Plant Quantitative Genetics

SLU, Uppsala, 25 March – 5 April 2019

I recently spent two weeks attending the Plant Quantitiative Genetics course instructed by Bruce Walsh, and held at SLU Uppsala. There was a lot of content covered and a fantastic group of people gathered, in this very brief time period. The content ranged from sire selection in cattle, to phenotype expression in second generation offspring, to gene linkage and inheritance. A good thing to note with a subject like genetics, is it is very broad, and in this case the attendees had a diverse range of projects and topics which all fit within this 'Plant Quantitative Genetics' subject. The course covered what I had hoped it would, and exceeded my expectations in terms of subject depth.

SLU has a large group of knowledgeable geneticists and PhD students, and some of them can be seen in this class photo. Many of them are using whole genome sequencing and looking at all the bases along the chromosomes for a particular species. They are using very advanced methods, new technologies, and complicated analysis in their projects, often to try to identify the genes responsible for trait expression. I have enjoyed hearing about their work, and the instructor covered the main principles behind this sort of analysis.

Bruce managed to mention a wide range of technologies and principles which underlie how genetics influences the phenotype (visual appearance) for an individual. It is beyond my current project scope to do any form of DNA analysis, although chromosome number is a good way to differentiate birch species and hybrids. This information could help during my later project looking at birch which has regenerated naturally, if chromosome number could be gained reliably, quickly and cheaply. I could also take samples for any trees which are difficult to identify and have them lab checked. This course has definitely given me something to think about, but with 28 and 56 chromosomes in Silver birch and Downy birch respectively, it is very unlikely I will manage to do something like genome sequencing.

I still need to use the software ASReml to estimate the heritability of acoustic velocity (AV) measurements for some of Skogforsk's silver birch families. This course has included some aspects of accounting for environmental influence on how an individual looks, which will help with this part of my work. I have the parent information, so should now be able to make a coefficient of co-ancestry for all of the trees measured and try to get information about the generations before, for a more detailed pedigree.

The course also included dealing with unbalanced data sets, and I will use mixed models and BLUP for estimating the effects of parent (m and f), site and phenotype, on AV. It has been useful to have some key assumptions listed to help decide when a particular test is better than another, and the course showed many cases where a certain model will be more accurate or more flexible than others. The participants were however constantly reminded that the 'best' way to model and test something depend on what you are aiming to get out at the end. Where precision can be sacrificed or is less important, there may be a more robust test, or a simpler test, which may be indicative.

I hope to do something similar to the initial plan, but feel like after taking this course I have a better understanding of why certain decisions have been made. My Skogforsk supervisor had already shown me the method for data analysis, but I was getting stuck on how the resulting numbers were obtained and what the alternatives were. This course went through a number of examples and showed how values could be derived and inferred from an initial data set. I definitely will do some more indepth reading, but currently plan to see what further family information is available from Skogforsk and start building my mixed model.

Cheers again! The course has been interesting, very rapid paced, and in-depth.