

Why should we care about the rumen microbiome in next animal breeding strategies

Óscar González-Recio

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75th EAAP Annual Meeting
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Rumen microbiome as a proxy of methane emissions



METHANE & GENETICS



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Rumen eukaryotes are the main phenotypic risk factors for larger methane emissions in dairy cattle.

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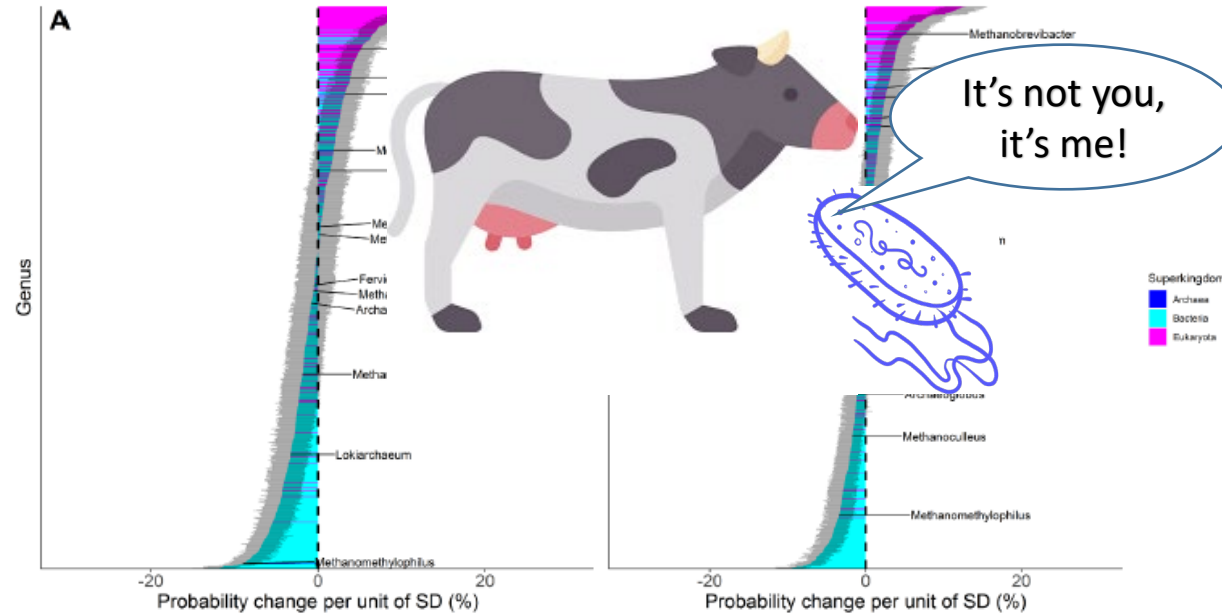


Fig. 3. Change in the probability of being classified in the upper quartile for (A) methane concentration (ppm CH₄) and (B) methane intensity (ppm CH₄/kg milk) per unit of standard deviation for relative abundance (%) of 1240 genera colored by superkingdom. Black dashed line indicates the baseline probability of being classified in the upper quartiles without any genus effect. All the archaea genera are explicitly indicated. Probability intervals based on posterior standard deviations are depicted in gray for all genera.

Wallace et al. BMC Genomics (2015) 16:839
DOI 10.1186/s12864-015-2032-0



RESEARCH ARTICLE

Open Access

The rumen microbial metagenome associated with high methane production in cattle

R. John Wallace^{1*}, John A. Rooke², Nest McKain¹, Carol-Anne Duthie², Jimmy J. Hyslop², David W. Ross², Anthony Waterhouse², Mick Watson^{3†} and Rainer Roehe^{2†}

Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine

Marina Martínez-Álvarez^{1,2*}, Marc D. Auffret^{1,2†}, Robert D. Stewart³, Richard J. Dewhurst¹, Carol-Anne Duthie¹, John A. Rooke¹, R. John Wallace⁴, Barbara Shih⁵, Tom C. Freeman⁵, Mick Watson^{3,5} and Rainer Roehe^{1*}



Applied and Environmental Microbiology®

MINIREVIEW

June 15, 2008 Volume 74 Issue 12
<https://doi.org/10.1128/AEM.02812-07>

Structure of the Archaeal Community of the Rumen

Peter H. Janssen^{*}, Marek Kirs[†]

Grasslands Research Centre, AgResearch Ltd., Palmerston North 4442, New Zealand



- [illegible]





Oral and rumen microbiome as proxies for feed efficiency

scientific reports

OPEN

Rumen and lower gut microbiomes relationship with feed efficiency and production traits throughout the lactation of Holstein dairy cows

Hugo F. Monteiro¹, Ziyao Zhou², Marilia S. Gomes³, Phillip M. G. Peixoto⁴, Erika C. R. Bonsaglia¹, Igor F. Canisso³, Bart C. Weimer¹ & Fabio S. Lima^{1,2}

[Check for updates](#)

Proc. Assoc. Advmt. Breed. Genet. 21: 89-92

PREDICTION OF RESIDUAL FEED INTAKE FROM GENOME AND METAGENOME PROFILES IN FIRST LACTATION HOLSTEIN-FRIESIAN DAIRY CATTLE

M. Wang¹, J. E. Pryce^{1,2}, Keith Savin¹ and B. J. Hayes^{1,2}

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²La Trobe University, Bundoora, VIC 3086, Australia

SCIENTIFIC REPORTS

Corrected: Author Correction

OPEN

Whole rumen metagenome sequencing allows classifying and predicting feed efficiency and intake levels in cattle

Beatriz Delgado¹, Alex Bach^{2,3}, Isabel Guasch⁴, Carmen González⁵, Guillermo Elcoso⁴, Jennie E. Pryce⁶ & Oscar Gonzalez-Recio^{1,5}

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The oral microbiome as a proxy for feed intake in dairy cattle

C. N. Marcos^{1,2*}, A. Bach^{3,†}, M. Gutiérrez-Rivas^{2,4} and O. González-Recio²

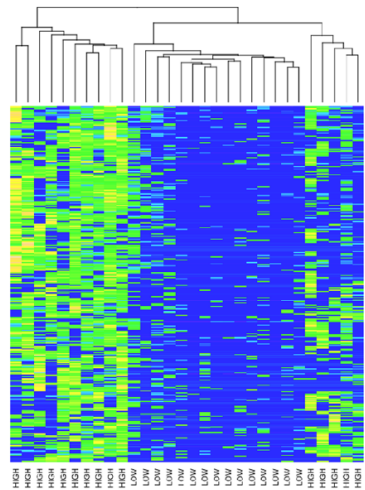
¹Departamento de Producción Agraria, ETSIAAB, Universidad Politécnica de Madrid, Ciudad Universitaria, 28040 Madrid, Spain

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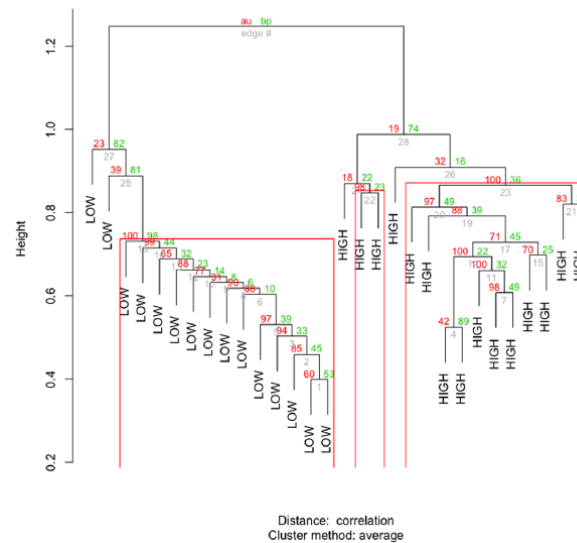
³ICREA, 08007 Barcelona, Spain

⁴Blanca from the Pyrenees, Hostalets de Tost, 25795 Lleida, Spain

b) Hierarchical clustering



Cluster dendrogram with AU/BP values (%)



Distance: correlation
Cluster method: average

SCIENTIFIC REPORTS

Corrected: Author Correction

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Whole rumen metagenome sequencing allows classifying and predicting feed efficiency and intake levels in cattle

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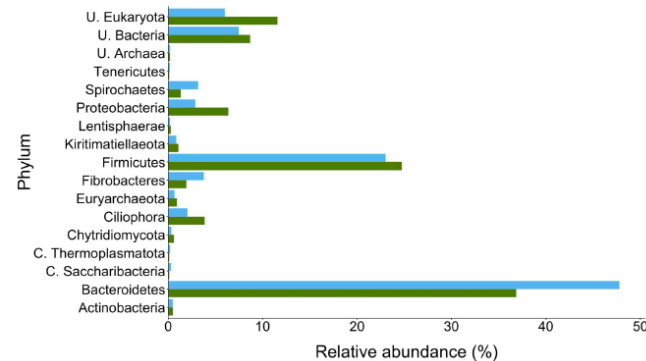
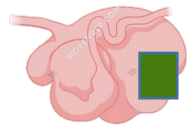


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The oral microbiome as a proxy for feed intake in dairy cattle

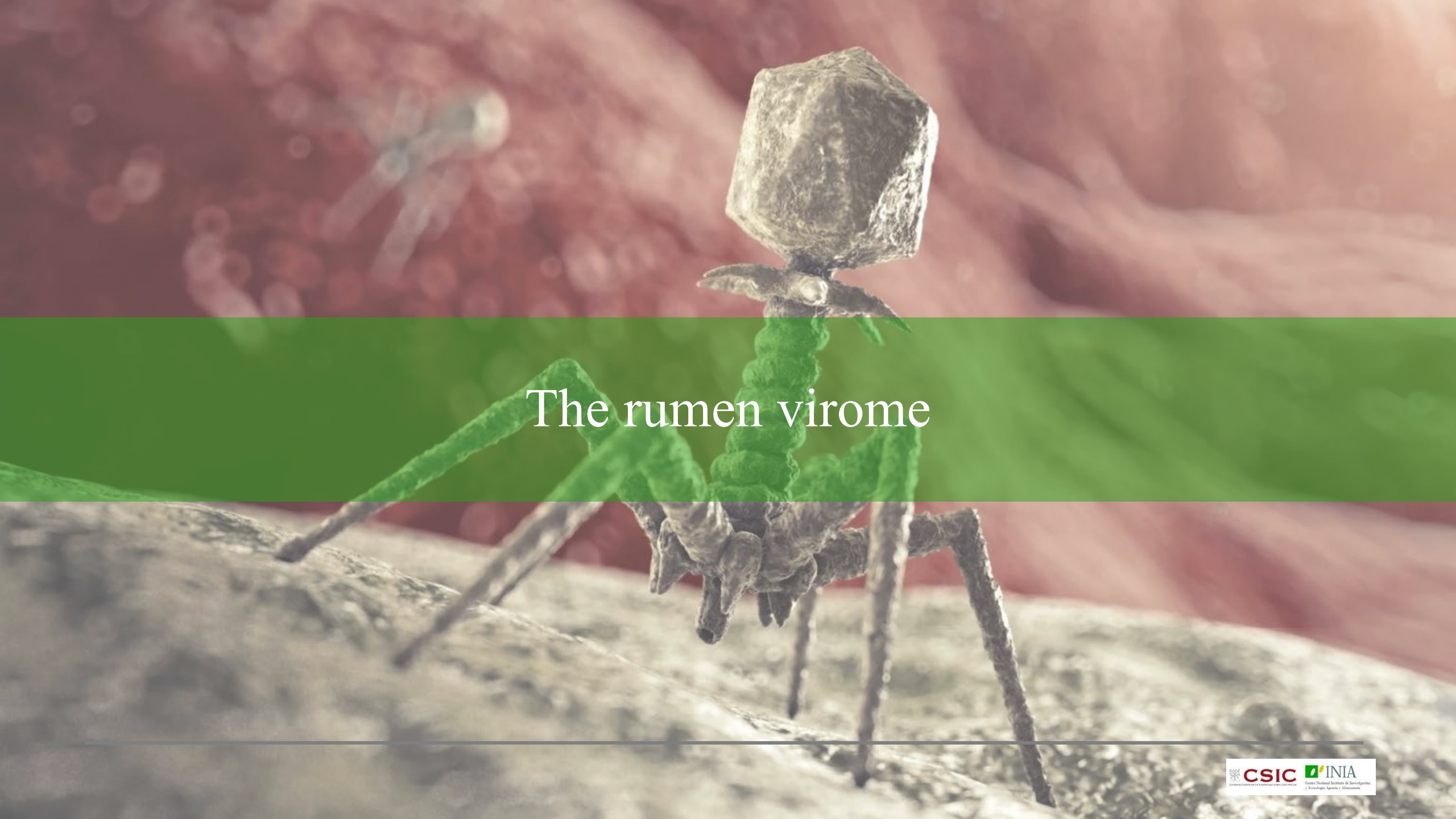
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¹Departamento de Producción Agraria, ETSIAAB, Universidad Politécnica de Madrid, Ciudad Universitaria, 28040 Madrid, Spain

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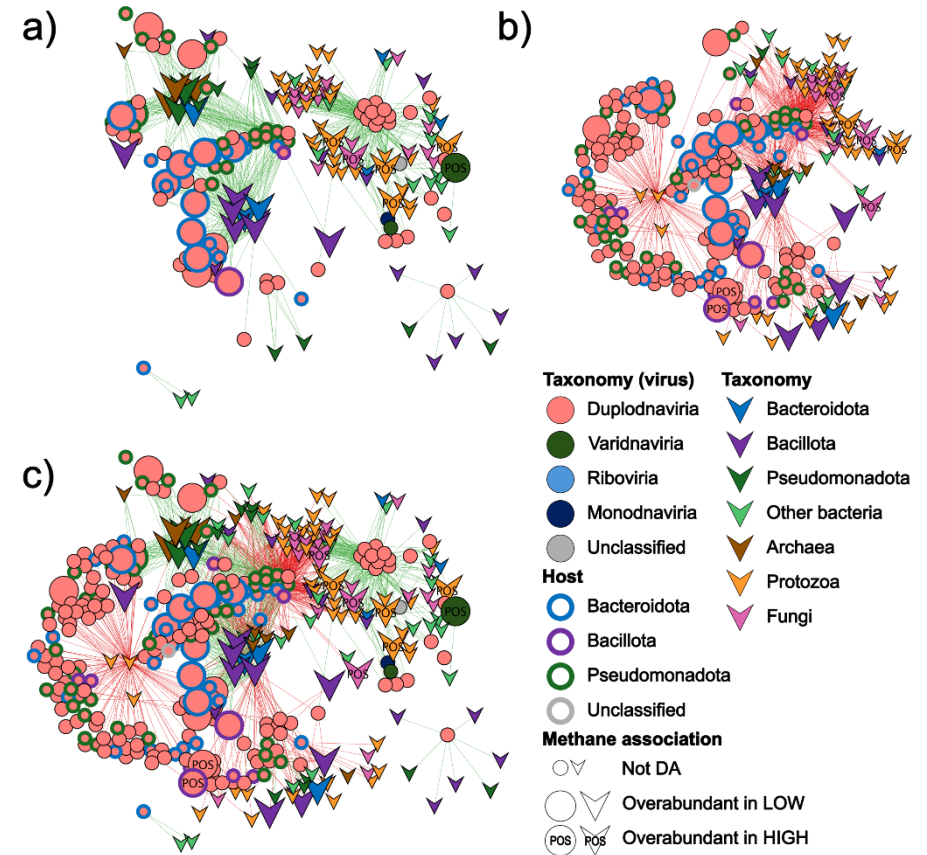
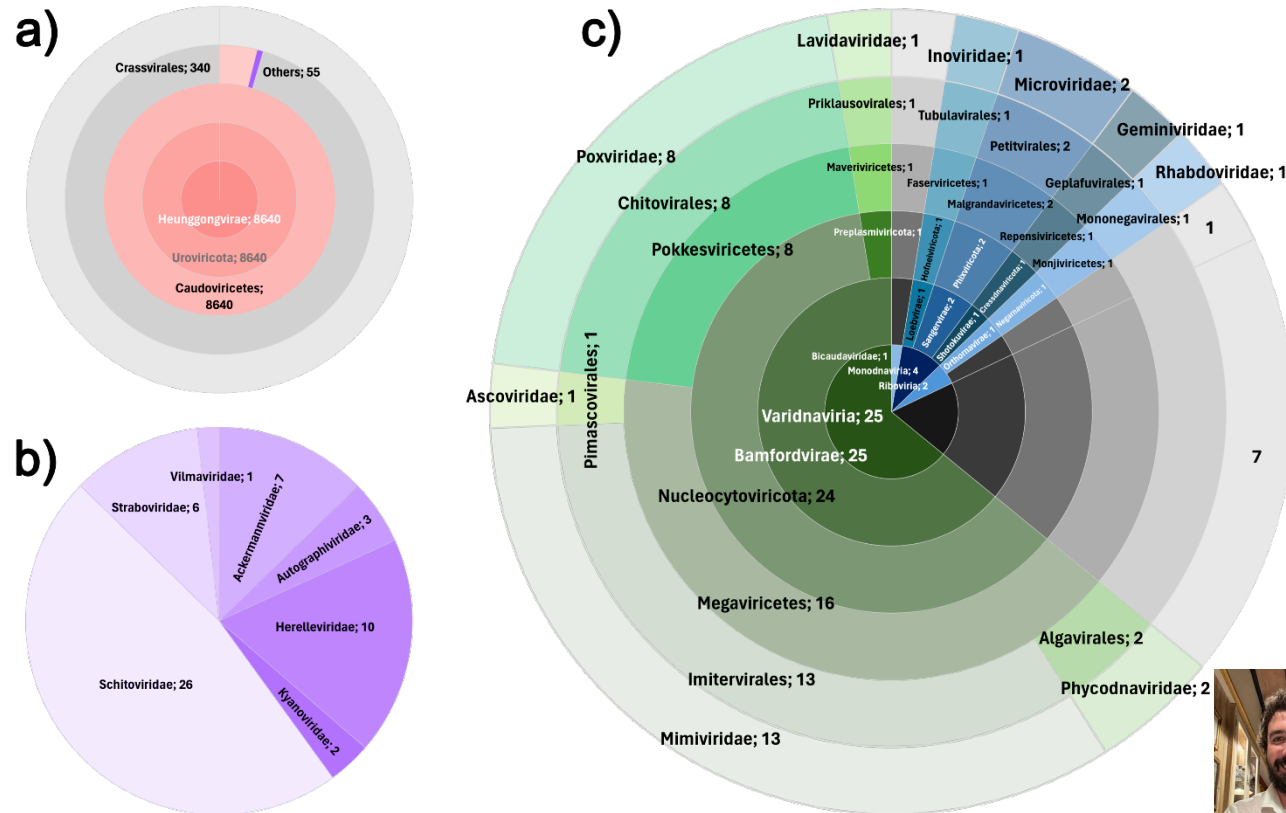
³ICREA, 08007 Barcelona, Spain

⁴Blanca from the Pyrenees, Hostalets de Tost, 25795 Lleida, Spain



The rumen virome

- A comprehensive exploration of the rumen virome unveiled a noteworthy population of phages and megaviruses potentially associated with methane emissions.





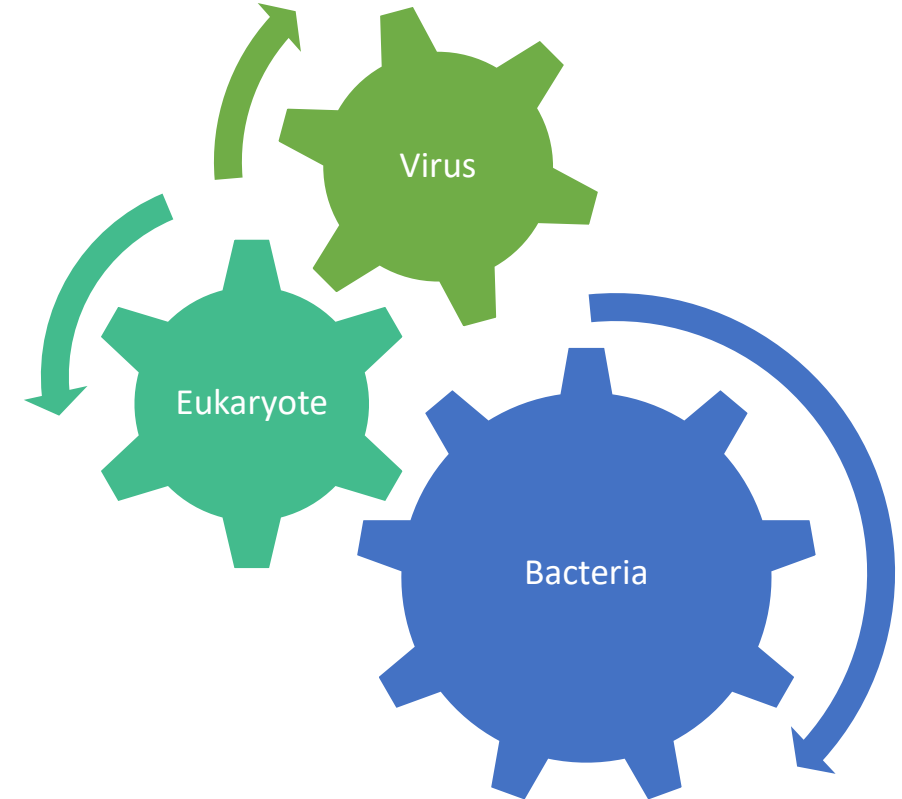
Objective



Should the rumen microbiome composition be included as a trait of interest in dairy (and beef) cattle



Large dimensionality, redundancy and interplay



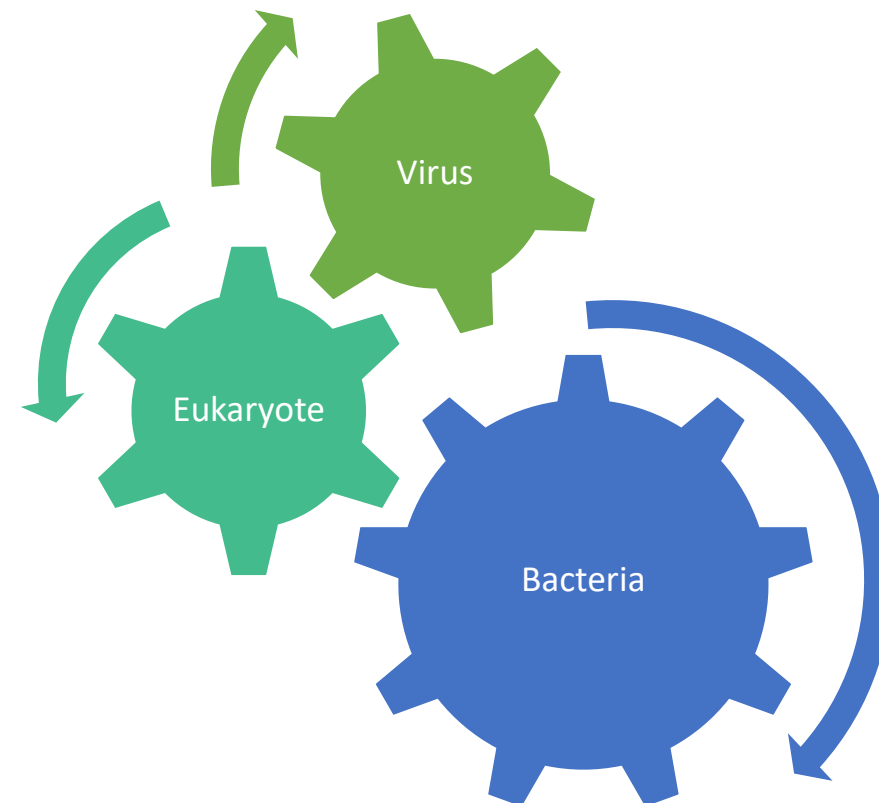
Rumen microbiome community



- **How to deal statistically in animal breeding?**

Large dimensionality, redundancy and interplay

Selection of features
based on genetic
correlations with traits
of interest



Aggregated variables with
Principal Component
Analysis

Heritability estimates between 0.20 and 0.30

RESEARCH ARTICLE

Open Access

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

Marina Martínez-Álvarez^{1,2*}, Jennifer Mattock³, Óscar González-Reco³, Alejandro Saborío-Montero⁴,
Ziqing Weng⁵, Joana Lima², Carol-Anne Duthie², Richard Dewhurst², Matthew A. Cleveland⁵, Mick Watson² and
Rainer Roehe^{2*}



J. Dairy Sci. 104:8135–8151

<https://doi.org/10.3168/jds.2020-20005>

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**A dimensional reduction approach to modulate the core ruminal
microbiome associated with methane emissions
via selective breeding**

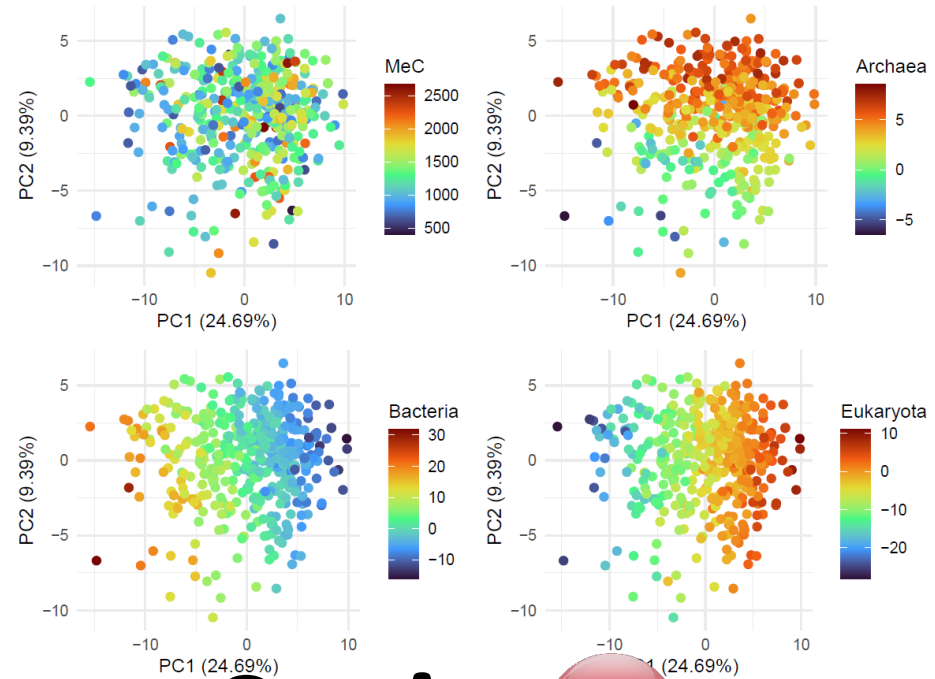
Alejandro Saborío-Montero,^{1,2} Adrián López-García,¹ Mónica Gutiérrez-Rivas,¹ Raquel Atxaerandio,³
Idoia Goñi,⁴ Aser García-Rodríguez,³ José A. Jiménez-Montero,⁴ Carmen González,¹ Javier Tamames,⁵
Fernando Puente-Sánchez,⁶ Luis Varona,⁴ Magdalena Serrano,¹ Cristina Ovilo,¹
and Oscar González-Reco^{1,7,*}

Transacciones de la Academia Española de Estadística, Estadística y Teoría de la Probabilidad, Vol. 10, No. 1, 2021, pp. 1-10.

Similar microbiome composition and relationship with methane under 2 different production systems



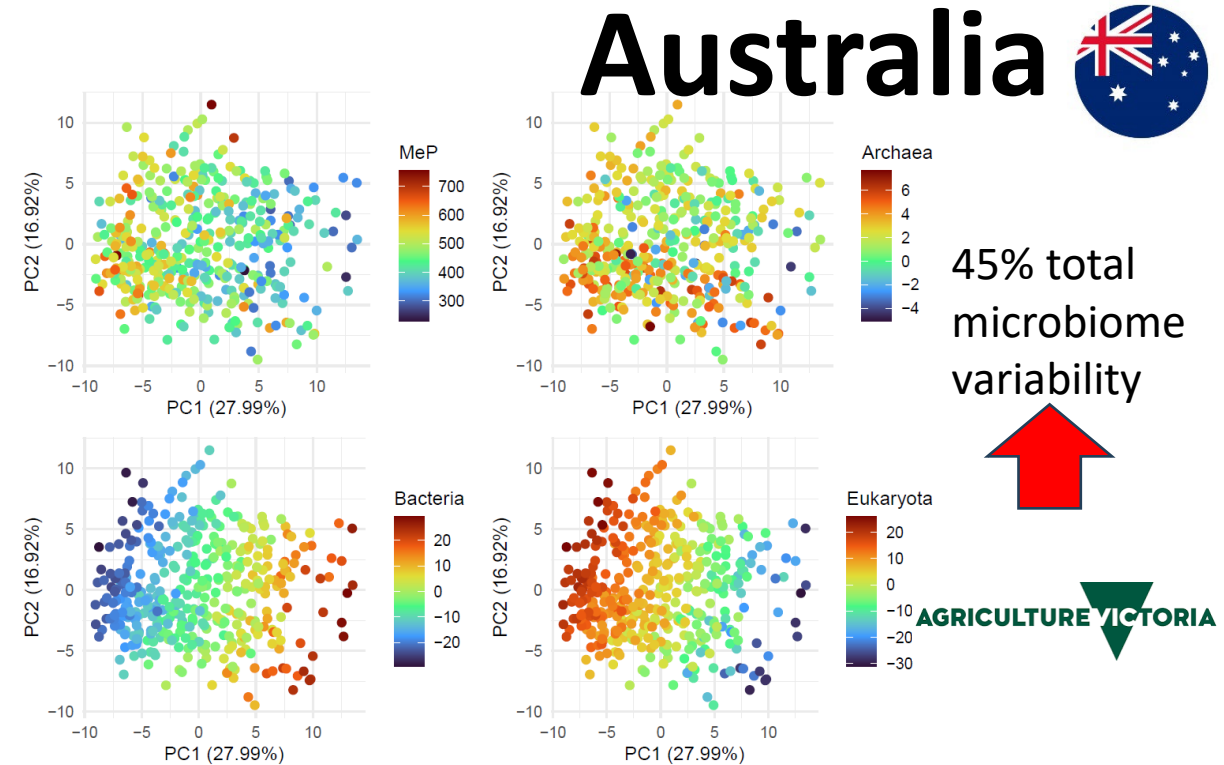
- Aggregated variables capture a relevant portion of microbial variability



Spain



33% total
microbiome
variability



Australia



45% total
microbiome
variability



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J. Dairy Sci. 104:8135–8151
<https://doi.org/10.3168/jds.2020-20005>

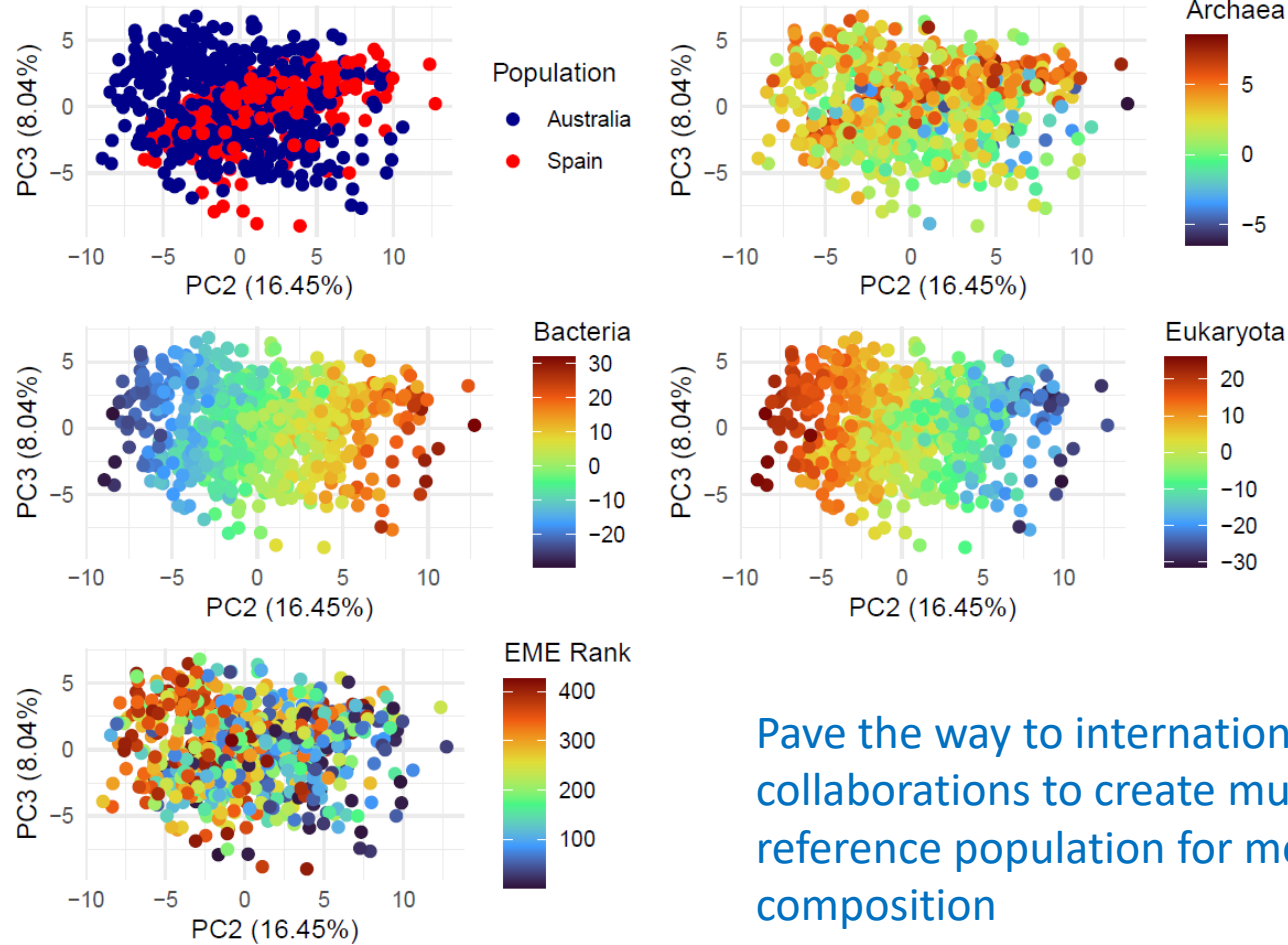
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A dimensional reduction approach to modulate the core ruminal microbiome associated with methane emissions via selective breeding

Alejandro Saborio-Montero,^{1,2} Adrian López-García,¹ Mónica Gutiérrez-Rivas,¹ Raquel Atxaerandio,³ Idoia Goiri,³ Aser García-Rodríguez,³ José A. Jiménez-Montero,⁴ Carmen González,¹ Javier Tamames,⁵ Fernando Puente-Sánchez,⁵ Luis Varona,⁶ Magdalena Serrano,³ Cristina Ovilo,¹ and Oscar González-Reco^{1,7,*}



Similar microbiome composition and relationship with methane under 2 different production systems



Joint population



Pave the way to international collaborations to create multi country reference population for metagenome composition

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(unpublished)

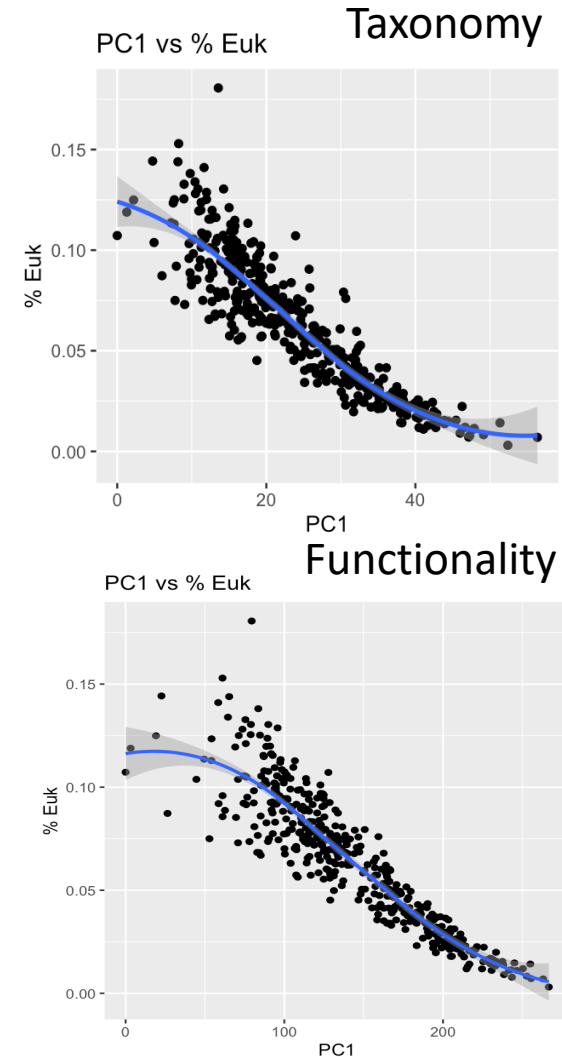
Agregated variables have a biological meaning



- First PC1 is related to Eukaryotes relative abundance

- PC2 is related to $\frac{Proteobacteria}{Firmicutes + Bacteroidetes}$

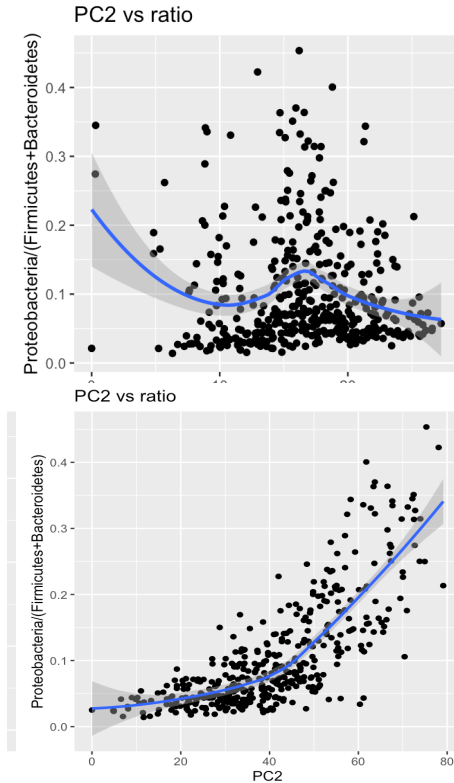
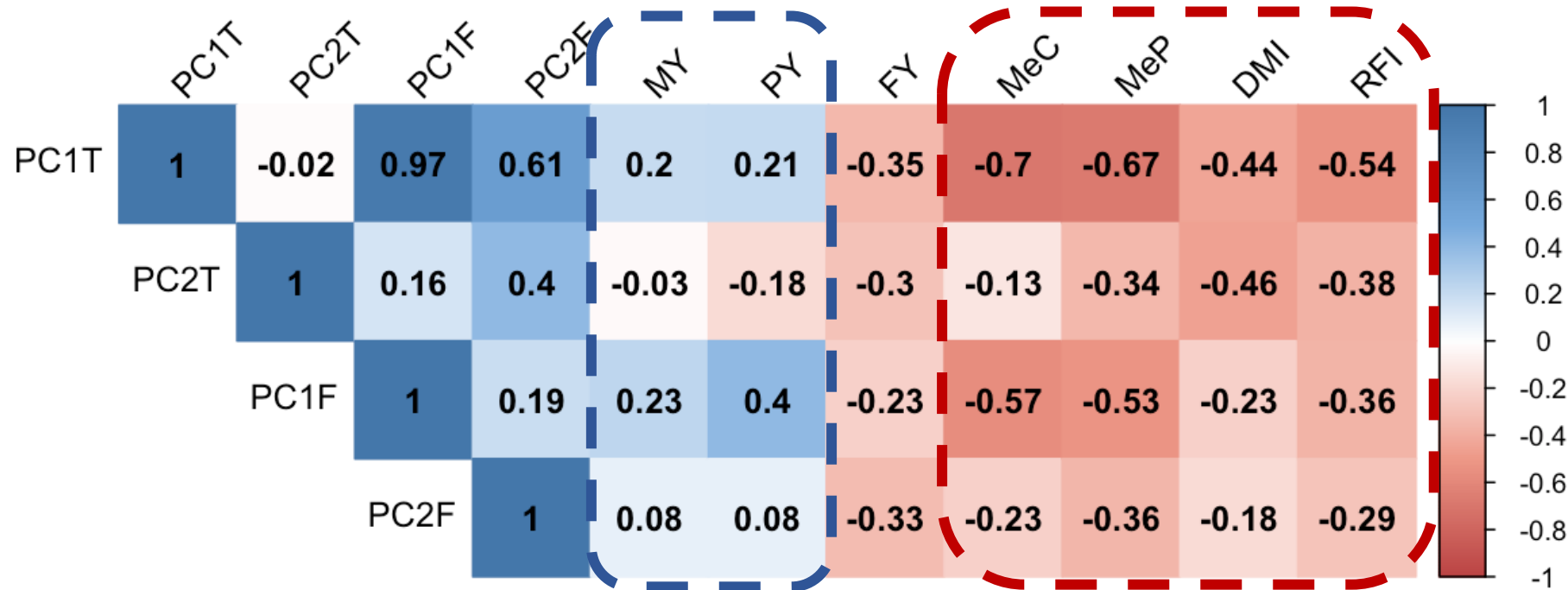
(Petri et al. 2013 & Auffret et al. 2017)



Rumen microbiome community



• Genetic correlation between PC and other traits

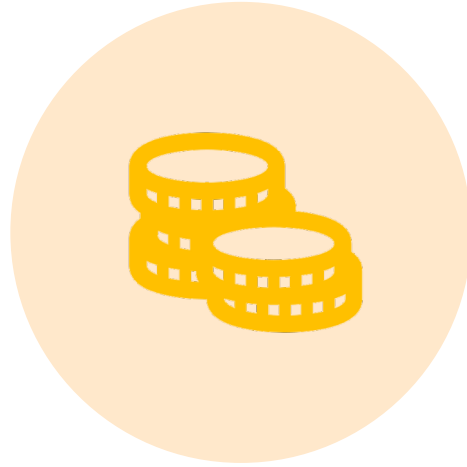


- Aggregated microbial variables are favorably genetically correlated with milk, protein, methane emissions and feed efficiency (unfavorable with fat)
- Breeding for lower methane or feed efficiency may impact microbiota composition (dysbiosis)
- What are the expected consequences?

Microbiome in breeding goals and selection indices



Challenges at selecting for microbiome composition



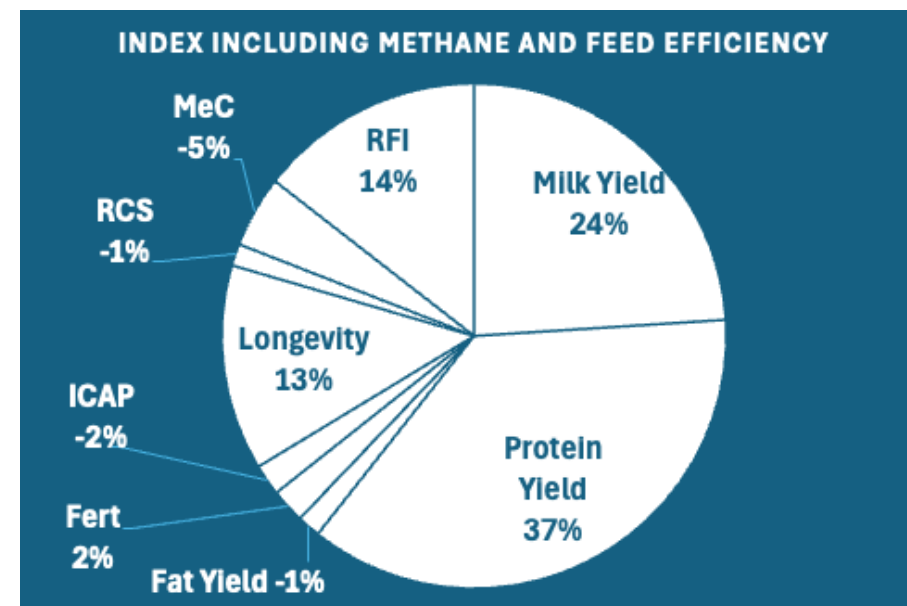
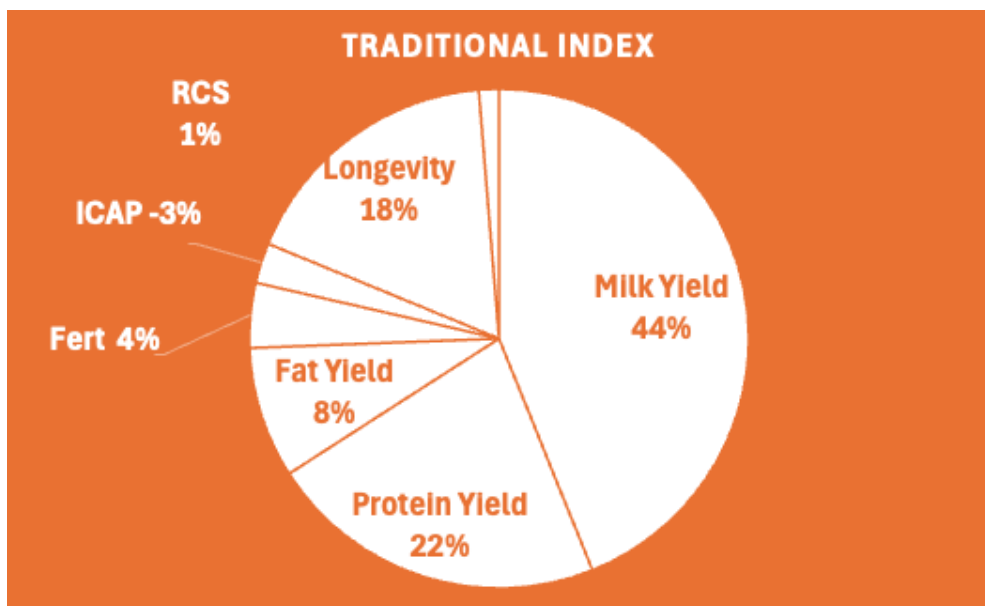
UNKNOWN ECONOMIC VALUE



**UNCERTAIN DIRECTION OF BREEDING
(COMPLEX MICROBIAL RELATIONSHIPS)**

Example of implementation

- **Efficiency and sustainability index in Spanish Dairy cattle**
 - Subindex (will be integrated in the total merit index)



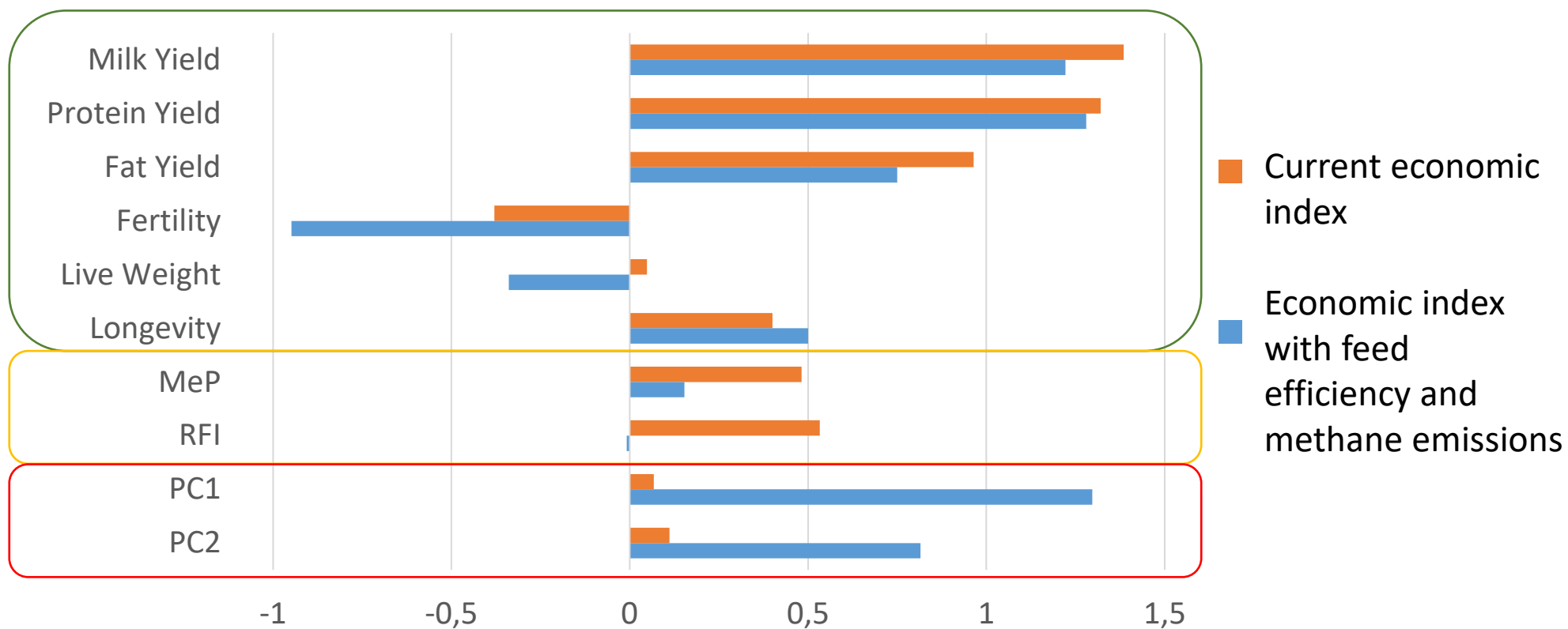
→ Calculate expected genetic gain for each trait, including the correlated response on the microbial aggregated variables.

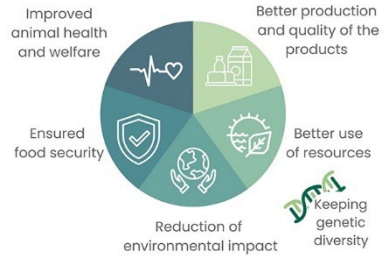
Example of implementation



- **Efficiency and sustainability index in Spanish Dairy cattle**
 - Subindex (will be integrated in the total merit index)

Expected genetic gain (additive standard deviation units)





Take home message for future metagenomic interventions in breeding programs

01

Selection for methane emissions and feed efficiency may shift rumen microbiota composition

So far, the consequences are uncertain. Need microbiome phenotyping to control changes.

02

Aggregated metagenome variables can capture a large rumen microbiome variability

Attractive as metagenomic traits in breeding programs.

03

International collaborations

Coming research efforts in this area.



Re-Livestock
RESILIENT FARMING SYSTEMS





A. Saborío-Montero
A. López-García
M. Gutiérrez-Rivas
C. González-Verdejo
N. Scrobota



I. Goiri
R. Atxaerandio
E. Ugarte
A. García-Rodríguez



J. López-Paredes
N. Charfeddine
J.A. Jiménez-Montero



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