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The ruminal microbiota plays a central role in the nutrition of its host, directly affecting milk production and animal health. There are no such studies in sheep that describes this link, thus the aim of our study was to determine differences in ruminal bacteria between divergent lines for somatic cells score and milk production persistency of Lacaune ewes.

We had rumen fluid samples of 700 dairy Lacaune ewes raised at the INRAE Experimental Farm of La Fage sampling between 2015 and 2019. These ewes were adult animals, mostly in their second lactation, and belonged to two divergent lines selected for somatic cells score (SCS) or milk production persistency during lactation (PERS). The phenotypes of ewes obtained from milk recording controls over the five years were somatic cells count, milk production, milk fat content, milk protein content and milk dry matter content. Ruminal metagenome was sequenced using 16s rRNA gene with Illumina Miseq technology. We analyzed microbiota sequences with FROGS pipeline to obtain relative abundances of OTUs (in proportion of total sequences per sample) and R Phyloseq package to estimate biodiversity indices. Thereafter we grouped OTUs according to phylum, family and genus levels.

Fixed effects would be included in the variance analyses were the lines (SCC+, SCC-, PERS+, PERS-), run sequencing effect, date of rumen fluid sampling, lactation number (2 up to 7 lactations), stage of lactation (45 to 133 DIM) and litter size (1, 2 or more lambs), moreover we tested also suckling method of the ewe (maternal or artificial). ANOVA of α-diversity and relative abundance of OTUs or taxa at different taxonomic levels were estimated by including the significant effects. Further, a discriminant analysis (with sPLS-DA) was applied on OTUs with divergent lines as discriminant factor, and some links were researched between phenotypes and OTUs (with sPLS), using MixOmics R-package.

With these analyses, we found several links between ewes' performances and rumen bacteria and we characterized the ruminal microbiota of divergent lines.