Host genotype influence methane emission, feed efficiency and rumen metagenomics

One of the greatest challenges we are facing is to generate enough food for a growing world population whilst decreasing the environmental footprint of the increased production. If we do not meet this challenge we will see increased political instability in numerous countries and/or migration from areas where it will no longer be possible to live due to e.g. drought or flood. Dairy cattle production both contribute to food production through milk and meat and environmental impact through methane and nitrogen.

A part of the solution is to use genetic selection both to decrease environmental impact but also to improve efficiency. Phenomics strategies have been used to investigate this since these traits are not currently under selection. We have been able to generate the largest dataset on individual methane measurements in dairy cattle in the world. Methane is produced by microbes in the rumen of the cow and therefore it is needed to make large scale rumen sampling to investigate host genotype-microbiome interaction. We have used 16s RNA methodology to estimate abundance of bacteria as well as archaea which is the microbe producing the majority of methane in the rumen. On the data we have generated we have done genome wide association studies, genomic prediction and estimated additive genetic and genomic parameters.

In this presentation I will show that i) methane emission can be measured in large scale in dairy cattle and it is under genetic control, ii) rumen microbial composition is influenced by host genotype, iii) it is possible to select for improved efficiency in dairy cattle.