



HAL
open science

Genetic determinism of dairy sheep ruminal microbiota

Christel Marie-Etancelin, Beatrice Gabinaud, Géraldine Pascal, Regis Tomas, Jean Marie Menras, Francis Enjalbert, Charlotte Allain, Helene Larroque, Rachel Rupp, Annabelle Meynadier

► To cite this version:

Christel Marie-Etancelin, Beatrice Gabinaud, Géraldine Pascal, Regis Tomas, Jean Marie Menras, et al.. Genetic determinism of dairy sheep ruminal microbiota. 69. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2018, Dubrovnik, Croatia. 705 p. hal-02737262

HAL Id: hal-02737262

<https://hal.inrae.fr/hal-02737262v1>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Genetic determinism of dairy sheep ruminal microbiota

C. Marie-Etancelin¹, B. Gabinaud¹, G. Pascal¹, R. Tomas², J.M. Menras², F. Enjalbert¹, C. Allain¹, H. Larroque¹, R. Rupp¹ and A. Meynadier¹.

¹ GenPhySE, INRA, INPT, ENVT, Université de Toulouse, Castanet-Tolosan, France.

² INRA, Experimental Unit of La Fage, Saint-Jean et Saint-Paul, France.

The microbiota of herbivorous animals plays a central role in the nutrition of its host, directly affecting his health and his ability to produce. Very few publications reported results concerning the impact of host genetics on the composition of ruminal microbiota (Rowe et al., 2015). Thus, we proposed to study the genetic determinism of bacterial relative abundances of sheep rumen microbiota.

369 dairy Lacaune ewes raised indoor at the INRA Experimental Farm of La Fage, had a sampling of their rumen fluid done. These ewes were adult animals, fed with a 93% hay-silage based diet and belonged to 4 different lines (lines divergently selected on somatic cells count or on milk persistency). Ruminal metagenome were sequenced using 16s rRNA gene with Illumina Miseq technology. Bioinformatics analysis of the microbiota sequences were implemented with FROGS pipeline to obtain relative abundances of bacteria (Escudié et al., 2017) and R Phyloseq package to estimate biodiversity indices. Fixed effects included in the genetic analyses of relative abundances were the “lines”, the “parity” and the “day of sampling” effects. Heritability estimates of the square root of relative abundances were computed in single trait using the VCE 6.0 software (Neumaier and Groeneveld, 1998).

FROGS pipeline allowed clustering the 4,944,307 informative sequences into 2,135 OTUs, which represented 247 bacteria taxas (140 genera, 50 families, 31 orders, 17 classes and 9 phyla). Significant differences between lines were observed: 4 bacteria generas have abundancies differences according to CCS lines (*Olsenella*, *Prevotella 1*, *Prevotellaceae Gaba1*, *Syntrophococcus* with always higher values for CCS+) and 4 others according to PERS lines (*Coprococcus 1*, *Olsenella*, *Succonivibrionaceae U2*, *Syntrophococcus*). At the genera scale, heritabilities estimates ranged from 0.00 to 0.49 with a standard error of 0.11 on average: 22% of genera had heritabilities higher than 0.1, which is lower than Estellé et al. (2015) on Large White (50% genera with $h^2 > 0.1$). The most heritable genera ($h^2 > 0.25$) were *RuminococcaceaeUCG002*, *Lachnospira*, *Atopobium* and *Oscillospira* which also were taxa with low abundances.