

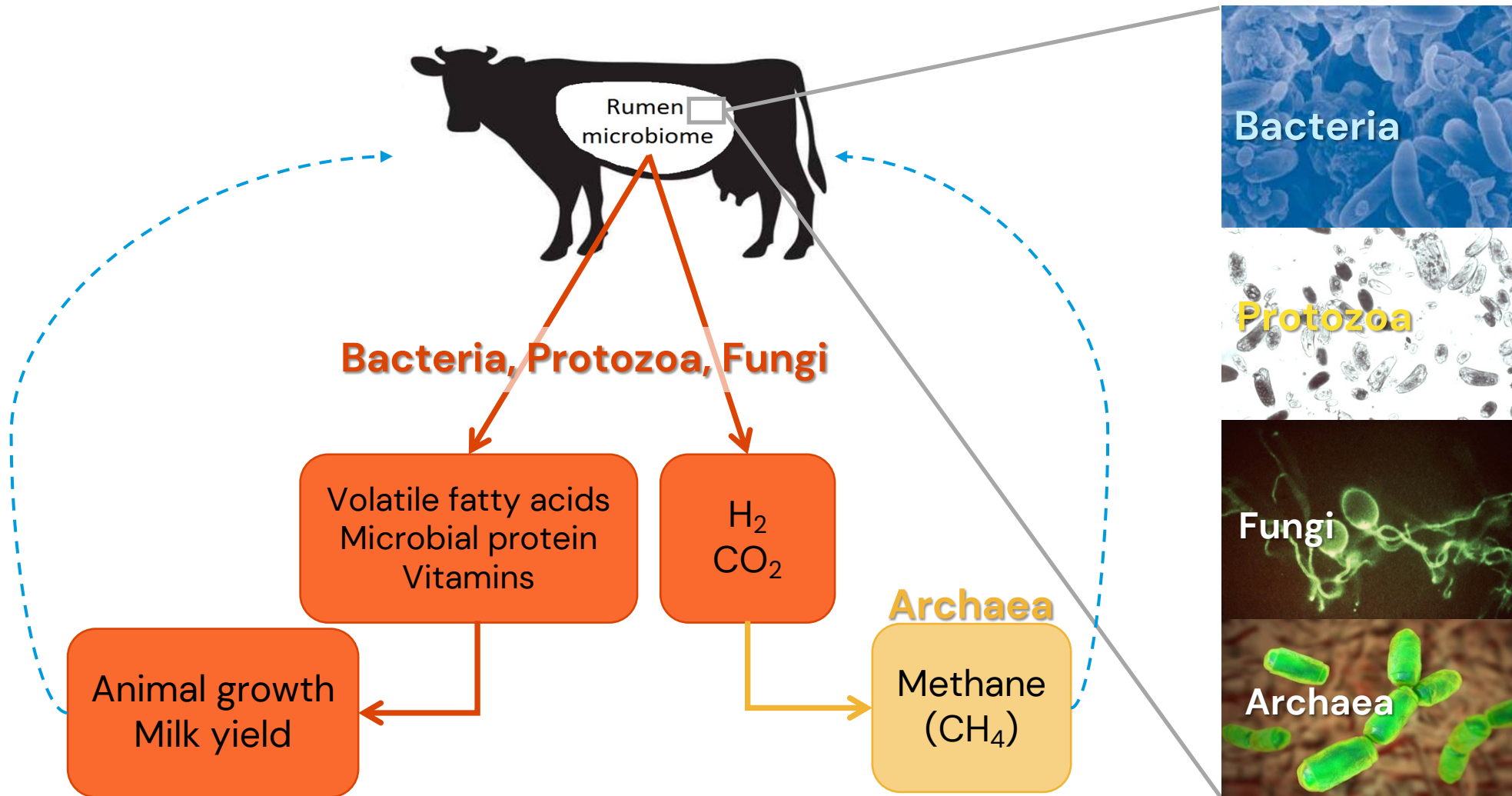


Rumen microbiome in cattle

Joana Lima

October 13th 2022

THE RUMEN MICROBIOME



Methane emissions in red clover and grass silage



Methane emissions and rumen metabolite concentrations in cattle fed two different silages

R. Bica^{1,2,7}, J. Palarea-Albaladejo^{3,6}, J. Lima^{1,2}, D. Uhrin⁴, G. A. Miller¹, J. M. Bowen¹, D. Pacheco⁵, A. Macrae² & R. J. Dewhurst¹

- Three main approaches to reduce CH₄ emissions:
 1. to **change the diet composition** which will alter VFA production, reducing the available H₂ produced during enteric fermentation
 2. to **increase the feed passage rate** through the rumen, altering the extent of rumen fermentation and VFA production patterns
 3. feeding **high quality diets**, thus decreasing CH₄ emissions in relation to productivity

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Grass silage (GS)

- CH₄ yield = 21.2 ± 4.61 g/kg DMI

Red-clover (RC)

- CH₄ yield = 17.8 ± 3.17 g/kg DMI

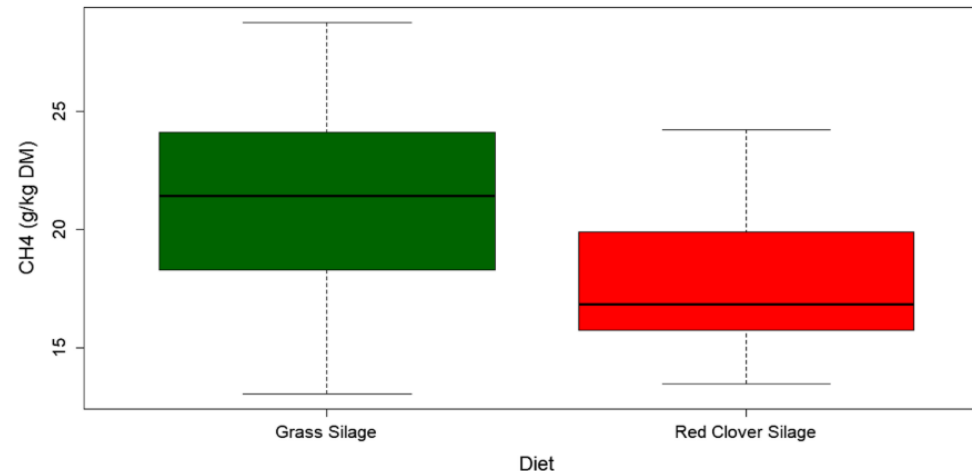


Figure 1. Boxplot of CH₄ yield (CH₄ g/kg DM) in grass silage and red clover silage fed animals.

Methane emissions in red clover and grass silage



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Grass silage (GS)

- CH₄ yield = 21.2 ± 4.61 g/kg DMI
- Richer in fibre and sugars

Red-clover (RC)

- CH₄ yield = 17.8 ± 3.17 g/kg DMI
- Richer in pectin, proteins

Methylotrophic
methanogenesis

Methane emissions in red clover and grass silage



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Grass silage (GS)

- CH₄ yield = 21.2 ± 4.61 g/kg DMI
- Richer in fibre and sugars
- Decreased passage rate

Red-clover (RC)

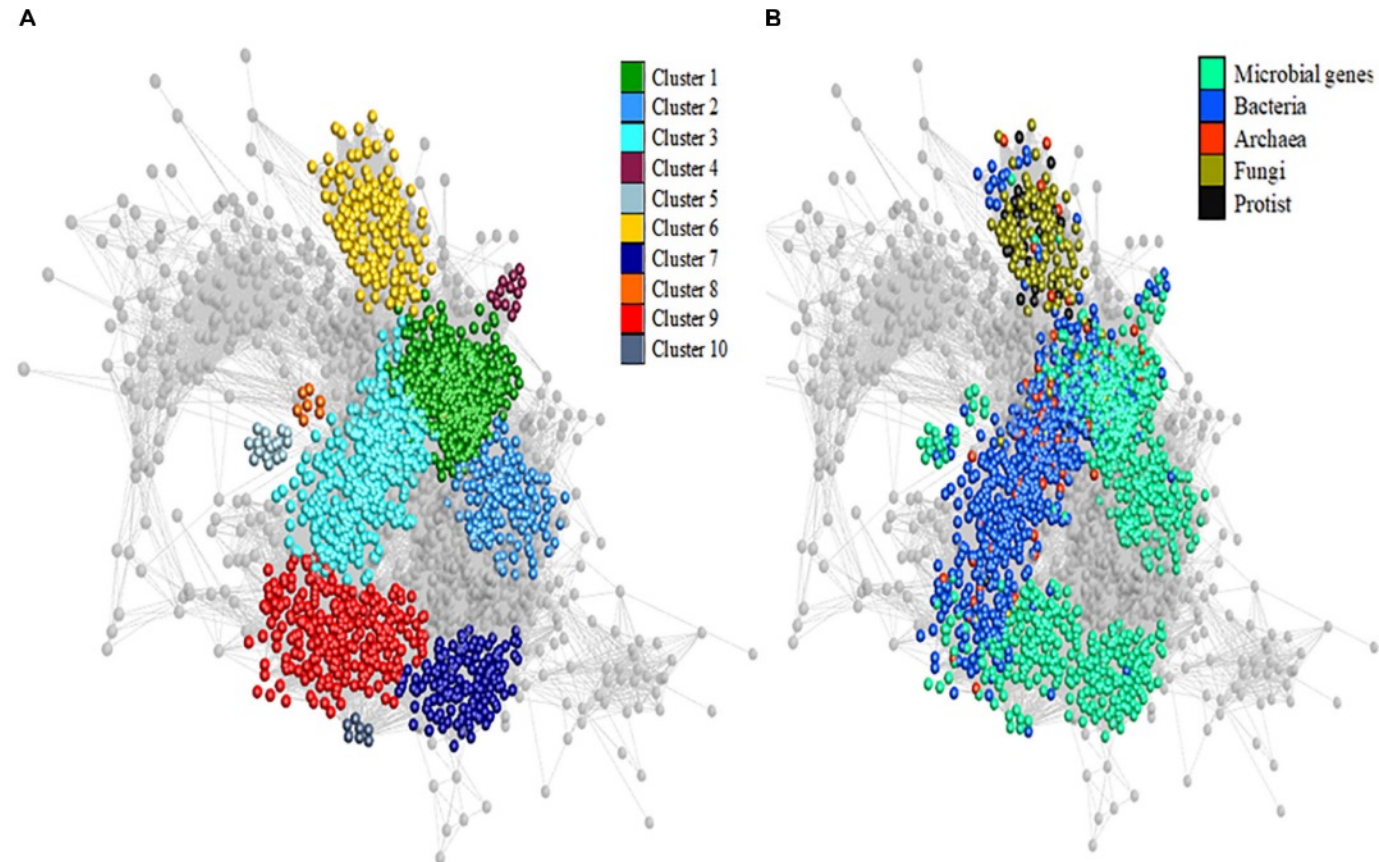
- CH₄ yield = 17.8 ± 3.17 g/kg DMI
- Richer in pectin, proteins
- Increased passage rate

| Metabolite | Red clover silage | Grass silage | ¹ FDRpvalue |
|--------------|---------------------|---------------------|------------------------|
| VFA | | | |
| Acetate* | 52,120.8 ± 14,159.8 | 73,265.6 ± 16,616.7 | 0.000† |
| Butyrate* | 4421.5 ± 1469.9 | 7718.7 ± 3857.4 | 0.028† |
| Isobutyrate* | 803.5 ± 251.8 | 1119.4 ± 515.8 | 0.100 |
| Isovalerate* | 456.6 ± 135.7 | 612.3 ± 243.8 | 0.100 |
| Propionate* | 11,449.1 ± 3832.0 | 18,722.8 ± 5408.5 | 0.001† |
| Valerate* | 615.2 ± 235.6 | 1298.7 ± 694.1 | 0.009† |

The rumen microbiome in methane emissions

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*†}, Robert D. Stewart³,
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Barbara Shih⁵, Tom C. Freeman⁵, Mick Watson^{3,5} and Rainer Roehe^{1*}



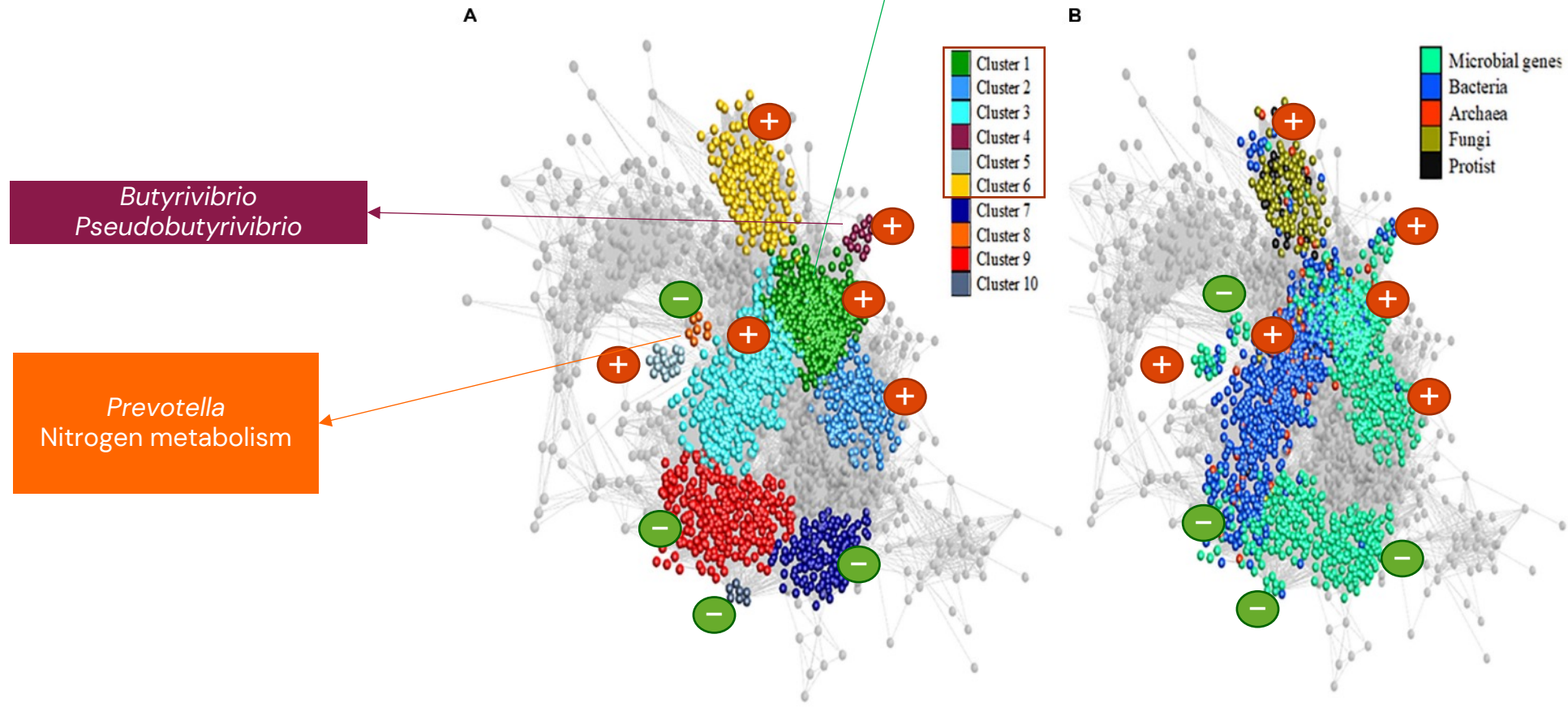
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Nitrogen fixation
Lignin degradation
Amino acid metabolism
Sugar metabolism

The methanogenesis cluster
57% methane yield variation



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High methane emitters (HME)

- Fewer hydrogenotrophic methanogenic Archaea (lower diversity) with lower number of interactions between variables

Low methane emitters (LME)

- More diverse methanogenic Archaea (hydrogenotrophic, methylotrophic and acetoclastic methanogenesis)
- Higher number of interactions between variables
- *Candidatus Methanomethylophilus* (methylotroph) was favoured in LME, and in the same cluster as acetogens *Eubacterium*, *Blautia* and *Acetitomaculum*, H₂ sinkers

The rumen microbiome in performance traits



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

Joana Lima^{1*}, Marc D. Auffret¹, Robert D. Stewart², Richard J. Dewhurst¹, Carol-Anne Duthie¹, Timothy J. Snelling³, Alan W. Walker³, Tom C. Freeman^{2†}, Mick Watson² and Rainer Roehe^{1*}

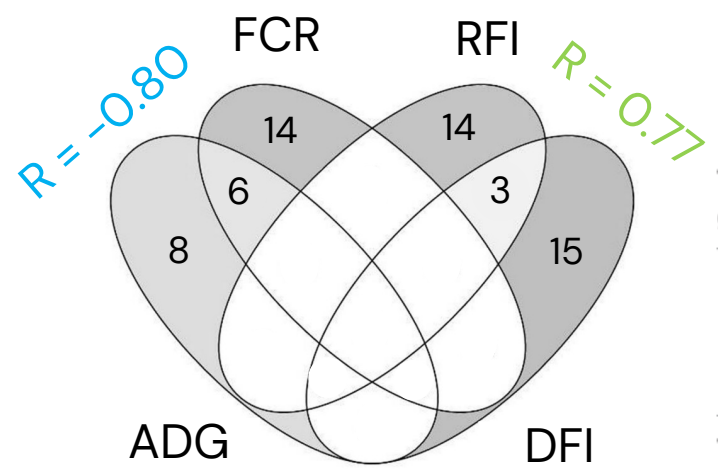


TABLE 1 | Percentage of variation in each trait explained by the microbial genes identified in the partial least squares (PLS).

| | | Percent variation accounted for by partial least squares factors | | | |
|-----------------------|-------------|--|-------|---------------------|-------|
| | | Model effects | | Dependent variables | |
| Trait | No. factors | Current | Total | Current | Total |
| Feed conversion ratio | 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 |
| Average daily gain | 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 |
| Residual feed intake | 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 |
| Daily feed intake | 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 |

- cell wall biosynthesis
- hemicellulose and cellulose degradation
- host-microbiome crosstalk

- vitamin B12 biosynthesis
- environmental information processing
- bacterial mobility

The rumen microbiome is heritable



Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance

Rainer Roehe^{1*}, Richard J. Dewhurst¹, Carol-Anne Duthie¹, John A. Rooke¹, Nest McKain², Dave W. Ross¹, Jimmy J. Hyslop¹, Anthony Waterhouse¹, Tom C. Freeman³, Mick Watson⁴, R. John Wallace²

20 microbial genes: 81% CH₄ g/kg DMI

49 microbial genes: 86% FCR

Ranking of sire progeny groups was consistent with ranking based on abundance of archaea.

R = 0.8 daily methane emissions

R = 0.65 methane yield

*The general consistency in ranking of sire progeny groups based on microbial and methane emissions levels provides evidence that there is an **additive genetic influence** of the host on the rumen microbial community and their metabolic activity to produce methane.*

The rumen microbiome is heritable

- 1 Bovine host genome acts on specific metabolism, communication and
- 2 genetic processes of rumen microbes host-genomically linked to methane
- 3 emissions

- 4 Marina Martínez-Álvaro¹, Marc D. Auffret¹, Carol-Anne Duthie¹, Richard J. Dewhurst¹,
- 5 Matthew A. Cleveland², Mick Watson³ and Rainer Roehe^{*1}

Genetic heritability of methane yield = 33%

Many microbial genera and genes were significantly heritable.

$R_{CH_4} > 0.4$

Amino acid transport and
metabolism

Could be a common host effect – maybe
on rumen passage rates?

Sugar fermentation

Fast sugars fermentation can lead to drop
in pH, affecting fibrolytic or maybe
methanogenic organisms

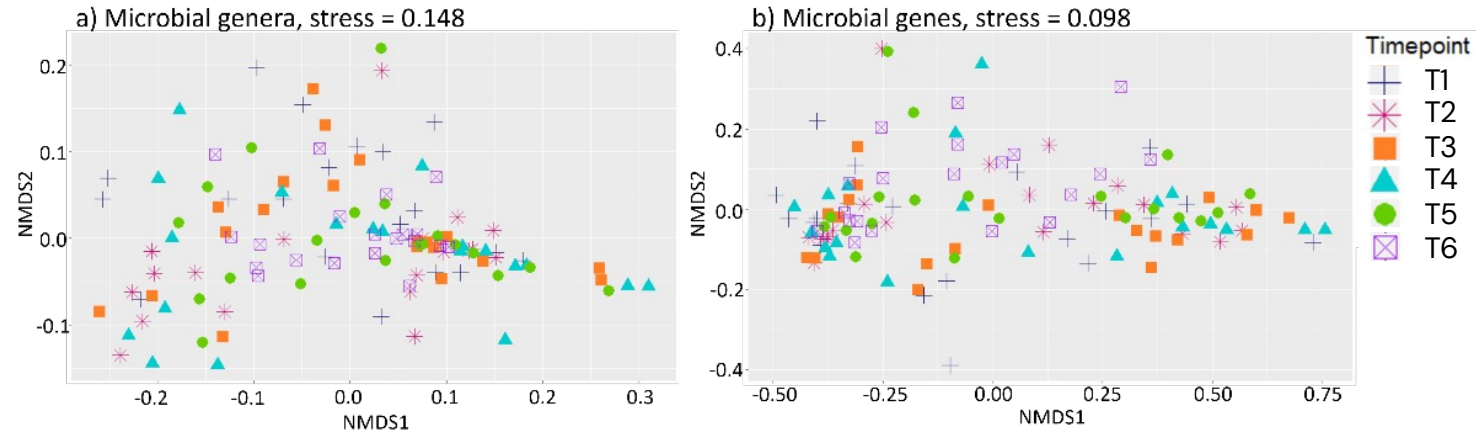
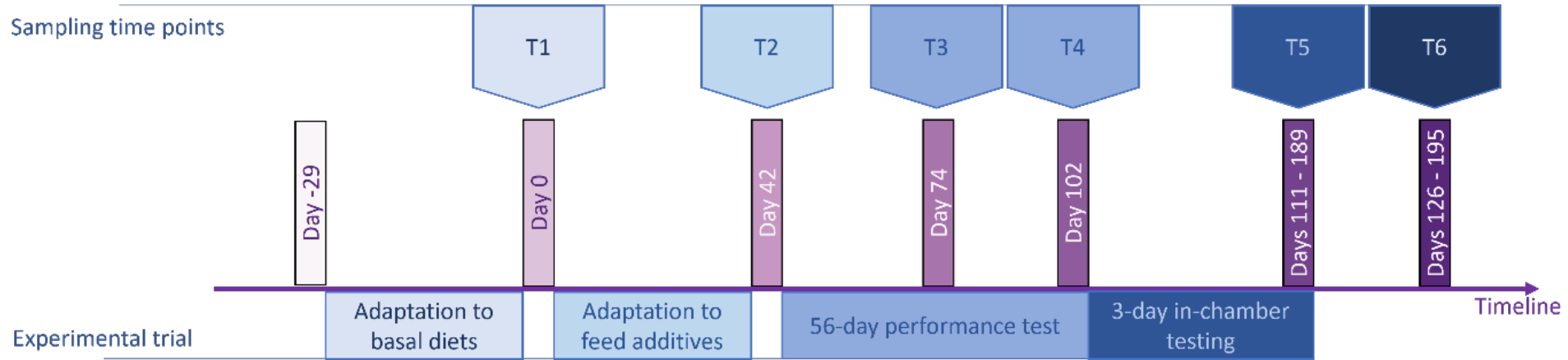
Acetogenesis

Microbial interactions and host
genomically influence rumen
environmental conditions may affect the
thermodynamics between
methanogenesis and acetogenesis

The rumen microbiome is temporally stable

97. Associations between the rumen microbiome and host performance traits are substantially stable throughout the finishing phase of beef cattle

J. Lima^{a,*}, M. Martinez-Alvaro^a, J. Mattock^b, M.D. Auffret^c, C.A. Duthie^a, M. Cleveland^d, R.J. Dewhurst^a, M. Watson^{a,e}, R. Roehe^a



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| Data | Timepoint | FCR | ADG | DFI | RFI | CH ₄ yield | Daily CH4 |
|------------------|---------------------------------|------|------|------|------|-----------------------|-----------|
| Microbial genera | Number of explanatory variables | 224 | 264 | 270 | 252 | 162 | 288 |
| | T1 | 57.2 | 54.1 | 73.2 | 57.8 | 60.9 | 72.7 |
| | T2 | 74.1 | 65.2 | 86.1 | 68.1 | 60.4 | 74.3 |
| | T3 | 54.5 | 67.6 | 66.5 | 53.2 | 70.6 | 64.1 |
| | T4 | 63.5 | 39.8 | 53.4 | 50.6 | 56.6 | 59.0 |
| | T5 | 70.9 | 63.4 | 81.8 | 70.3 | 52.4 | 71.6 |
| | T6 | 53.0 | 53.7 | 71.7 | 64.5 | 49.3 | 52.0 |
| | Average | 62.2 | 57.3 | 72.1 | 60.7 | 58.4 | 65.6 |
| | SD | 8.8 | 10.3 | 11.6 | 8.1 | 7.5 | 8.9 |

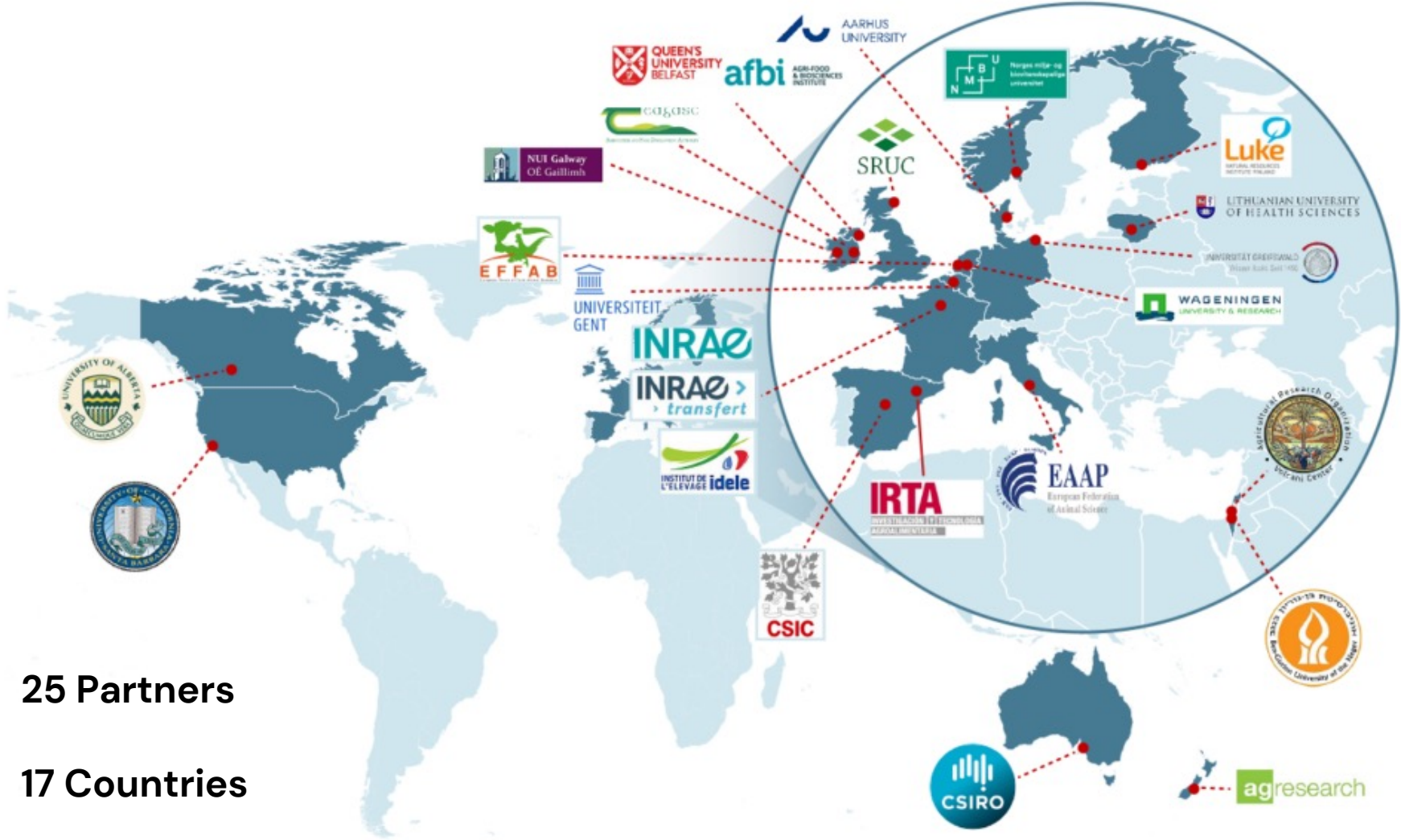
| Data | Timepoint | FCR | ADG | DFI | RFI | CH ₄ yield | Daily CH4 |
|-----------------|---------------------------------|------|------|------|------|-----------------------|-----------|
| Microbial genes | Number of explanatory variables | 144 | 133 | 194 | 214 | 223 | 204 |
| | T1 | 66.8 | 60.7 | 71.5 | 73.8 | 73.4 | 82.1 |
| | T2 | 53.0 | 55.5 | 74.7 | 61.9 | 86.8 | 54.1 |
| | T3 | 68.4 | 62.9 | 63.6 | 62.8 | 82.0 | 77.6 |
| | T4 | 82.0 | 70.4 | 67.6 | 56.5 | 61.9 | 75.2 |
| | T5 | 87.4 | 72.1 | 63.3 | 69.9 | 65.1 | 70.4 |
| | T6 | 56.7 | 71.6 | 55.9 | 58.3 | 70.3 | 71.5 |
| | Average | 69.0 | 65.5 | 66.1 | 63.9 | 73.3 | 71.8 |
| | SD | 13.6 | 6.9 | 6.7 | 6.7 | 9.6 | 9.7 |

Main aims

- Characterize ruminant-associated microbiomes
- Influence of microbiomes on **host animal in early life** – establishment and maintenance
- Influence of microbiomes throughout fundamental life events with impact on **animal production, health, and welfare**:
 - Weaning
 - Feed transitions
 - Lactation
- Facilitate adoption of novel practices and innovations



The HoloRuminant concept



25 Partners

17 Countries

- Australia
- Belgium
- Canada
- Denmark
- Finland
- France
- Germany
- Ireland
- Israel
- Italy
- Lithuania
- Netherlands
- New Zealand
- Norway
- Spain
- United States of America
- United Kingdom



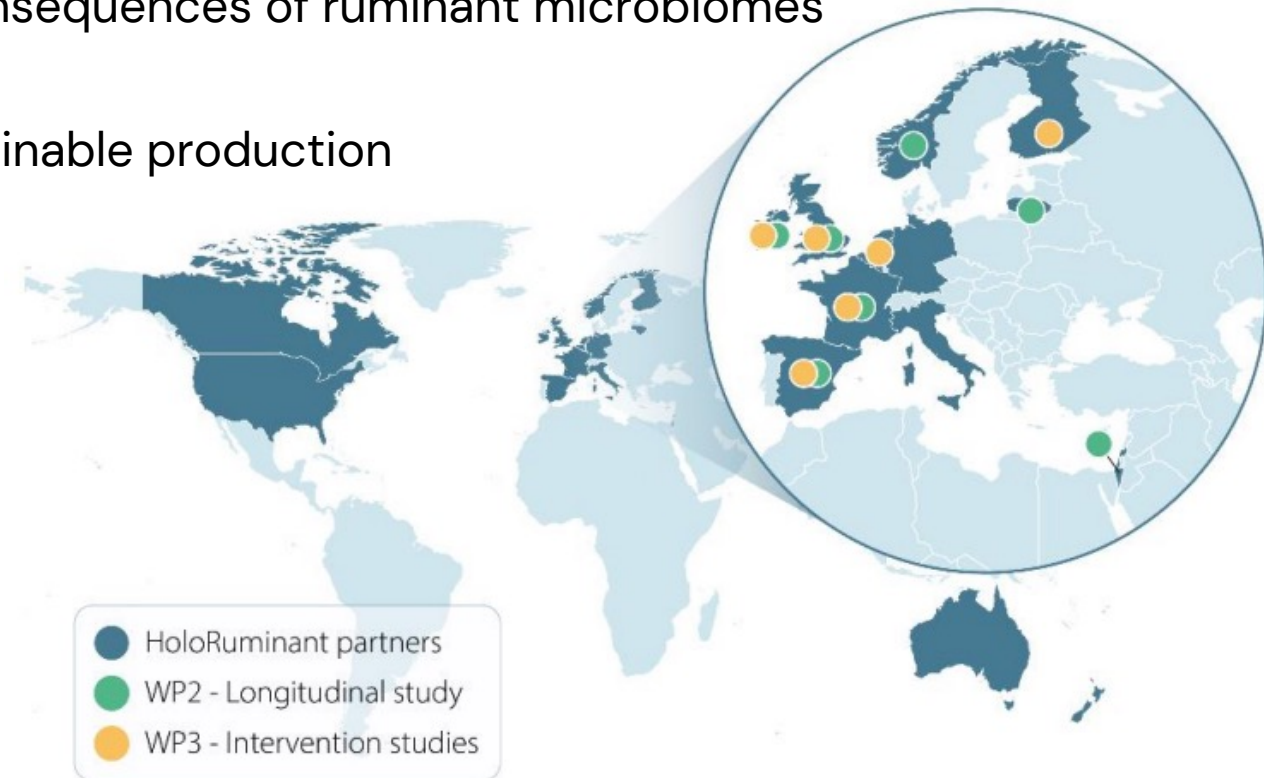
HoloRuminant @ SRUC

Work Package 2

Colonisation, persistence and consequences of ruminant microbiomes

Work Package 3

Ruminant microbiomes and sustainable production





HoloRuminant @ SRUC



Richard Dewhurst

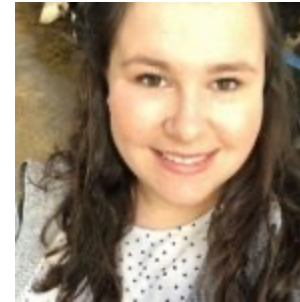
Professor of Ruminant Nutrition &
Production Systems

Head of the Dairy Research Centre



Rainer Roehe

Professor of Animal Genetics and
Microbiome



Holly Ferguson

Precision Dairying Scientist



Joana Lima

Microbiome

Partners




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