, relating to oat surface wax, and oat hormones and development respectively. Plant surface wax helps plants conserve water and also ensures that water does not stick to the plant surface, and may also play a role in defense against pathogens. Plant hormones control innumerable aspects of plant development, and understanding this interplay may help produce oats with higher yields or improved stress resistance.

This thesis provides a look at how to find genes in plants with large genetic sequence, as well as a first peek of what researchers will be able to achieve with access to the oat genes and genetic sequence. Hopefully they will prove a valuable resource to researchers and breeders alike, and hopefully it will let them create better oats, helping to ensure that people have food to eat in spite of the ongoing climate crisis.