Ruminal bacteria heritabilities: Which is the impact of different data processing ?

Guillermo Martinez Boggio, Annabelle Meynadier, Charlotte Allain, Christel Marie-Etancelin

▶ To cite this version:

> Guillermo Martinez Boggio, Annabelle Meynadier, Charlotte Allain, Christel Marie-Etancelin. Ruminal bacteria heritabilities: Which is the impact of different data processing ?. EAAP 2021, Aug 2021, Davos, Switzerland. hal-03480858

HAL Id: hal-03480858
https://hal.inrae.fr/hal-03480858v1

Submitted on 14 Dec 2021

Ruminal bacteria heritabilities:
Which is the impact of different data processing ?

Guillermo Martinez Boggio[1], Annabelle Meynadier[1], Charlotte Allain[2], Christel Marie-Etancelin[1]
[1]GenPhySE, Université de Toulouse, INRAE, ENVT, France. [2]INRAE, Experimental Unit of La Fage, France

guillermo.martinez-boggio@inrae.fr

Introduction and objective

Microbiome data is **compositional**: the information is found in the operational taxonomic unit (OTU) **ratios**.

As high-dimensional data with zeros, it is necessary to replace the zeros, and apply value transformation.

To compare **data processing methods** in terms of **heritability** estimates (h^2).

Materials and methods

Rumen samples of 795 Lacaune ewes
Metabarcoding 16s rRNA gene

Table 1. *Data processing methods to be compare.*

	GBM	C1	Z01
CLR	GBM-CLR	C1-CLR	Z01-CLR
Log	GBM-Log	C1-Log	Z01-Log

Zeros replacement:
GBM= Geometric Bayesian Method
C1= Add constant equal 1
Z01= Replace only zeros with 0.001

Data transformation:
CLR= Centred Log-Ratio transformation
Log= Logarithm transformation

Heritability estimates*:

$$y = Xb + Za + e$$

y: OTU abundances processed with each of the 6 methods.
b: fixed effects lactation stage, litter size, year, number of lactation, sequencing run, sampling order and total nb. sequences.
a: random animal effect ~ $N(0, \sigma^2_a A)$.
e: residual ~ $N(0,\sigma^2_e I)$.

**The threshold of significance obtained by phenotype-animal permutation*

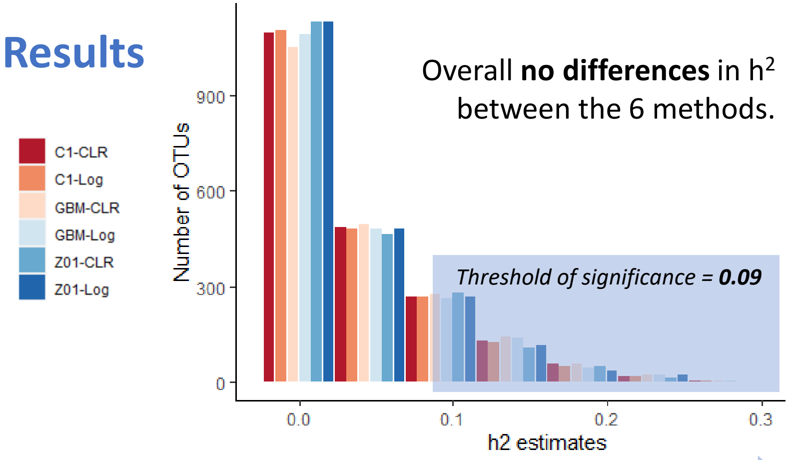
Conclusions

Ruminal bacteria h^2 are affected by data processing.

Zeros replacement impact the most the number of heritable OTUs.

GBM leads to less difference between the two data transformation.

Results



Overall **no differences** in h^2 between the 6 methods.

But, the number of **heritable OTUs** defined by the methods were **variable**.

Table 2. *Number of heritable* OTUs by processing data method.*

	GBM	C1	Z01
CLR	**326**	**293**	**249**
Log	**294**	**274**	**254**

GBM > C1 > Z01

By **replacing only the zeros** we obtain lower number of heritable OTUs.

% OTUs in common between CLR and Log

78% **72%**

Using **GBM** the differences between CLR and Log are lesser than with C1.