



# Microbiota and productive performance in ruminants

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21 November 2024

Holoruminant Stakeholder Event  
IRTA, Caldes de Montbui

# Why microbiome?

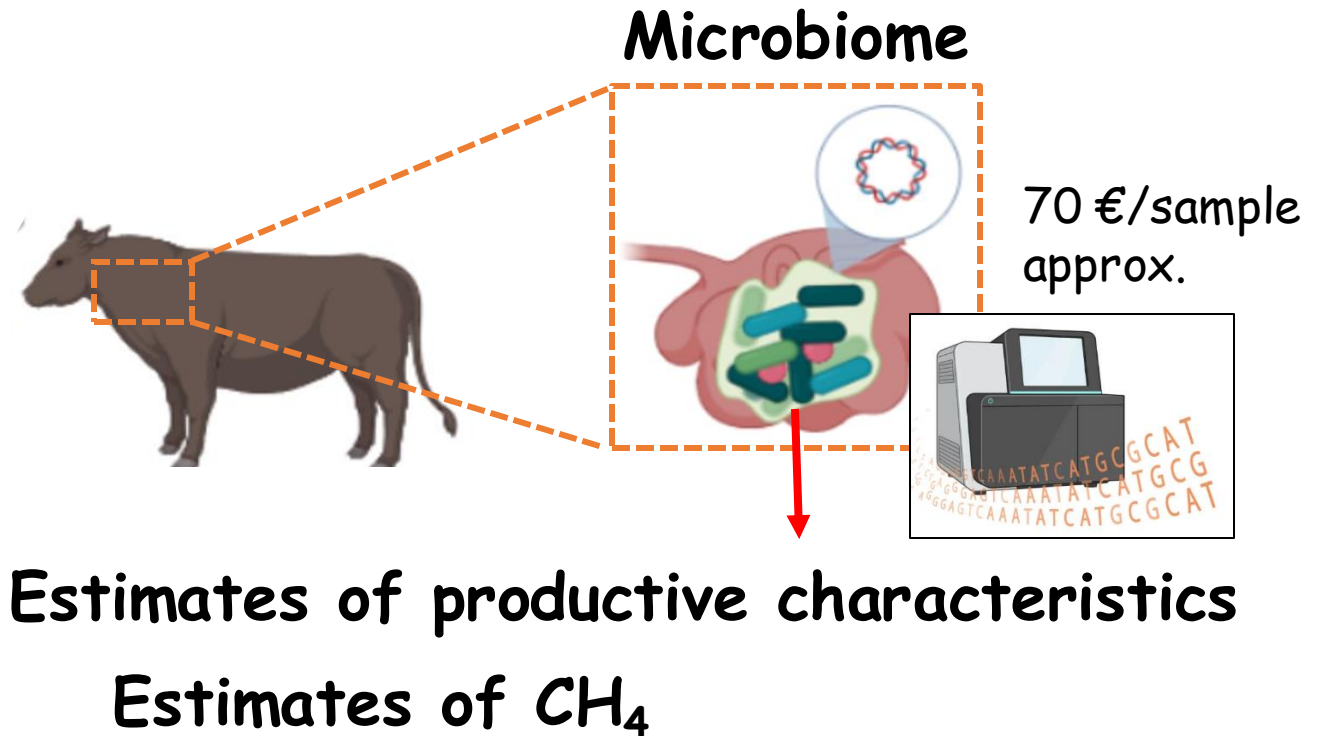
- Cattle obtain ~70% of their energy requirements from VFA produced by microbial fermentation.
- Between 50% and 80% of their amino acid req. from microbial proteins.
- Microbial metabolites -> regulators in the gut-brain and gut-liver axes, which can influence body composition, bone density, feeding behaviour, etc.
- Variations in microbial composition -> production, efficiency, emissions and health

# Objective 1: prediction of production trait phenotypes and microbiome data

## Practical utility:

1) Possibility of intervening on the microbiome to improve production efficiency

2) Proxies for phenotypes that are more costly to measure (in money and time): application in breeding programmes.



# What information do we need?

## Information on animals

### Factors that may affect phenotypes/microbiome

- Diet
- Race
- Type of holding



## Phenotype

- $S$
- ADG
- DMI
- IC
- $CH_4$



## Metagenotypes

- Rumen content samples (slaughterhouse)
- Illumina Hi-seq4000 DNA Sequencing
- Data processing
- Data transformation



Core Microbiome:  
3000 microbial gene abundances + 1500  
microbial genus abundances present in >70%  
samples

# What predictive accuracy do we expect?

**TABLE 1** | Percentage of variation in each trait explained by the microbial genes identified in the partial least squares (PLS).

Trait	No. factors	Percent variation accounted for by partial least squares factors			
		Model effects		Dependent variables	
		Current	Total	Current	Total
FCR	1	41.59	41.59	35.46	35.46
	2	6.35	47.94	21.19	56.65
	3	7.57	55.51	6.72	63.37
ADG	1	39.42	39.42	49.26	49.26
	2	9.60	49.02	11.47	60.73
	3	7.97	56.99	4.67	65.40
RFI	1	24.04	24.04	44.32	44.32
	2	13.95	37.99	16.80	61.12
	3	16.72	54.71	4.52	65.63
DFI	1	28.98	28.98	44.94	44.94
	2	21.25	50.23	19.94	64.88
	3	7.86	58.09	8.05	72.93

The number of factors refers to the number of latent variables in which the total number of microbial genes (independent variables) were projected in the PLS procedure, and each factor accounts for a portion of the total explained variation. The "Model Effects" columns refer to the percent variability of the independent variables matrix that relates to the respective percent variability presented in the "Dependent Variables" columns. The "Current" columns present values for each extracted factor individually, and the "Total" columns present the subtotal variation. The cells colored in gray contain the values of percent variation explained by the three latent variables for each trait. FCR, feed conversion ratio; ADG, average daily gain; RFI, residual feed intake; DFI, daily feed intake.

$R^2 \sim 0.6 - 0.7$   
ADG, IC, RFI, DFI

We can use the microbiome to predict various traits ...

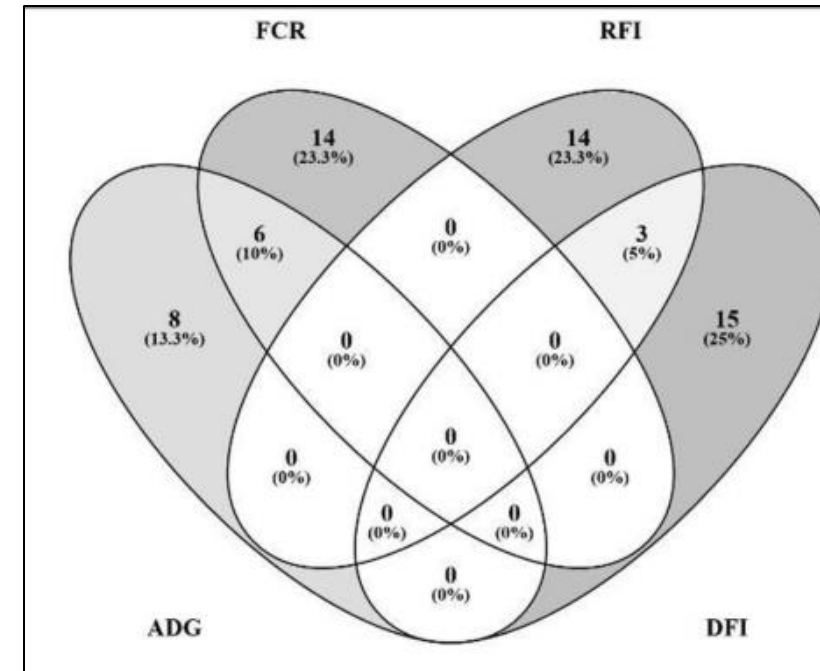
## Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle

Joana Lima<sup>1\*</sup>, Marc D. Auffret<sup>1</sup>, Robert D. Stewart<sup>2</sup>, Richard J. Dewhurst<sup>1</sup>, Carol-Anne Duthie<sup>1</sup>, Timothy J. Snelling<sup>2</sup>, Alan W. Walker<sup>2</sup>, Tom C. Freeman<sup>2\*</sup>, Mick Watson<sup>2</sup> and Rainer Roehe<sup>1\*</sup>

OPEN ACCESS

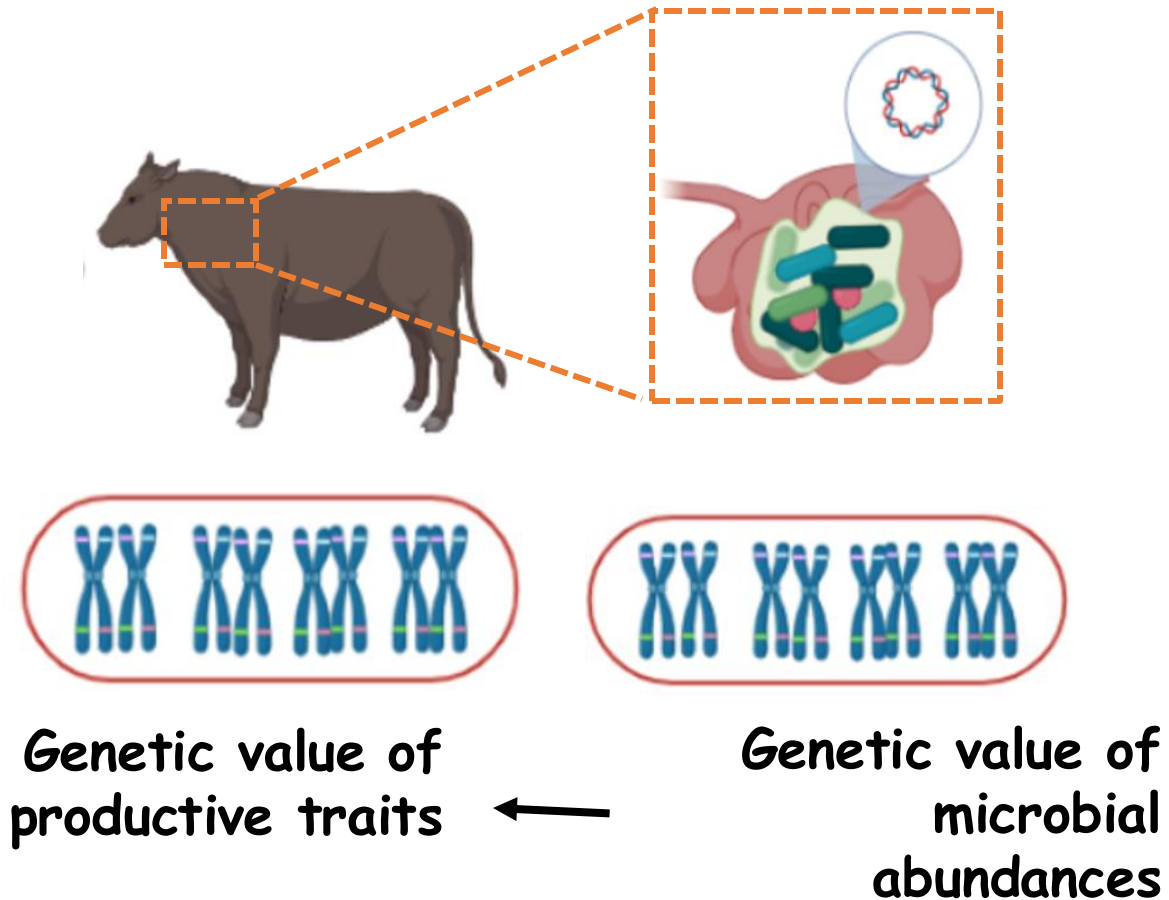
<sup>1</sup> Beef and Sheep Research Centre, Future Farming Systems Group, Scotland's Rural College, Edinburgh, United Kingdom, <sup>2</sup> Division of Genetics and Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom, Edited by: Robert J. Schaefer, <sup>3</sup> The Rowett Institute, University of Aberdeen, Aberdeen, United Kingdom

## Overlap between microbial genes chosen as predictors



... although the microbial predictors in each case are different.

# Objective 2: prediction of breeding values for productive traits with microbiome data



**Practicality: speeding up the response to screening**

**Hypothesis:**

1) Is the microbiome heritable  $h^2$ ?

2) Is there a genetic correlation between microbial abundances and productive traits?

3) Can we use microbial information to estimate breeding values for productive traits?

# What information do we need?

## Information on animals

### Factors that may affect phenotypes/microbiome

- Diet
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## Phenotyp

- ADG
- IMD
- IC
- CH<sub>4</sub>



## Metagenotype

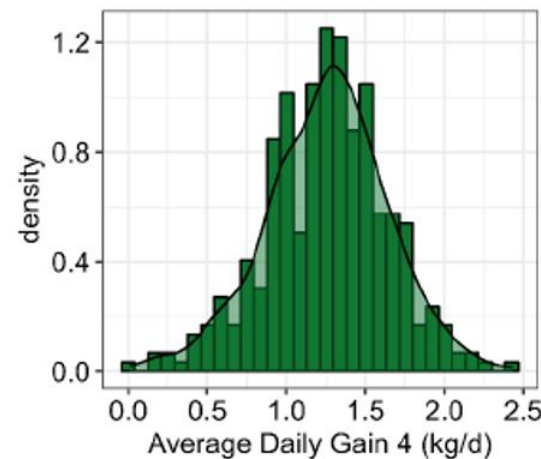
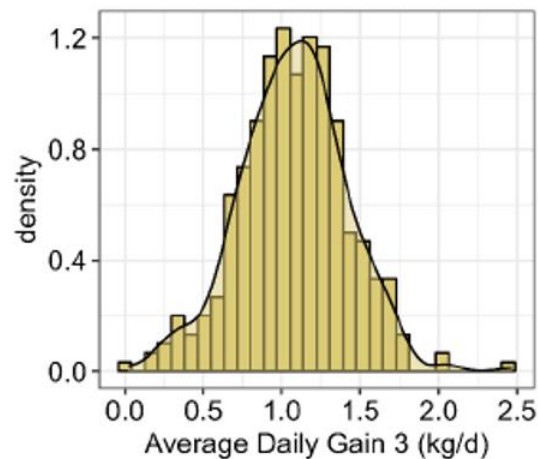
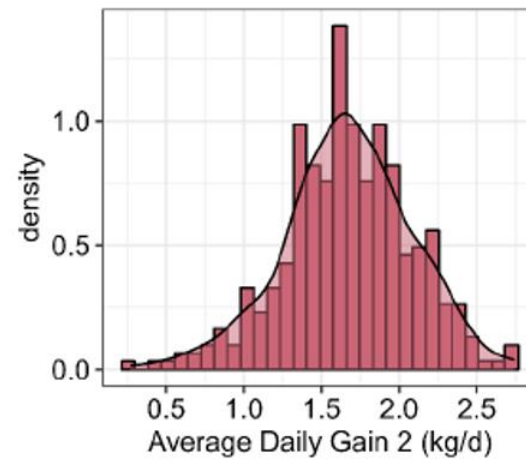
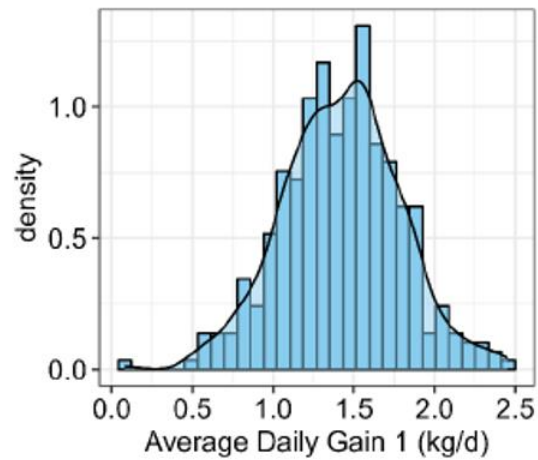
- Rumen content samples (slaughterhouse)
- Illumina Hi-seq4000 DNA Sequencing
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## Genotypes / Pedigree

- BovineSNP50k Chip

# Example: ADG at different stages in beef cattle

## Los fenotipos: ADG mensual





## Genetic parameters

Heritabilities (diag), genomic (upp-diag) and environmental (low-diag) correlations

X	ADG1	ADG2	ADG3	ADG4
ADG1	0.31	0.27	0.39	0.07
ADG2	-0.11	0.27	0.13	0.20
ADG3	-0.12	-0.17	0.29	-0.13
ADG4	0.05	0.05	-0.09	0.27

Research Article | [Open access](#) | Published: 15 March 2024

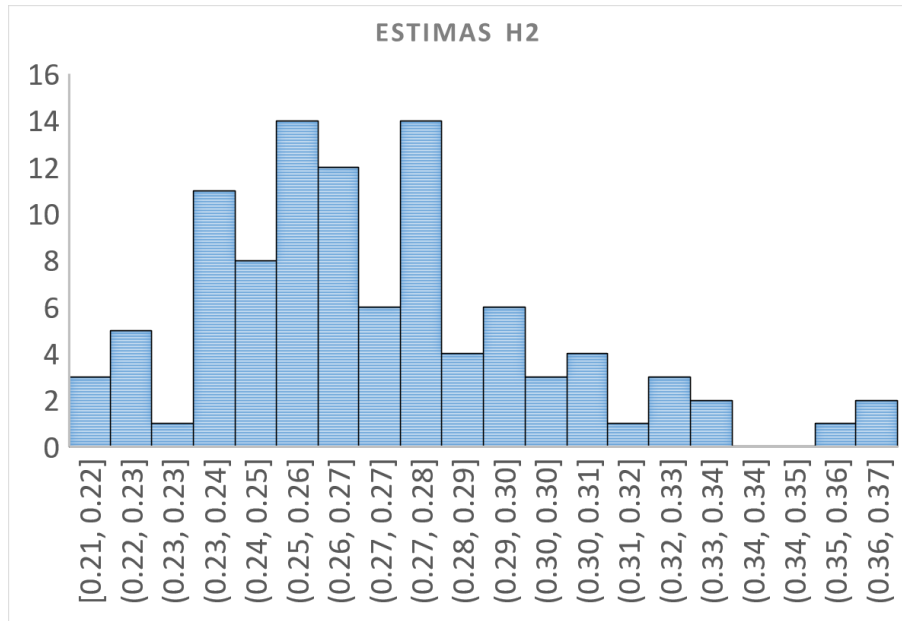
**Including microbiome information in a multi-trait genomic evaluation: a case study on longitudinal growth performance in beef cattle**

Marina Martínez-Álvaro , Jennifer Mattock, Óscar González-Recio, Alejandro Saborío-Montero, Ziqing Weng, Joana Lima, Carol-Anne Duthie, Richard Dewhurst, Matthew A. Cleveland, Mick Watson & Rainer Roehe 

*Genetics Selection Evolution* 56, Article number: 19 (2024) | [Cite this article](#)

# Calculation of $h^2$ and $r_g$ of microbial traits

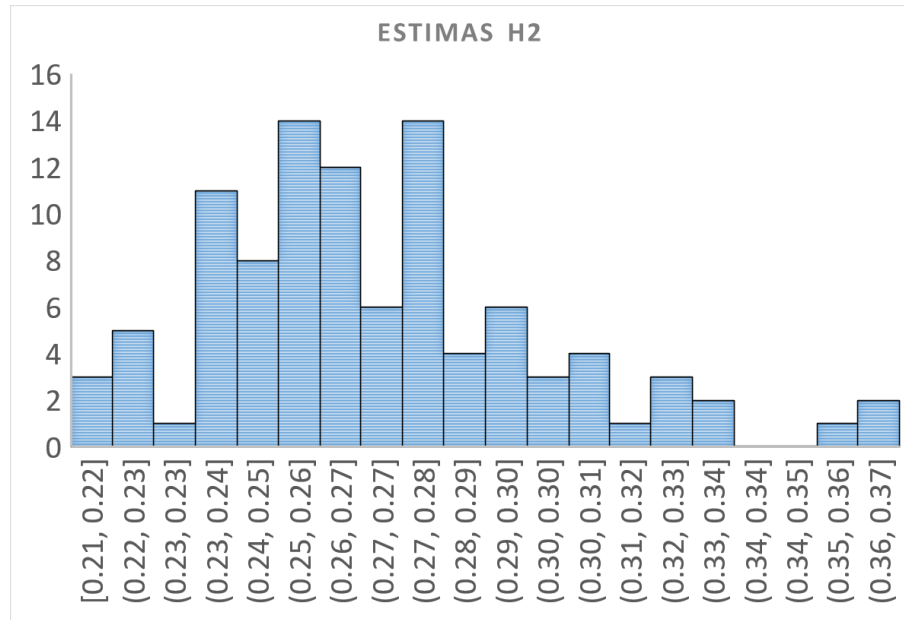
## Heredabilities



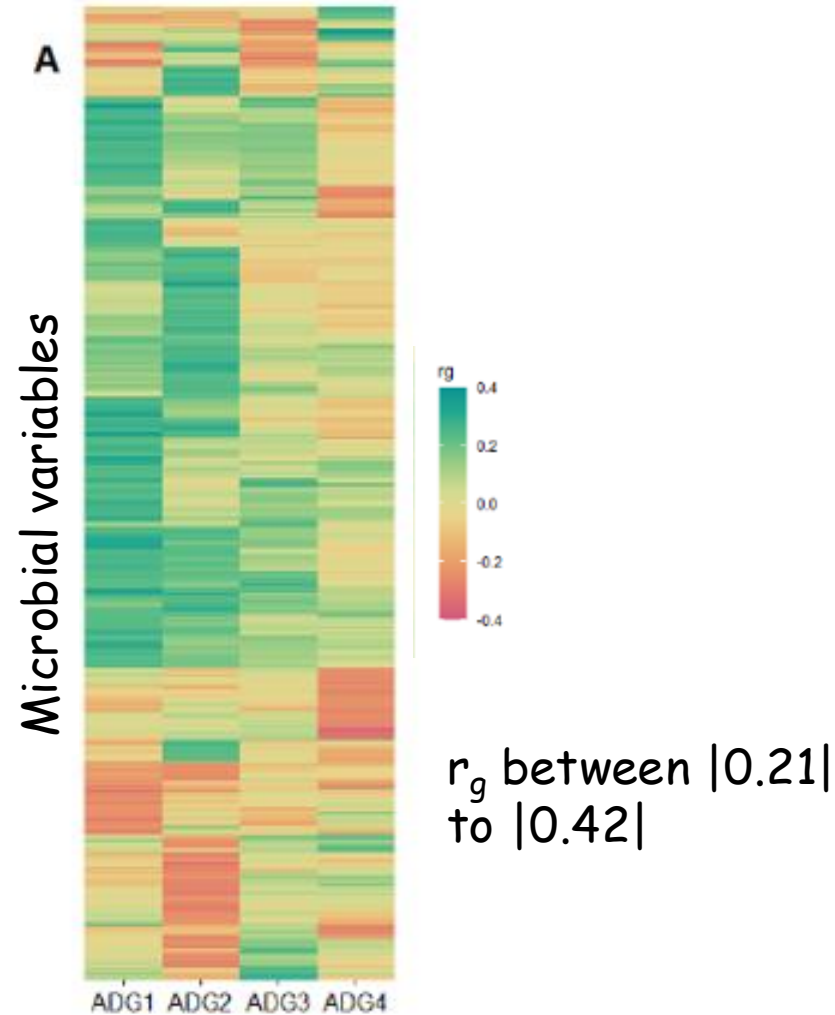
$h^2$  from 0.19 to 0.44

# Calculation of $h^2$ and $r_g$ of microbial traits

## Heredabilities

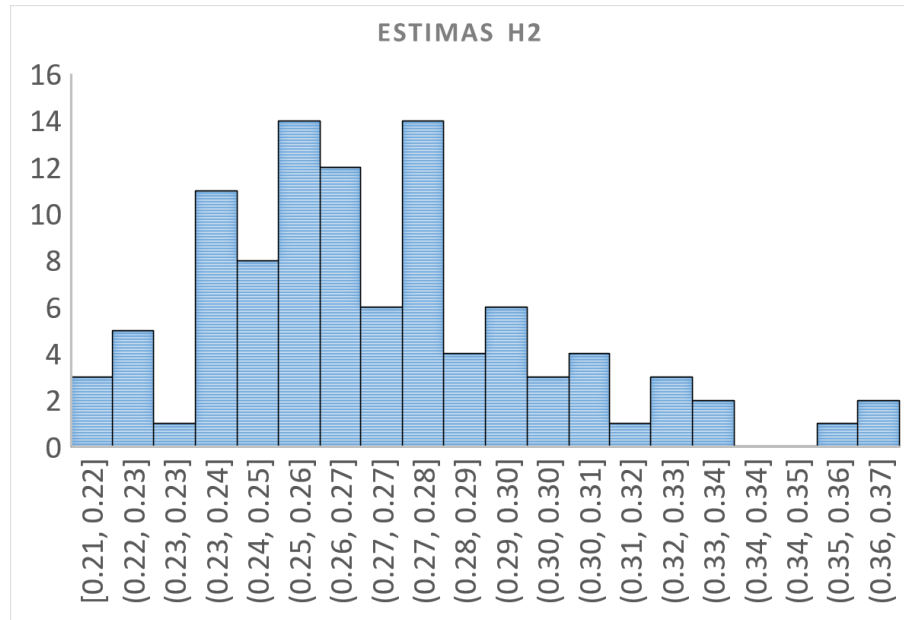


## Genetic correlations between microbial variables and ADGs



# Calculation of $h^2$ and $r_g$ of microbial traits

## Heredabilities



## Genetic correlations between microbial variables and ADGs

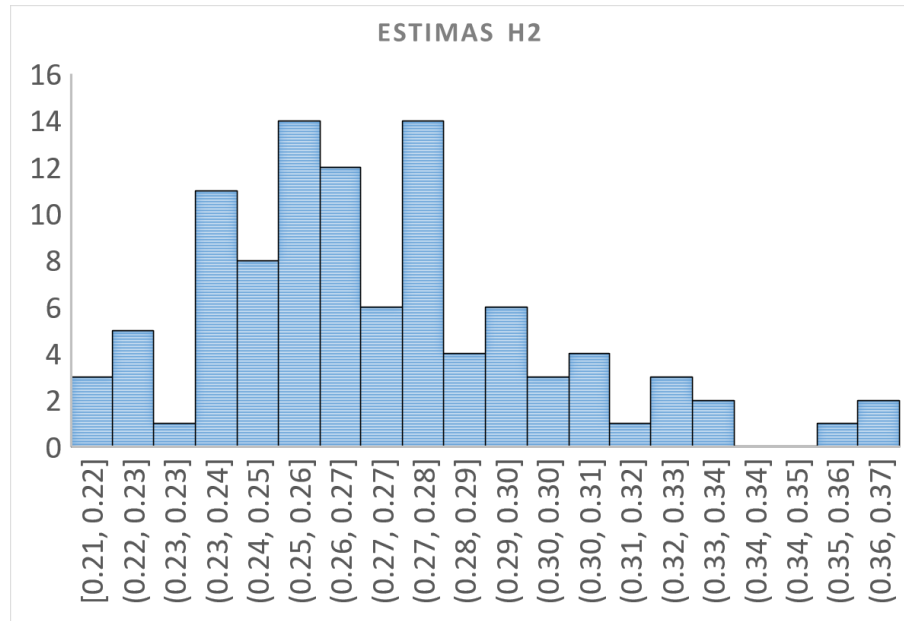


- Sulphur metabolism (Fe-S aa centres)
- synthesis of aa: phenylalanine, tryptophan, arginine, cysteine, methionine
- Lipopolysaccharides and peptidoglycans
- F-type H<sup>+</sup> transporting ATPase

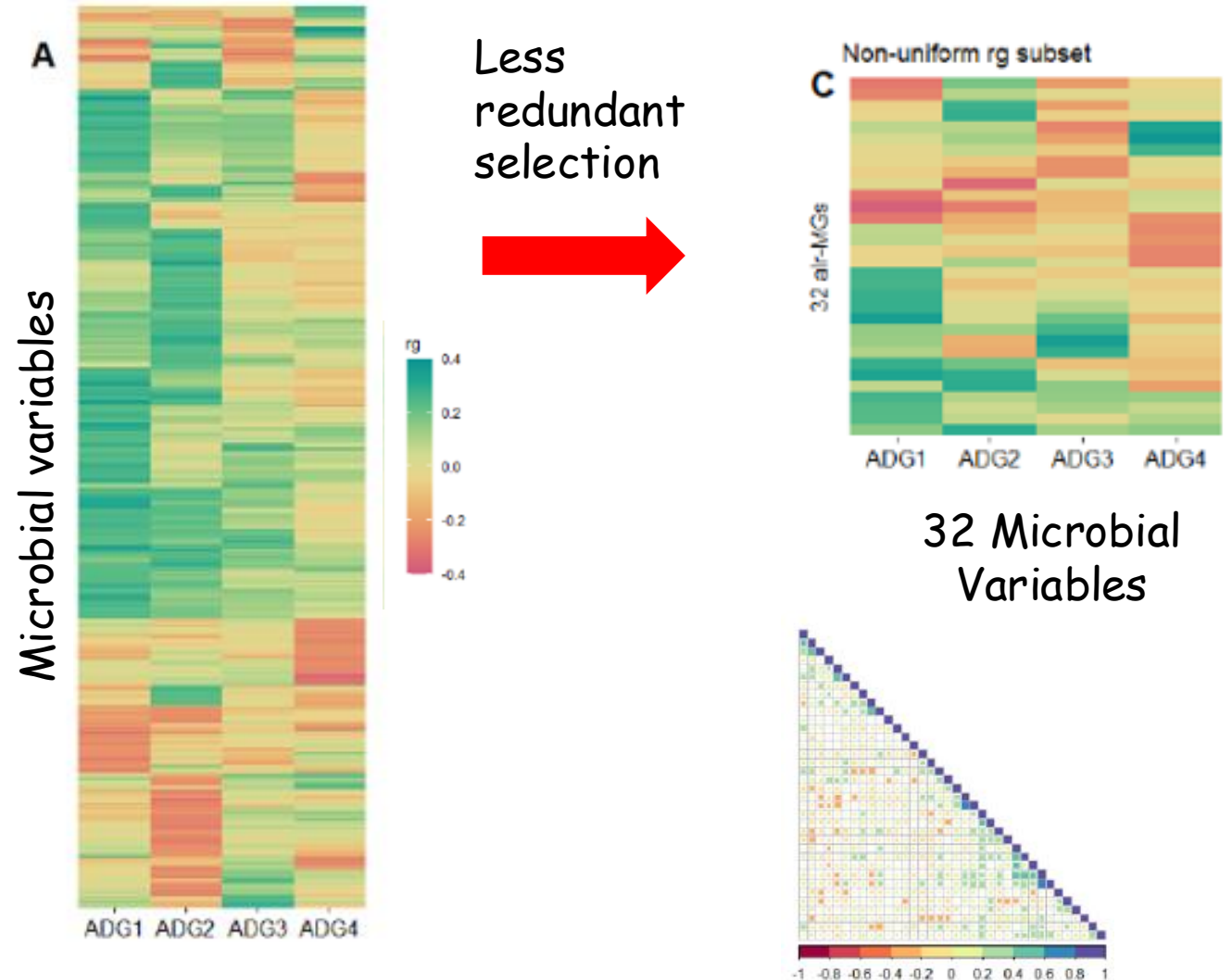
$r_g$  between |0.21|  
to |0.42|

# Calculation of $h^2$ and $r_g$ of microbial traits

## Heredabilities



## Genetic correlations between microbial variables and ADGs



# Accuracy of breeding value estimates

Accuracy Breeding Values

**+11% to +22%.**

Character	Direct	Combined	% Increm.
ADG1	0.56	0.64	15%
ADG2	0.51	0.57	11%
ADG3	0.53	0.58	11%
ADG4	0.48	0.59	21%

Training set (50%): choice of microbial traits

Testing set (50%): computer breeding values

Strategies

Direct: ADG

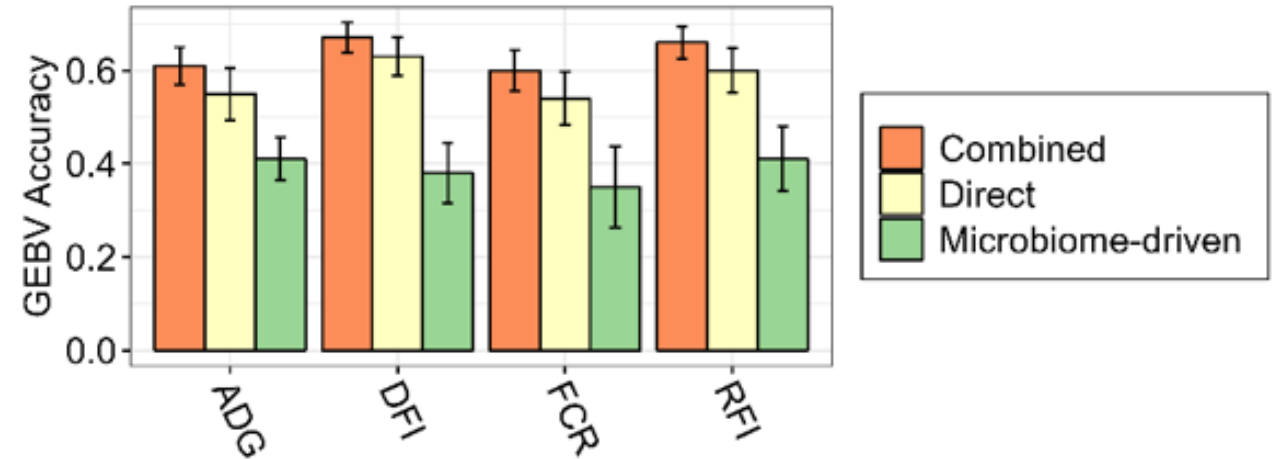
Combined: ADG + 32 microbial characters

# Results in other characters

## Accuracy of breeding values for other production traits

Direct vs. Combined Strategy

<u>Character</u>	<u>%Increase</u>
IC	10.6
GMD	11.9
RFI	11.3
DMI	7.6
CH <sub>4</sub>	18.0



**communications**  
biology

ARTICLE



<https://doi.org/10.1038/s42003-022-03293-0> OPEN

Bovine host genome acts on rumen microbiome function linked to methane emissions

Marina Martínez-Álvarez<sup>1</sup>, Marc D. Auffret<sup>2</sup>, Carol-Anne Duthie<sup>1</sup>, Richard J. Dewhurst<sup>1</sup>, Matthew A. Cleveland<sup>3</sup>, Mick Watson<sup>4</sup> & Rainer Roehe<sup>1</sup>

Critical points to  
consider in practice

# Prices

Whole metagenome sequencing: 120 €/sample approx.

16S targeted sequencing: 60 €/sample approx.

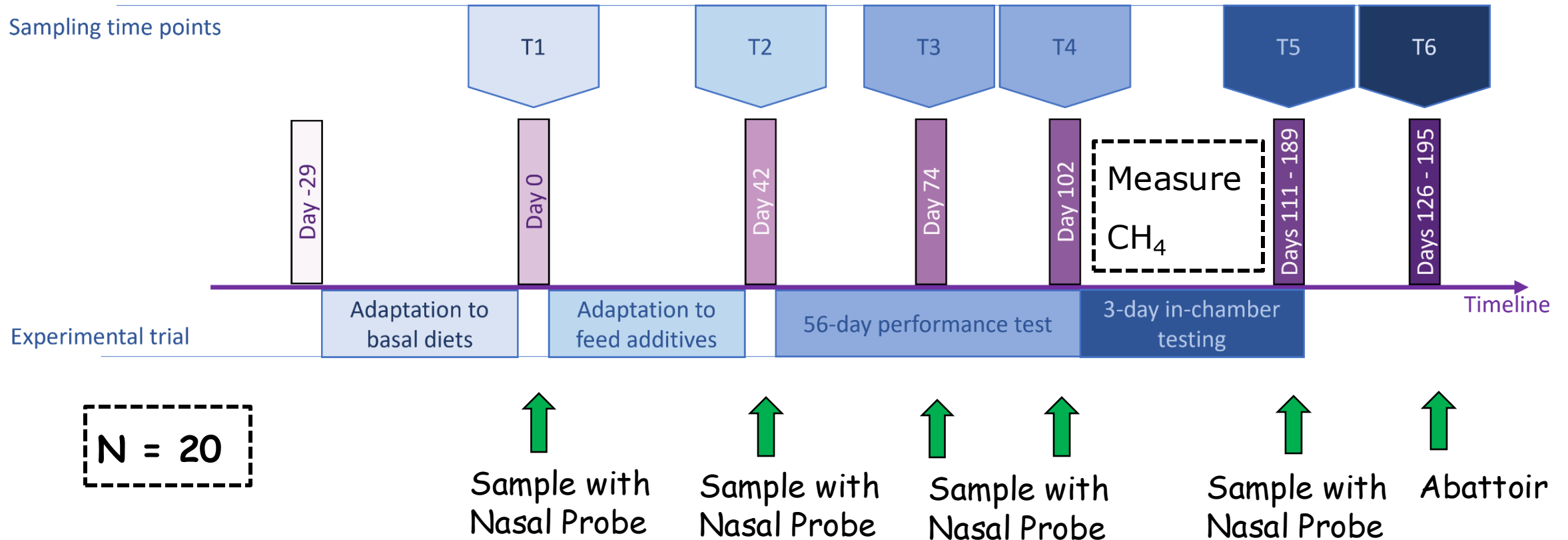
Transcriptomics (3'): €150/sample approx.

Metabolomics: 250 €/sample approx.



# When do we measure the microbiome?

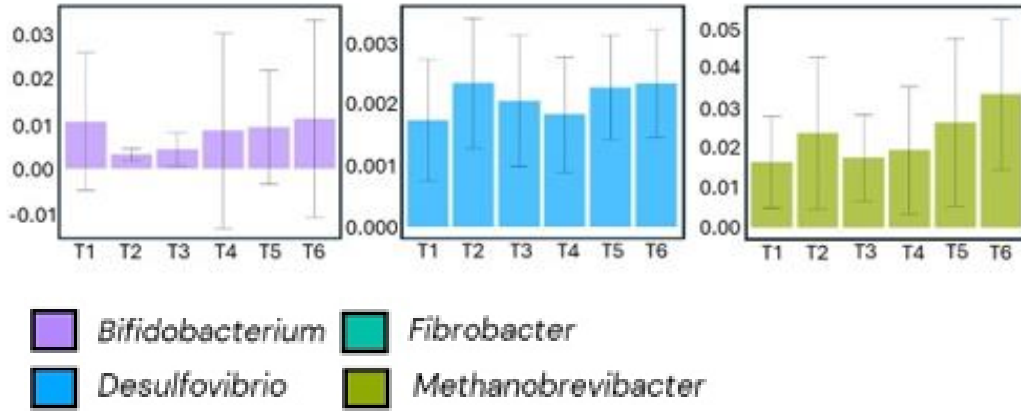
## Longitudinal study of the rumen microbiome at 6 sites



# When do we measure the microbiome?

## Longitudinal study of the rumen microbiome at 6 sites

Many of the gene and microbial genome abundances are not stable...



...but overall they show **stable** predictive capabilities!!!

	R <sup>2</sup> IC	R <sup>2</sup> ADG	R <sup>2</sup> DMI	R <sup>2</sup> CH4(g/kg DMI)	R <sup>2</sup> CH4 (g/day)
T1	0.74	0.67	0.86	0.71	0.74
T2	0.71	0.65	0.81	0.61	0.73
T3	0.63	0.63	0.73	0.50	0.71
T4	0.57	0.54	0.71	0.57	0.64
T5	0.54	0.53	0.66	0.52	0.59
T6	0.53	0.39	0.53	0.49	0.52

Article | [Open access](#) | Published: 05 September 2024

**Temporal stability of the rumen microbiome and its longitudinal associations with performance traits in beef cattle**

Joana Lima , Marina Martínez-Álvaro, Jennifer Mattock, Marc D. Auffret, Carol-Anne Duthie, Matthew A. Cleveland, Richard J. Dewhurst, Mick Watson & Rainer Roehe 

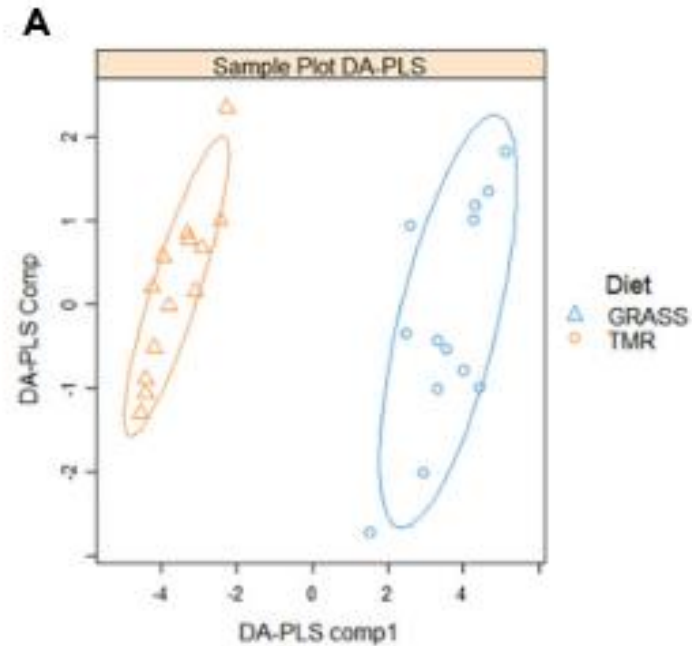
*Scientific Reports* 14, Article number: 20772 (2024) | [Cite this article](#)

829 Accesses | 3 Altmetric | [Metrics](#)

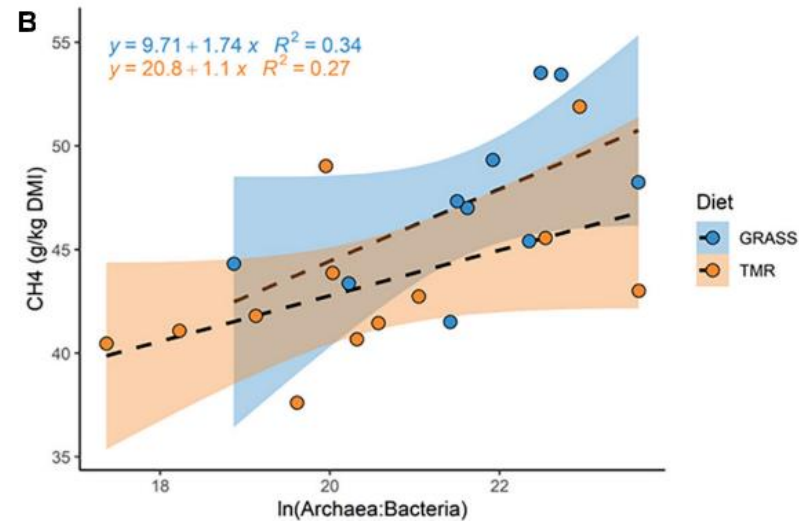
# What happens if the animals have been fed different diets?

## CONCENTRATE VS. FORAGE

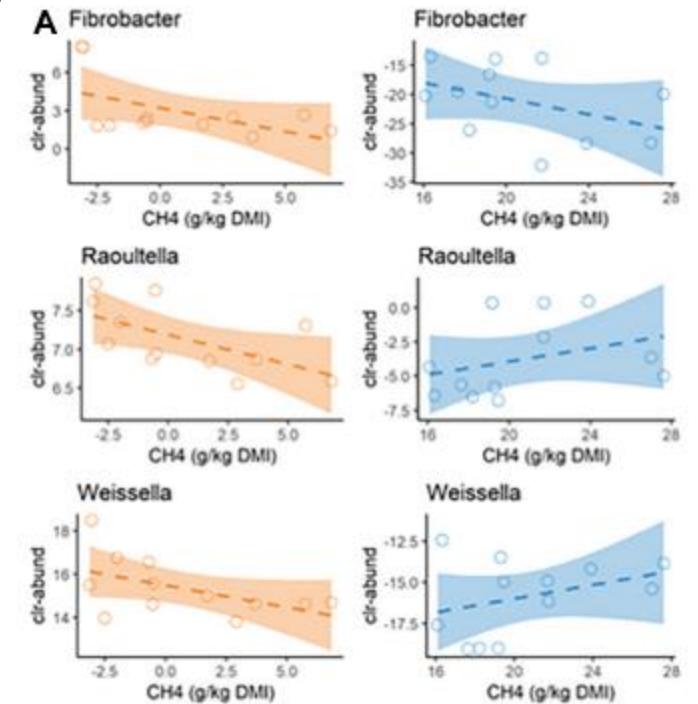
Clearly differentiated  
in their microbial  
composition



The log(Archaea:Bacteria)  
ratio correlated with CH<sub>4</sub> in  
both diets.



There are microbes with  
different tendencies depending  
on diet.



Different microbial genera drive  
methane emissions in beef cattle  
fed with two extreme diets

Gemma A. Miller<sup>1\*</sup>, Marc D. Auffret<sup>2</sup>, Rainer Roehe<sup>1</sup>,  
Holly Nisbet<sup>1</sup> and Marina Martínez-Álvarez<sup>3\*</sup>

<sup>1</sup>Scotland's Rural College (SRUC), Edinburgh, United Kingdom, <sup>2</sup>Agrifirm, Drogen, Belgium, <sup>3</sup>Institute for Animal Science and Technology, Universitat Politècnica de València, Valencia, Spain

# CONCLUSIONS



The microbiome can be used as a proxy for productive traits and methane.



Including microbiome traits in assessments can improve the accuracy of estimating breeding values.



Take stock of benefits (you will need a lot of data)



Considers environmental effects (especially uncontrolled ones!)

# Acknowledgements

Joana Lima<sup>ts</sup>  
Marc Auffret  
Jennifer Mattock  
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Carol-Anne Duthie  
Richard Dewhurst  
Matthew A. Cleveland  
Mick Watson  
Rainer Roehle



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DE VALÈNCIA

# Thank you!

