

Reducing dairy cattle enteric methane emissions using rumen metagenome

Boris Sepulveda,

Oscar González-Recio,

Amanda Chamberlain, Benjamin Cocks,
Jianghui Wang, Claire Prowse-Wilkins, Majid
Khansefid, Ruidong Xiang, Leah Marett, Richard
Williams, Joe Jacobs, Aser García-Rodríguez,
Jose Jiménez-Montero &

Jennie Pryce

May 2024



The rumen microbiota is a target trait in genomic selection to reduce enteric methane emissions

Methane



Image from www.hankkija.com

A potent greenhouse gas

Energy lost

CH₄ traits are sometimes weakly correlated but...

The nature of all traits is the same

Ruminal microbes



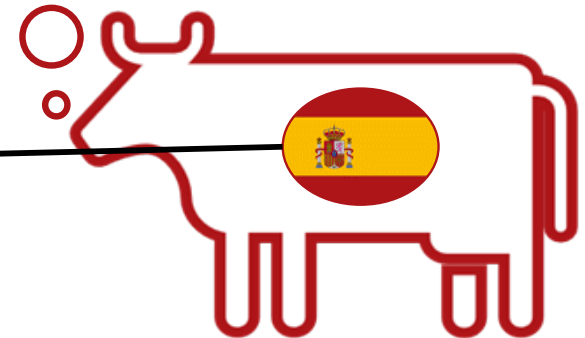
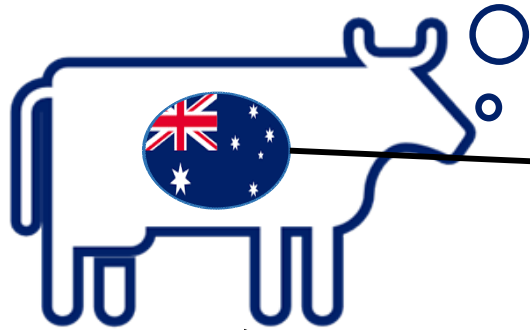
Prof Jennie Pryce
Agriculture Victoria



Dr Oscar González Recio
INIA - CSIC

MeP (g/d) with SF₆

MeC (ppm) with sniffers



Rumen metagenome



Cow genome

>400 Holstein dairy cows
1 research farm

>400 Holstein dairy cows
Multiple commercial farms



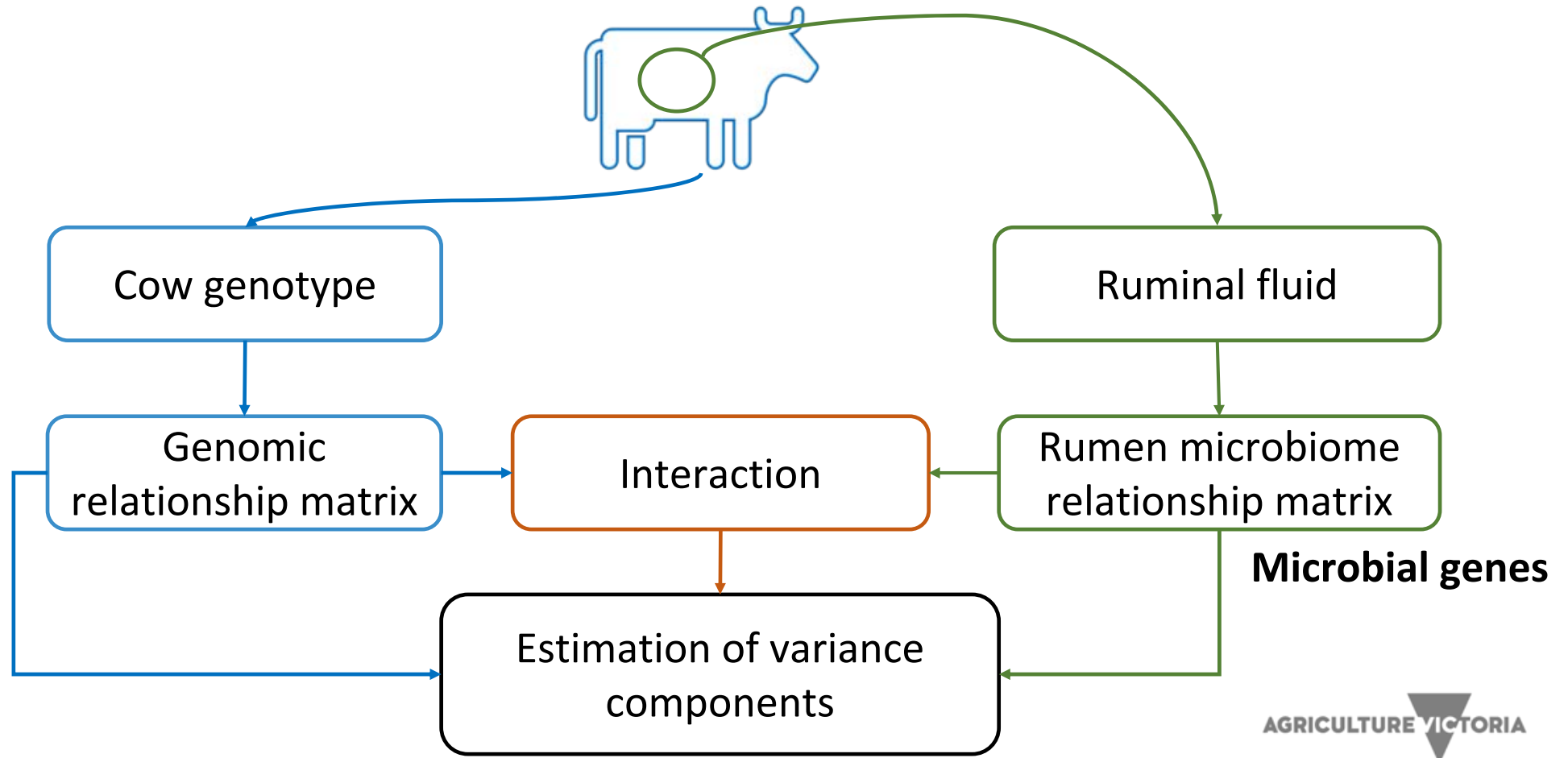
Variance components in methane emissions

- Cow genetics
- Rumen microbiome
- Interaction

- Holobiont model

Saborío-Montero et al. (2021). *Livestock Science*, 250, 104538

$$\text{Methane} = \mathbf{1}'\mu + \mathbf{Zg} + \mathbf{Um} + \mathbf{T}(\mathbf{g} \times \mathbf{m}) + \text{other effects} + \text{residual}$$



Other effects



Fixed

- Cohort (11 levels)
- Dry matter intake
- Days in milk
- Energy corrected milk
- Daily body weight change during the experiment



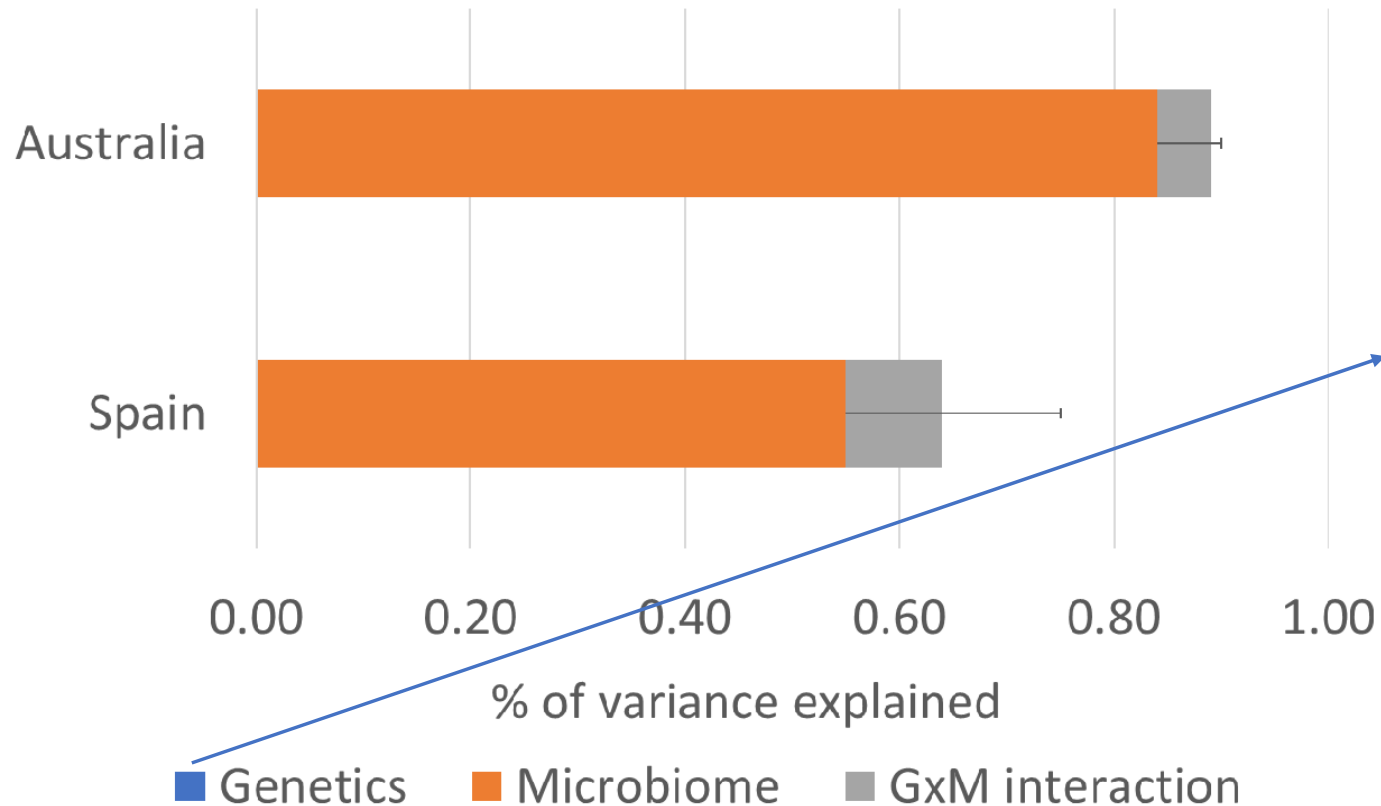
Random

- Sniffer nested within farms (24 levels)

Fixed

- Lactation number (2 levels)
- Stage of lactation (3 levels)

Variance in enteric methane emissions

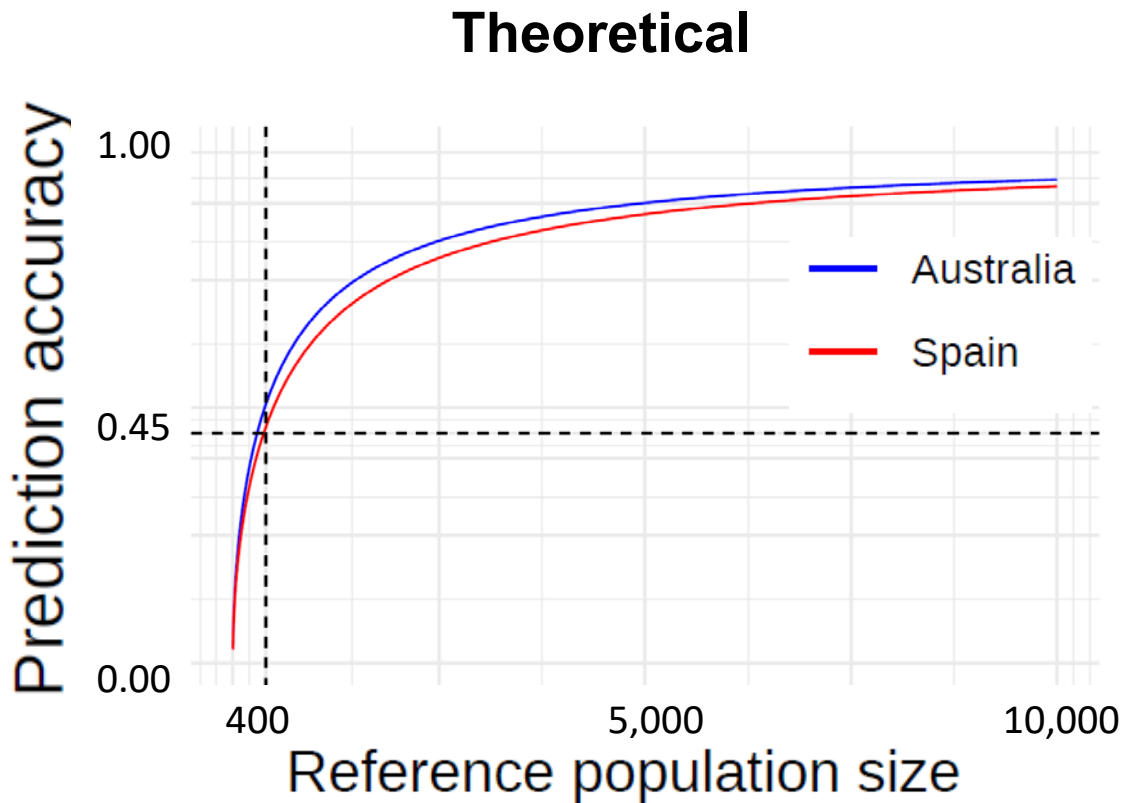


Consistent with the nature of the trait

The role of genetics is modulating the microbiome

Consistent with the literature

Prediction accuracy



Actual
(cross-validation within population)

- Australia: ~0.40
- Spain: ~0.20

Our proposed methodology

- Agrees with the trait's biology
 - Methane is not an intrinsic trait of cows
 - But a “trait” of the ruminal microbiome
- The role of genetics is modulating this microbiome
 - Consistent with the literature

Heritability and correlations

- For each microbial gene:
 - Heritability and breeding values with univariate GBLUP **within** population
- microbial gene** = $\mathbf{1}'\mu + \mathbf{Zg}$ + other effects + residual
- Phenotypic correlation: correlation between raw phenotypes
 - Genetic correlation: correlation between breeding values

Other effects



Fixed

- Cohort (11 levels)
- Dry matter intake
- Days in milk
- Energy corrected milk
- Daily body weight change during the experiment



Random

- Sniffer nested within farms (24 levels)

Fixed

- Lactation number (2 levels)
- Stage of lactation (3 levels)

Selection response

3 scenarios (Martínez-Álvaro et al. 2022. Commun. Biol, 5(1))

1. Directly selection against methane records only

2. Indirectly selecting on microbial genes only

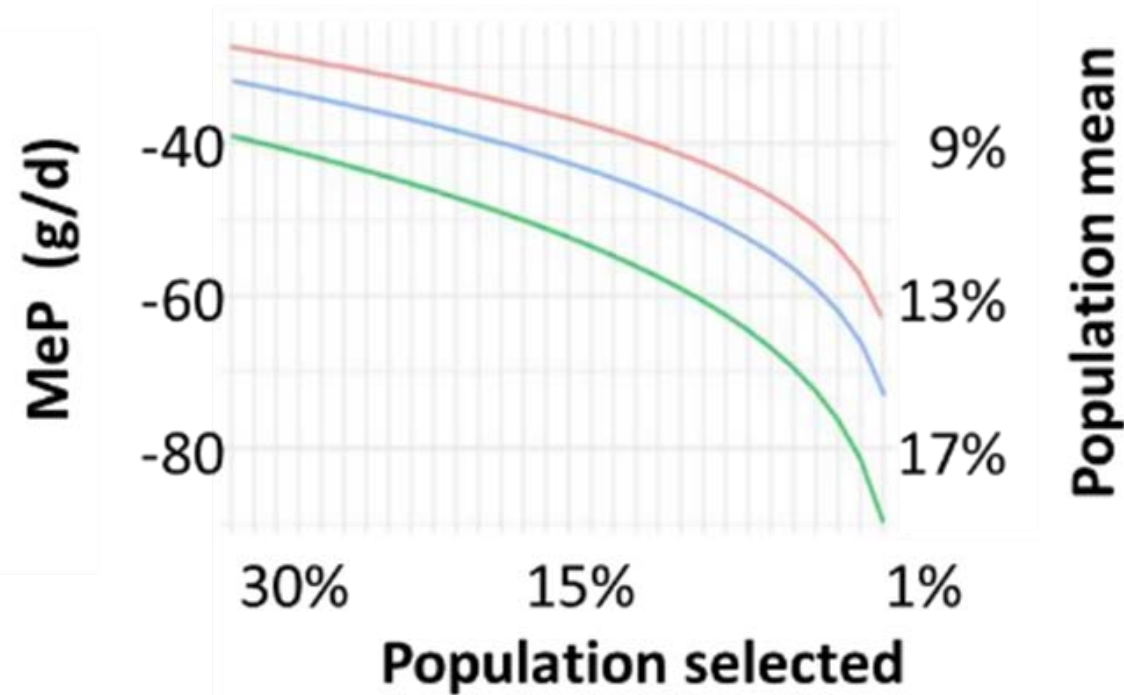
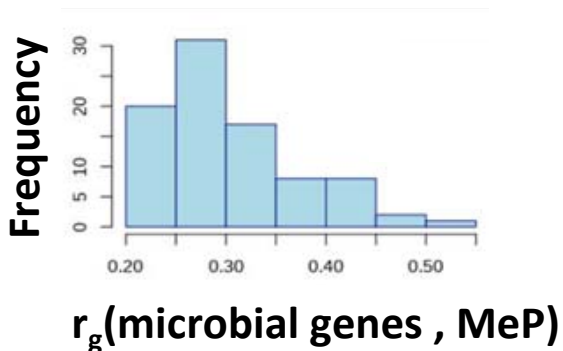
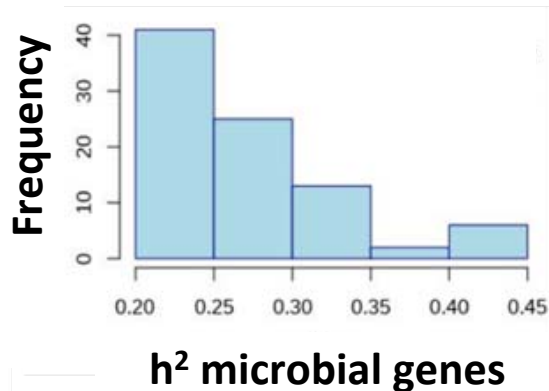
Selection index approach (Cameron, 1997).

microbial genes with h^2 and $r_g \geq 0.20$

3. Combination of scenarios 1 and 2

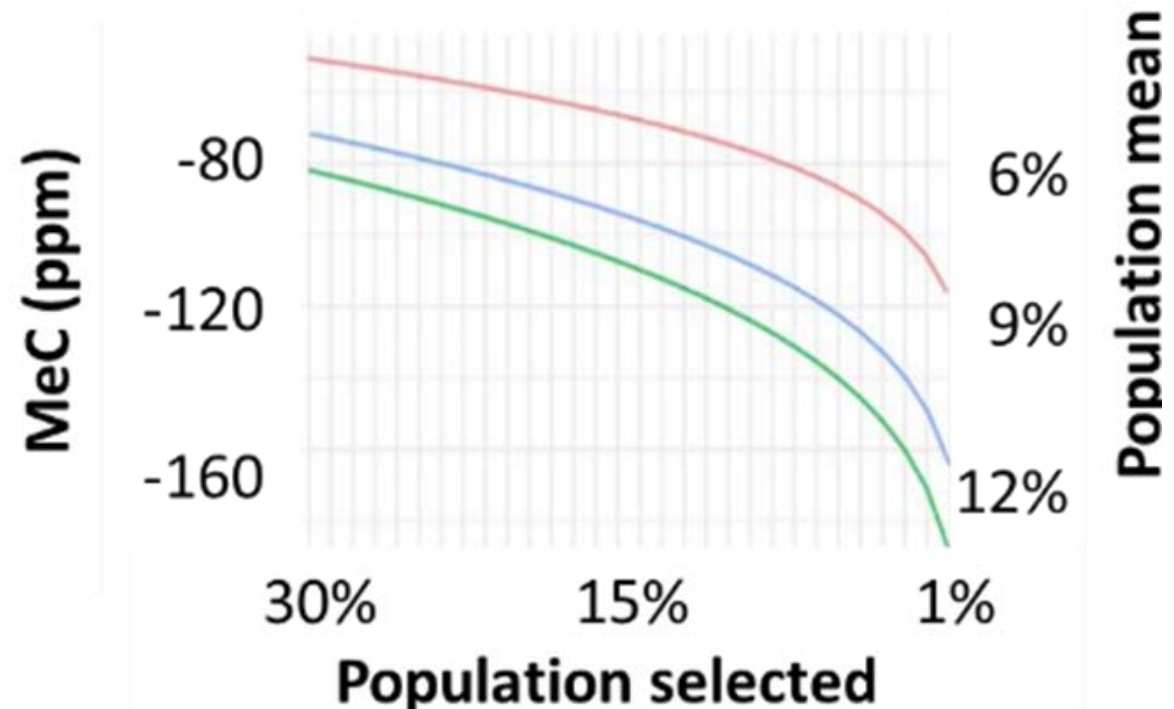
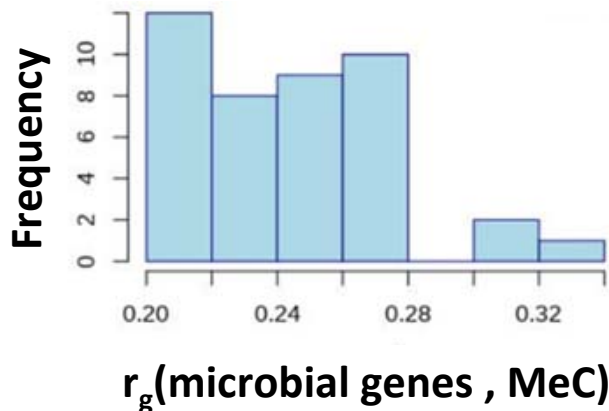
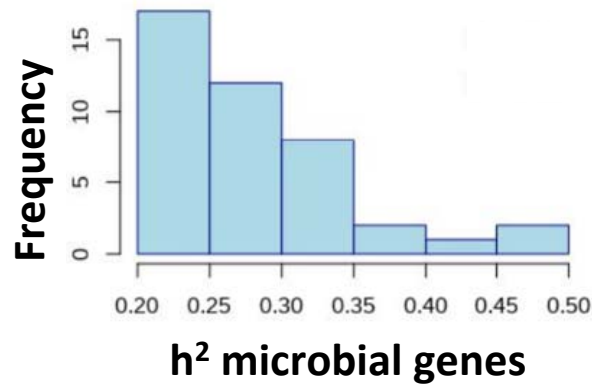
30% to 1% of the population with the lowest emissions is selected

Response to selection - Australia



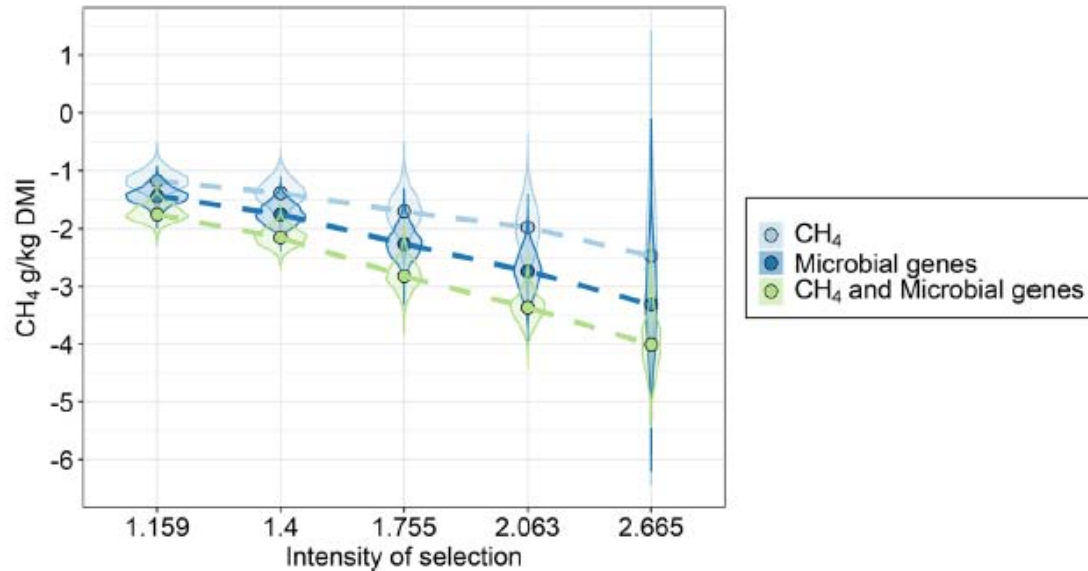
- Methane records
- Microbial genes
- Methane records and Microbial genes

Response to selection - Spain



- Methane records
- Microbial genes
- Methane records and Microbial genes

Agree with literature



communications biology

ARTICLE

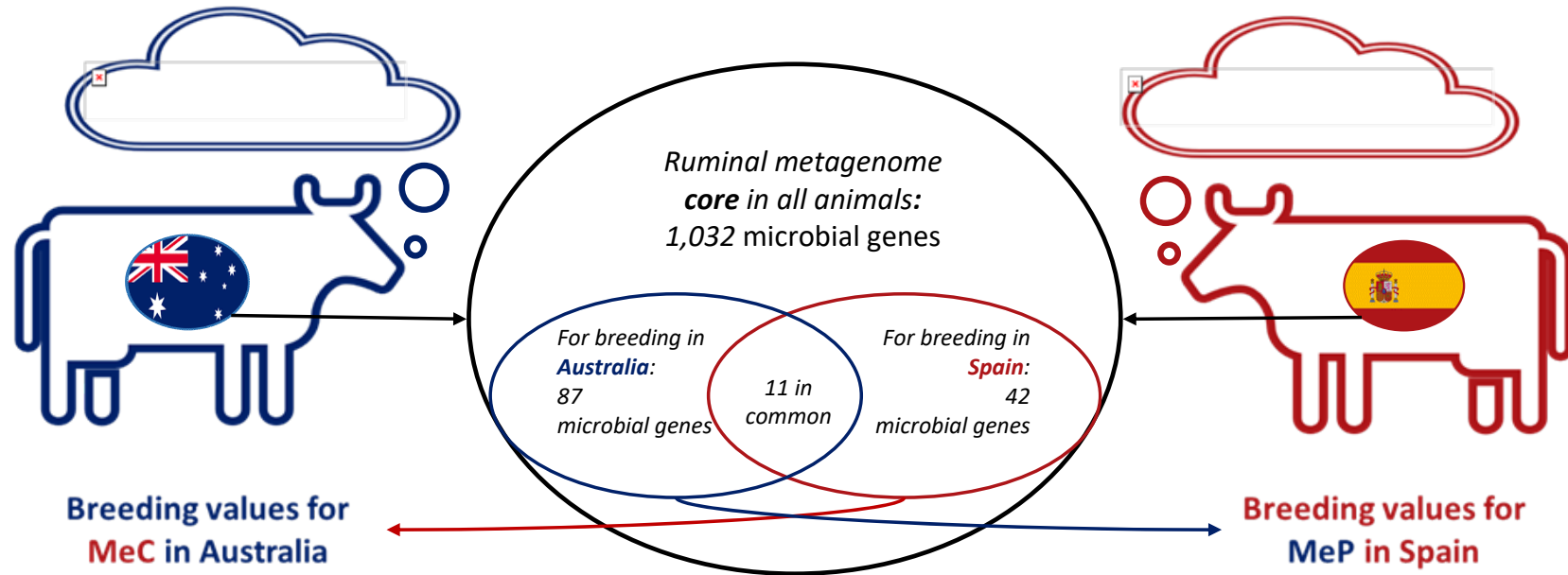
<https://doi.org/10.1038/s42003-022-03293-0>

OPEN

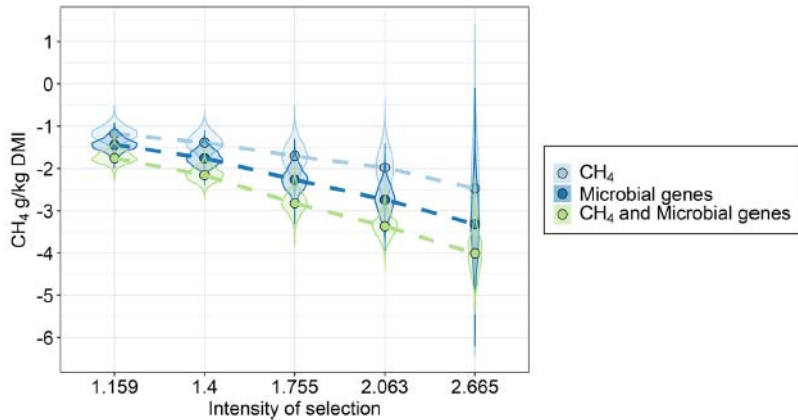
Bovine host genome acts on rumen microbiome function linked to methane emissions

Marina Martínez-Álvaro¹, Marc D. Auffret², Carol-Anne Duthie¹, Richard J. Dewhurst¹, Matthew A. Cleveland³, Mick Watson⁴ & Rainer Roehe^{1,5}

Microbiome connect populations with different emission traits ...



... and can even connect dairy and beef



communications biology

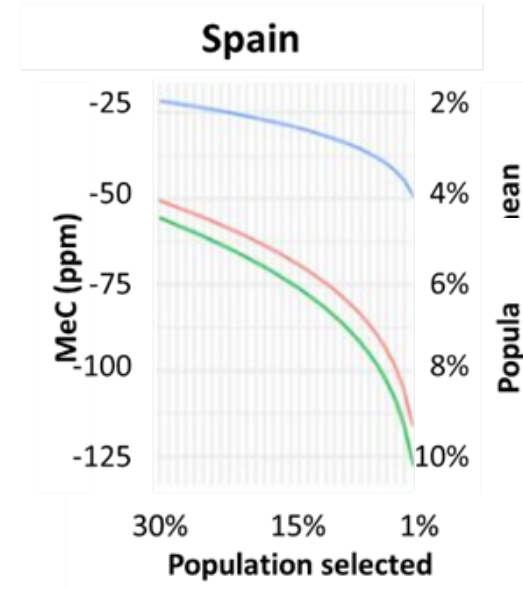
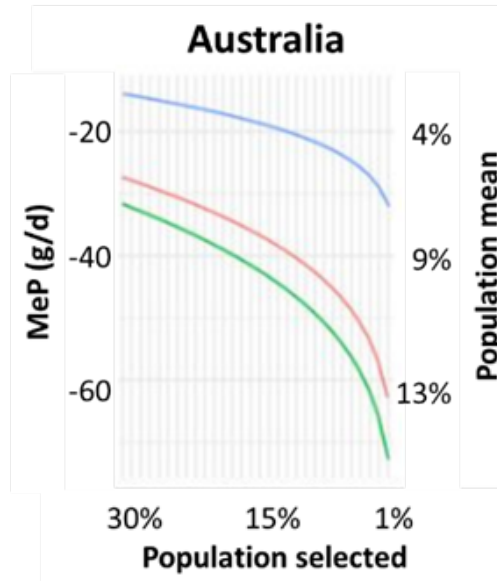
ARTICLE

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

OPEN

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

Marina Martínez-Álvarez¹, Marc D. Auffret², Carol-Anne Duthie¹, Richard J. Dewhurst¹, Matthew A. Cleveland³, Mick Watson⁴ & Rainer Roehe^{1,5*}



- Methane records
- Microbial genes
- Methane records and Microbial genes

Conclusions

- Rumen microbiome explain most of the variation in methane emissions
- Genetics affects indirectly by modulating the microbiome
- The rumen microbiome could be a target trait to reduce emissions
- Microbiome could connect populations and emission traits
- Microbes do not replace emissions records. They are complementary.

Conclusions

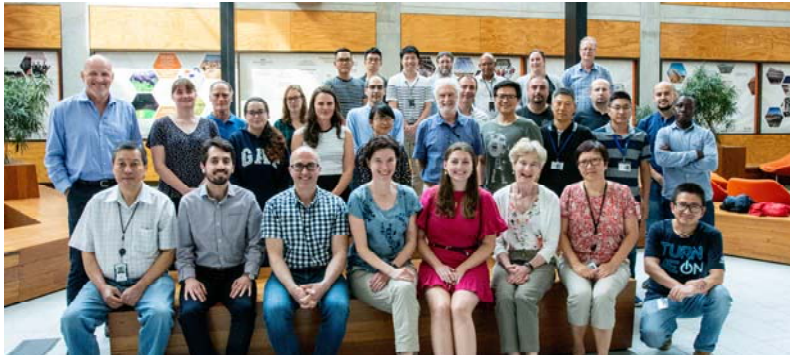
- Rumen microbiome explain most of the variation in methane emissions
- Genetics affects indirectly by modulating the microbiome
- The rumen microbiome could be a target trait to reduce emissions
- Microbiome could connect populations and emission traits
- **Microbes do not replace emissions records. They are complementary.**

Before implementation

- The results need validation
 - Larger population
 - Commercial conditions
 - Multivariate models to estimate heritability and genetic correlations
- Effect of modulating microbiome on:
 - Other traits
 - Health

A **global effort** to validate a **common core** of ruminal features to reduce enteric methane emissions is required

Acknowledgment



Computational Biology Group

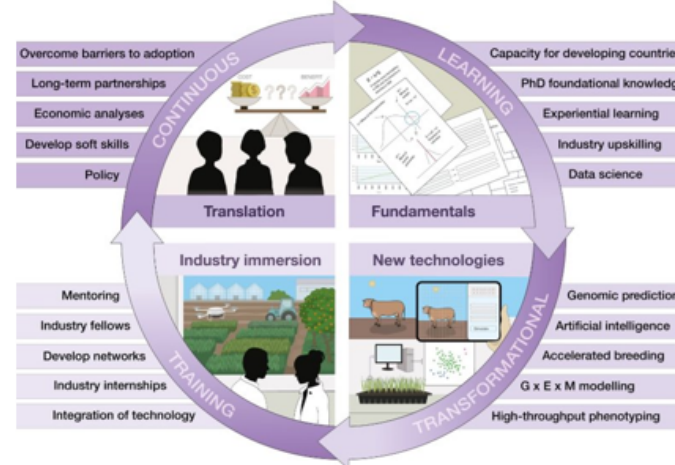
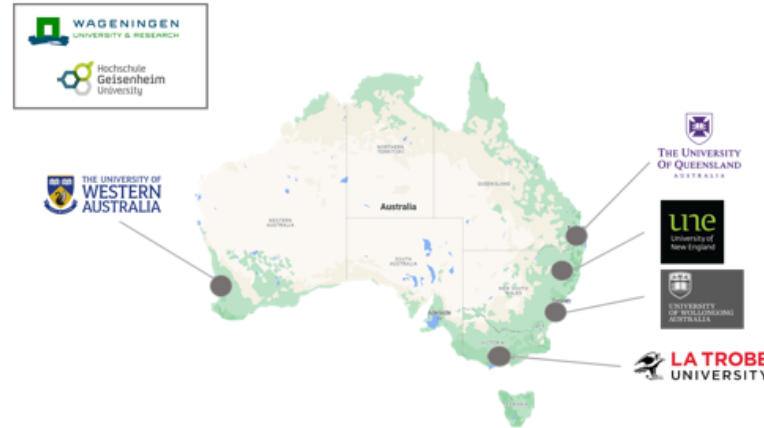


Ellinbank and Green Cow teams



ARC Training Centre in Predictive Breeding for Agricultural Futures

- The world's first centre dedicated to **training the next generation of plant and animal breeders** is being established at The University of Queensland
- The Centre consists of seven University Nodes and over 30 industry and government partners
- **38 PhD studentships and postdoctoral positions** are available within the Centre and projects focus on **21 agriculturally important species/commodities**
- Projects include a **placement with our leading industry partners**, access to **short courses**, and an opportunity to learn and apply **cutting-edge technologies** to help solve real world problems
- **Recruitment** will commence shortly – email predictivebreeding@uq.edu.au to be part of this exciting new Centre!

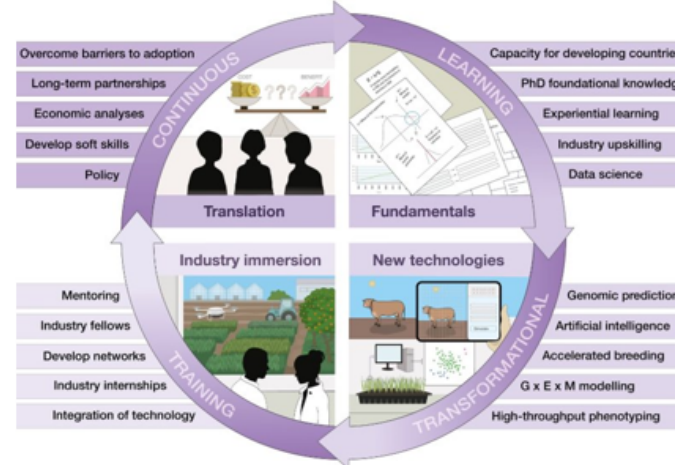


Thank you



ARC Training Centre in Predictive Breeding for Agricultural Futures

- The world's first centre dedicated to **training the next generation of plant and animal breeders** is being established at The University of Queensland
- The Centre consists of seven University Nodes and over 30 industry and government partners
- **38 PhD studentships and postdoctoral positions** are available within the Centre and projects focus on **21 agriculturally important species/commodities**
- Projects include a **placement with our leading industry partners**, access to **short courses**, and an opportunity to learn and apply **cutting-edge technologies** to help solve real world problems
- **Recruitment** will commence shortly – email predictivebreeding@uq.edu.au to be part of this exciting new Centre!





Theoretical accuracy

$$r_{EMV} = \sqrt{\frac{N_p m^2}{N_p m^2 + P}}$$

Ross and Hayes (2022). fgen, 13

Where (N_p) is the number of animals in the reference population with phenotype and metagenomics, m^2 is microbiability, and P is the number of ruminal features (KOs).