Association between rumen and faecal microbiome and enteric methane emissions in dairy cattle

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October 2025

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Dairy Australia

Dairy Bio

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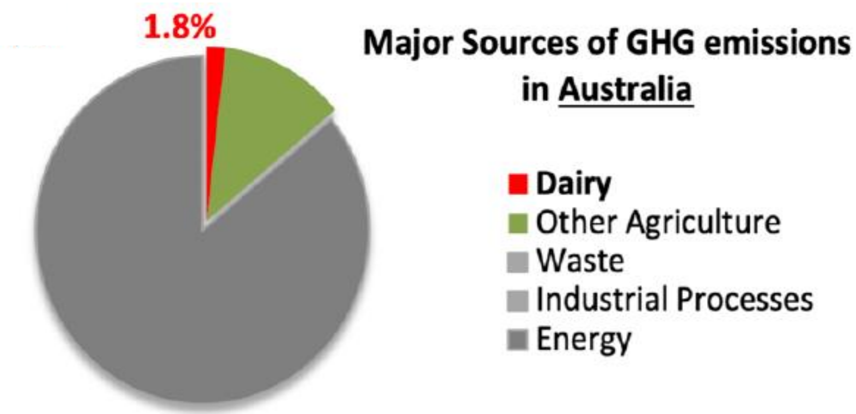
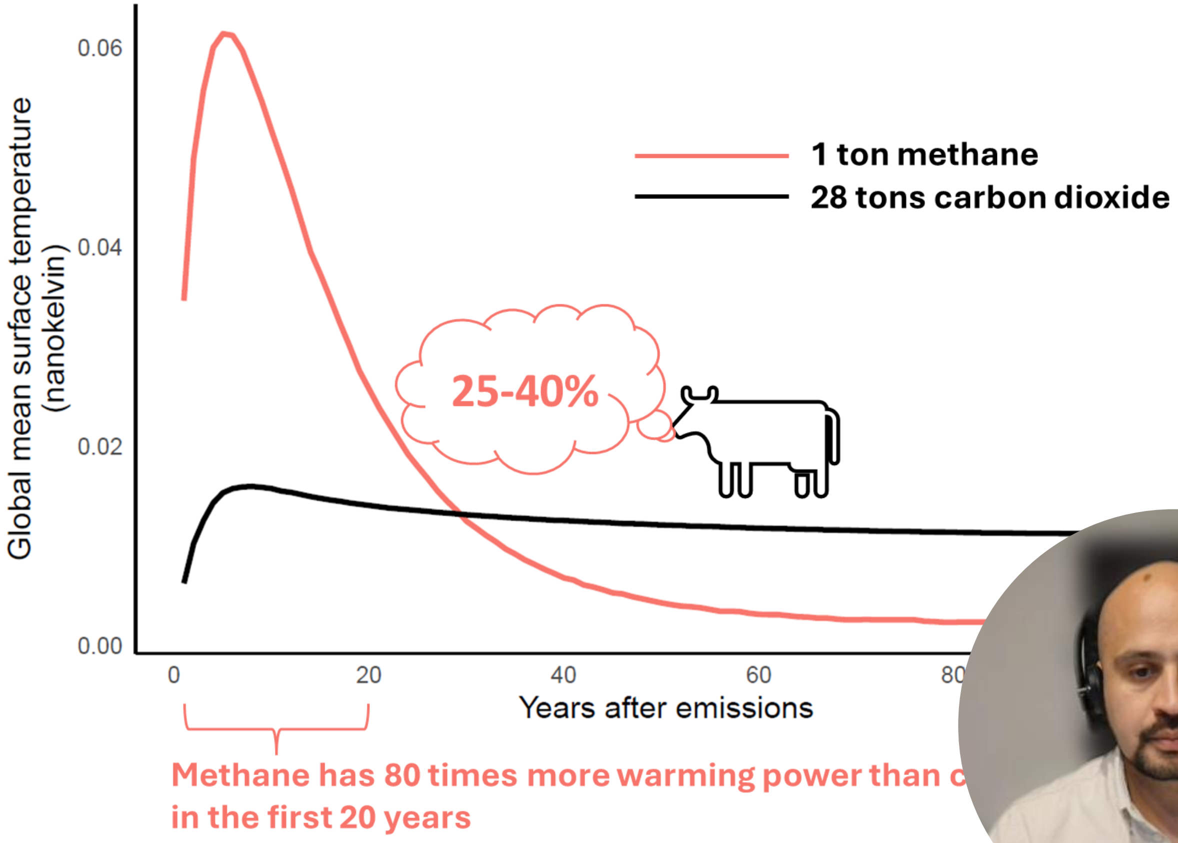
DairyFeedbase

Cows: NOT the main polluter, but a key solution



Richardson, 2020. PhD Thesis, La Trobe University



Sepulveda, 2024. PhD Thesis, La Tr

Rumen microbes and methane

Recording methane is costly and impractical

Ruminal microbes indicate methane emissions

J. Dairy Sci. TBC:1–19
https://doi.org/10.3168/jds.2024-25436

Rumen metagenome as a genomic selection target to reduce enteric methane emissions

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RESEARCH ARTICLE | Open Access

Rumen metagenome profiles are heritable and rank the New Zealand national sheep flock for enteric methane emissions

Timothy P. Bilton[1*], Setegn W. Alemu[1], Ken G. Dodds[1], Hannah Henry[1], Melanie K. Hess[1], Ronan Jordan[1], Fern Booker[1], Sharon M. Hickey[2], Neville Amyes[2], Kevin Knowler[1], Edgar Sandoval[3], Jacqueline Peers-Adams[1], Tracey C. van Stijn[1], Hayley Baird[1], Trevor Watson[2], Wendy Bain[1], Barry Veenvliet[1], Gerard Pile[1], Brooke Bryson[4], Shannon M. Clarke[1], Patricia L. Johnson[1], John C. McEwan[1] and Suzanne J. Rowe[1]

ORIGINAL ARTICLE

Journal of Animal Breeding and Genetics | WILEY

Structural equation models to disentangle the biological relationship between microbiota and complex traits: Methane production in dairy cattle as a case of study

Alejandro Saborío-Montero[1,2] | Mónica Gutiérrez-Rivas[1] | Aser García-Rodríguez[3] | Raquel Atxaerandio[3] | Idoia Goiri[3] | Evangelina López de Maturana[4] | José Antonio Jiménez-Montero[5] | Rafael Alenda[6] | Oscar González-Recio[1,6]

J. Dairy Sci. 106:2198–2212
https://doi.org/10.3168/jds.2022-22578

***Invited review:* Recursive models in animal breedin
Interpretation, limitations, and extensions**

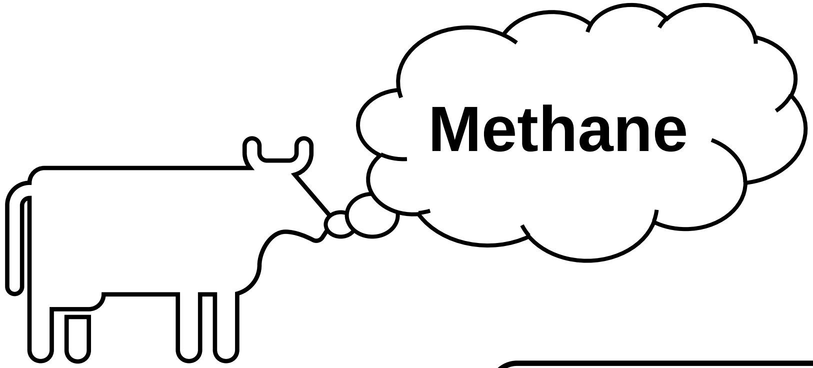
L. Varona[1*] and O. González-Recio[2]

OFFICIAL

Rumen and faecal microbes and methane

- Rumen sampling is invasive
- Faecal samples are easer to
- Could faecal microbes indicat
- Could faecal microbes indicat
  intake, etc

A stomach tube is passed orally down the
into the reticulo-rumen. *Photos provided by*



25 Holstein dairy cows

Rumen and faecal sampling

Laboratory processing

Extract DNA

Long-read sequencing with Oxford Nanopore Technologies

Bioinformatics

Assign taxa and functions to the sequenced DNA using SqueezeMeta*

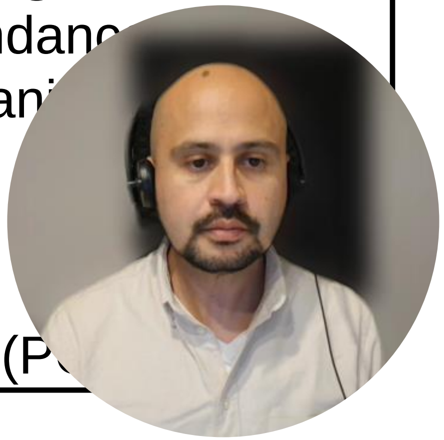
* doi.org/10.3389/fmicb.2018.03349

Data processing

- Remove non-microbial abundanc
- Features in at least 90% of ani
- Impute zeros
- Abundance to proportions
- Normalization (CLR)
- 5 first principal components (P

Phenotypic correlation between PC and methane adjusted by:

- Experiment (2 levels)
- Feed intake
- Days in milk
- Parity
- Production
- Body weight



Correlations between PC and methane

Faeces - methane: up to 0.35 ± 0.18

Faeces - rumen

- Type of microbes: -0.37 ± 0.17 to -0.52 ± 0.16
- Genes of microbes: -0.34 ± 0.17 to -0.62 ± 0.12
- |0.62| faeces – PC1 of rumen microbial genes.
    - 46% of variation in rumen

For details:

Proc. Assoc. Advmt. Anim. Breed. Genet. 26: 221-224

ASSOCIATION BETWEEN RUMEN AND FAECAL MICROBIOME AND ENTERIC METHANE EMISSIONS IN DAIRY CATTLE

B.J. Sepulveda[1], C.J. Vander Jagt[1], A.J. Chamberlain[1,3], J. Wang[1], L.C. Marett[2], S.R.O. Williams[2], J.L. Jacobs[2,3] and J.E. Pryce[1,3]

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Current and next steps

- 1,500 samples (83 animals) with methane + rumen + faeces
- Even more animals coming
- Not only principal components
- Heritability, genetic correlations, response to selection

Higher genetic correlations are expected

Example of correlations between rumen metagenome and methane

Rumen feature	Phenotypic correlation with methane	Genetic correlation with methane
Bacteria	-0.47 ± 0.04	-0.91 ± 0.20
Genus *Methanobrevibacter*	0.29 ± 0.05	0.68 ± 0.29

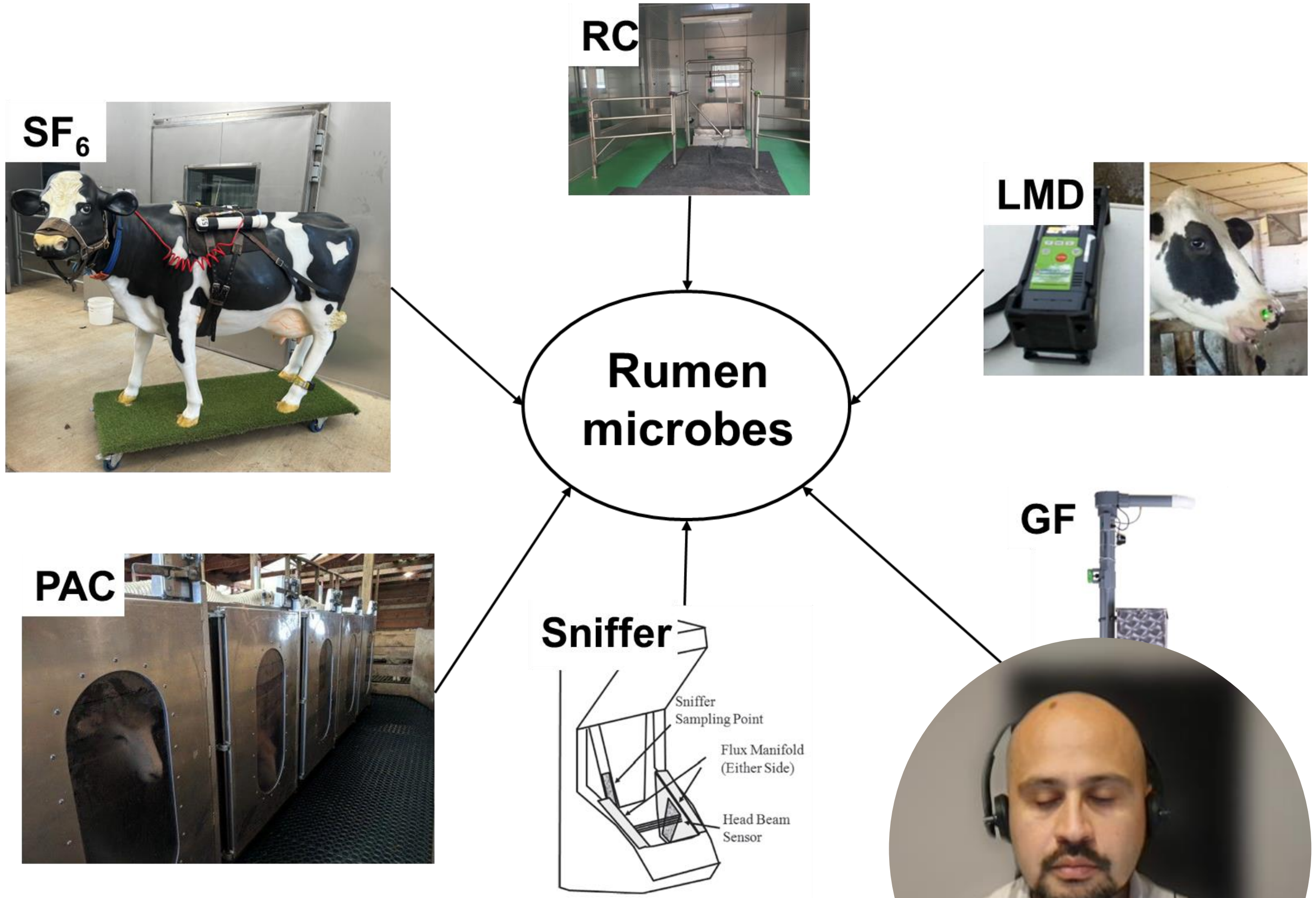
https://doi.org/10.3168/jds.2024-25436

Next step?

Global Methane Genetics MicroHUB

50 + teams
25 countries
>20K cattle and sheep

Some with faecal samples
for further studies
out of microHub



Images from Ellinbank SmartFarm, www.c-lockinc.com, www.nzagrc.org.nz, 10.3168/jds.2014-

Take home messages

Encouraging results (methane-faeces phenotypic correlations up to 0.35)

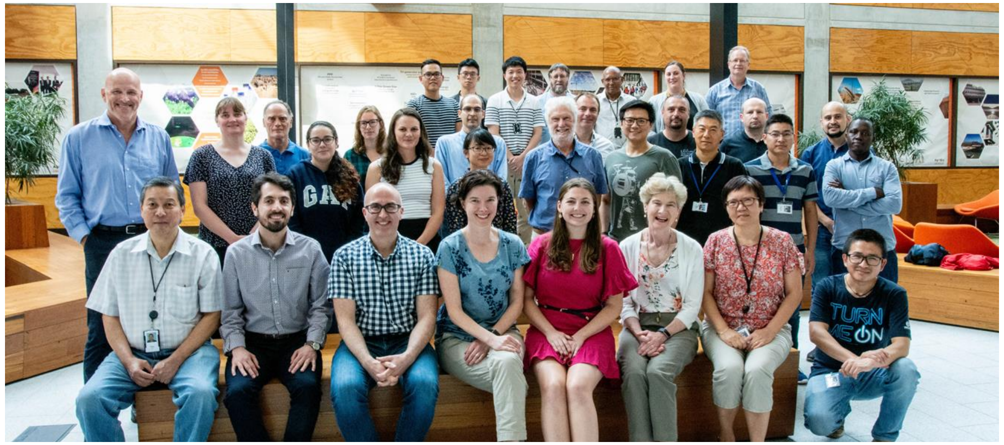
Higher genetic correlations are expected

Microbes from faeces and rumen are associated

Current and next steps:

- Include more animals
- Analyse more phenotypes from microbes
- Estimate genetic parameters

Acknowledgements



Computational Biology Group

Molecular Genetics Goup

Ellinbank and Green Cow tea

Dairy Australia

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Thanks

Dairy Australia

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Take home messages

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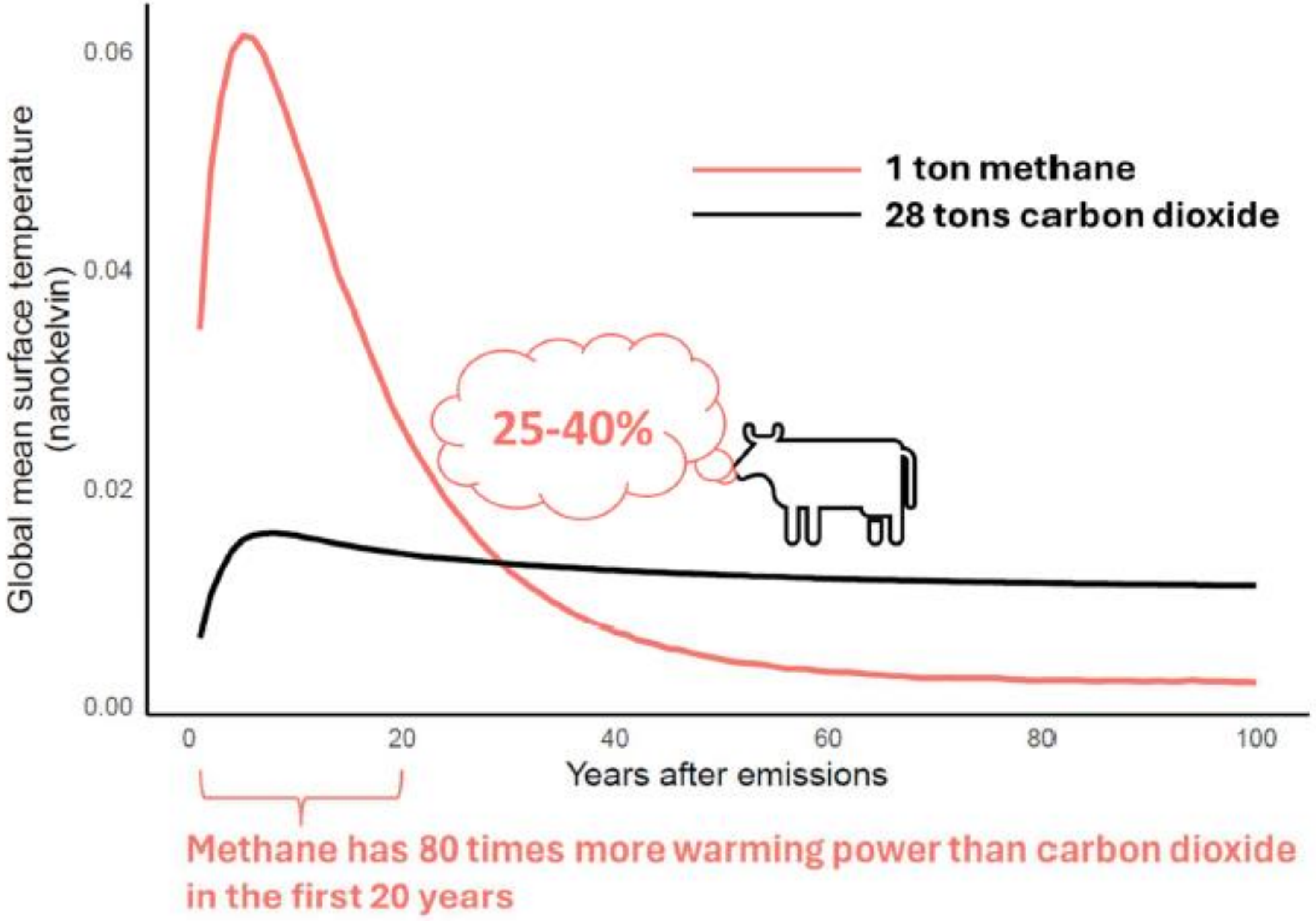

Figure 2. *Impact of methane and carbon dioxide emissions on global surface warming (IPCC, 2021, Azar et al., 2023). The effect of methane is more intense and shorter than the effect of carbon dioxide (Mar et al., 2022). Enteric methane emissions from ruminants contributed with up to 40% of anthropogenic methane emissions (Moss et al., 2000, EPA, 2022).*

https://www.fao.org/in-action/enteric-methane/background/en/

https://asm.org/articles/2023/june/ruminant-methanogens-as-a-climate-change-target

Table 1. phenotypic correlations (r_p) ± standard error (SE), and corresponding *p*-value between the first five principal components (PC1 to PC5) calculated from the content of features from the faecal and ruminal metagenome and methane production (MeP). FE: Fixed effects with significant effect fitted in the prediction model. KO: KEGG Orthology groups. COG: Clusters of Orthologous Genes. Variance explained by each principal component is shown in parenthesis.

Features	**Faeces**	**Rumen**	**FE**	**r_p ± SE**	***p*-value**
Genera	PC1 (16%)	PC3 (6%)	-	-0.52 ± 0.16	1.2×10^{-3}
Genera	PC2 (13%)	PC2 (15%)	parity,ECM	-0.48 ± 0.15	1.4×10^{-3}
Genera	PC4 (7%)	PC3 (6%)	experiment,DMI, parity, ECM	-0.43 ± 0.17	1.1×10^{-2}
Genera	PC5 (6%)	PC1 (29%)	-	-0.40 ± 0.18	2.6×10^{-2}
Genera	PC5 (6%)	PC2 (15%)	experiment,DMI, parity, ECM	-0.47 ± 0.16	3.3×10^{-3}
Genera	PC5 (6%)	PC5 (4%)	parity	-0.37 ± 0.17	3.0×10^{-2}
KO	PC2 (11%)	PC3 (6%)	experiment,ECM	-0.35 ± 0.17	4.0×10^{-2}
KO	PC3 (7%)	PC1 (46%)	experiment,DMI,ECM	-0.35 ± 0.17	4.0×10^{-2}
KO	PC3 (7%)	PC2 (9%)	DMI, parity	-0.46 ± 0.16	4.0×10^{-3}
KO	PC5 (4%)	PC1 (46%)	experiment,parity	-0.62 ± 0.12	2.4×10^{-7}
COG	PC2 (11%)	PC3 (7%)	DMI,parity,ECM	-0.37 ± 0.18	4.0×10^{-2}
COG	PC4 (5%)	PC3 (7%)	DMI,parity	-0.39 ± 0.17	2.2×10^{-2}
COG	PC5 (5%)	PC1 (29%)	experiment	-0.34 ± 0.17	4.6×10^{-2}
Features	**Faeces**	**Final trait**	**FE**	**r_p ± SE**	***p*-value**
Genera	PC5 (6%)	MeP	experiment	0.35 ± 0.18	5.2×10^{-2}
Features	**Rumen**	**Final trait**	**FE**	**r_p ± SE**	***p*-value**
Genera	PC4 (5%)	MeP	-	0.37 ± 0.20	6.4×10^{-2}