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► 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

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



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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

Conclusions

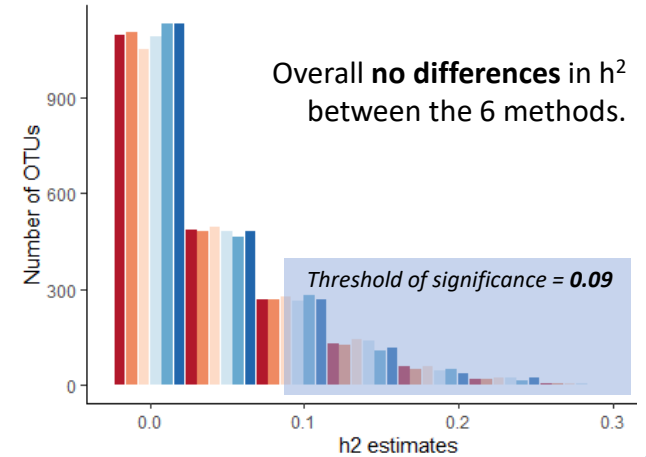
Ruminal bacteria h^2 are affected by data processing.

Zeros replacement impact the most the number of heritable OTUs.

GBM leads to less difference between the two data transformation.

Results

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



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.

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 $\sim N(0, \sigma_a^2 A)$.
e: residual $\sim N(0, \sigma_e^2 I)$.

*The threshold of significance obtained by phenotype-animal permutation