



Rumen bacteria in sheep : first evidence of host's genetic control

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► To cite this version:

Annabelle Meynadier, Beatrice Gabinaud, Regis Tomas, Jean Marie Menras, Géraldine Pascal, et al.. Rumen bacteria in sheep : first evidence of host's genetic control. 10. International Symposium on the Nutrition of Herbivores (ISNH10), Sep 2018, Clermont-Ferrand, France. Cambridge University Press, *Advances in Animal Biosciences*, 9 (3), 2018, 10th. International Symposium on the Nutrition of Herbivores (ISNH10). hal-02737229

HAL Id: hal-02737229

<https://hal.inrae.fr/hal-02737229>

Submitted on 2 Jun 2020

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Rumen bacteria in sheep: first evidence of host's genetic control

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Take home Message: Some low-frequency bacterial genera in rumen may be modulated by sheep genes.

Introduction

The microbiota of herbivorous animals plays a central role in the nutrition of its host: it directly affects his health and his ability to produce both products of interest for the human diet and undesirable products such as methane. Studies on ruminal microbiota point out a significant effect of the “host” factor, but very few publications reported results concerning the impact of host genetics on the composition of ruminal microbiota. On sheep, Rowe et al. (2015) showed that the first component of a principal component analysis of the ruminal bacterial community was heritable (h^2 of 0.24). Thus, we proposed to study the genetic determinism of bacterial relative abundances of sheep rumen microbiota.

Material and methods

In 2015 and 2016, 369 dairy Lacaune ewes raised indoor at the INRA Experimental Farm of La Fage, had a sampling of their rumen fluid done thanks to gastroesophageal tube and a vacuum pump on 4 different days. These ewes were adult animals (at least 2nd lambing) at about 3 month of milking and belonged to 4 different lines (lines divergently selected on somatic cells count or on milk persistency). They were fed with a 93% hay-silage based diet. Ruminal metagenome were sequenced using 16s rRNA gene with Illumina Miseq technology at the Genomic Platform (INRA, Toulouse, France). Bio-informatic analysis of the microbiota sequences were implemented with FROGS pipeline to obtain relative abundances of bacteria (Escudié et al., 2017). 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).

Results & Discussion

FROGS pipeline allowed clustering the 4,944,307 informative sequences into 2,135 OTUs, which represented 247 bacteria taxa: 140 different genera, belonging to 50 families, 31 orders, 17 classes and 9 phyla (Figure 1). The main representative bacteria phyla were *Bacteroidetes* and *Firmicutes* (50.8 and 38.0%, resp.). At the phylum scale, heritabilities estimates ranged from 0 (for *Bacteroidetes* and *Firmicutes*) to 0.17 (for *Spirochaetae*). At the genera scale, heritabilities values varied from 0.00 to 0.49 with a standard error of 0.11 on average: 22% of genera had heritabilities higher than 0.1 (Figure 2). Estellé et al. (2015) on Large White obtained 50% of the genera with heritabilities higher than 0.1, but on 63 selected bacterial genera. The most heritable genera ($h^2 > 0.25$) with coherent data distributions were *Ruminococcaceae* UCG002, *Lachnospira*, *Atopobium* and *Oscillospira* which also were taxa with low abundances.

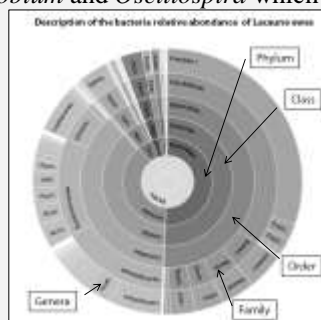


Figure 1

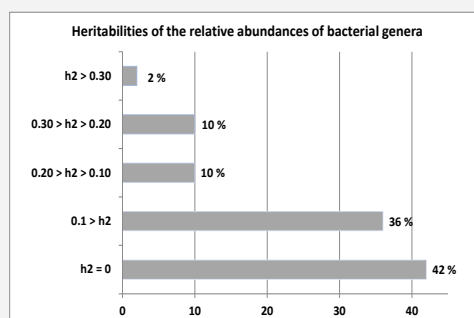


Figure 2

Conclusion

We confirm that bacterial abundances are, for some of them, heritable. Highly represented bacterial taxa that aggregated many subgroups appeared to be weakly heritable, but some quantitatively minor taxa, that could shape ruminal function, are partly controlled by host genetics.

Acknowledgements

This work was supported by grants from INRA-PHASE and INRA-GA divisions.

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