The rumen microbiota is modified in lambs divergently selected for residual feed intake

Quentin Le Graverand, Flavie Tortereau, Annabelle Meynadier, Didier Marcon, Christel Marie- Etancelin

The rumen microbiota is modified in lambs divergently selected for residual feed intake

Quentin Le Graverand*, Flavie Tortereau[1], Annabelle Meynadier[1], Didier Marcon[2], Christel Marie-Etancelin[1]

*quentin.le-graverand@inrae.fr

[1]GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326 Castanet Tolosan, France

[2]INRAE, Experimental Unit P3R, F-18390 Osmoy, France

The ruminal microbiota plays a central role in the nutrition of its host. Significant links between the rumen bacteria abundances and host performances (growth or feed efficiency) have been demonstrated in cattle, but few is known in sheep. Residual feed intake (RFI) is commonly used as a criterion to improve feed efficiency. At the INRAE P3R, divergent lines on RFI are being developed in the Romane meat sheep breed: individuals belong either to the RFI+ (inefficient) or RFI- (efficient) line. We proposed to investigate the ruminal population (bacteria, archaea, protozoa and fungi) of 277 lambs belonging to the 2nd (in 2018) or 3rd (in 2019 and 2020) generations of RFI selection. A first rumen fluid sample (C-sample) was taken at 4-5 months of age, after 6 weeks of feed efficiency control under a concentrate diet. Then, 167 out of these lambs were tested during 6 weeks under a forage-based diet (2/3 forage + 1/3 concentrate), after which a second sample of rumen fluid was taken (F-sample). During each of the 2 periods of control, feed intake, body weights and body composition traits were recorded. After DNA amplification, the ruminal microbiota was analysed by sequencing the 16s rRNA gene for bacteria and archaea, and the 18s rRNA gene for protozoa and fungi. Sequences were analysed with the FROGS pipeline to obtain relative abundances of OTUs (in proportion of total sequences per sample) which were then labelled according to phylum, family and genus levels.

Due to the huge impact of diet type, C-samples and F-samples were considered separately in the statistical analyses. After a CLR transformation of the OTUs abundances to consider their compositional nature, ANOVAs were performed with a covariate, the age at sampling and the fixed effects of the year, the pen and the sequencing depth. Finally, discriminant analyses such as sPLS-DA (with MixOmics R package) were performed with the divergent line as the discriminant factor. As expected, more OTUs were identified in F-samples than in C-samples. Differences in the composition of the ruminal microbiota were highlighted between divergent lines under the different diets.