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Rowett Institute of Nutrition and Health

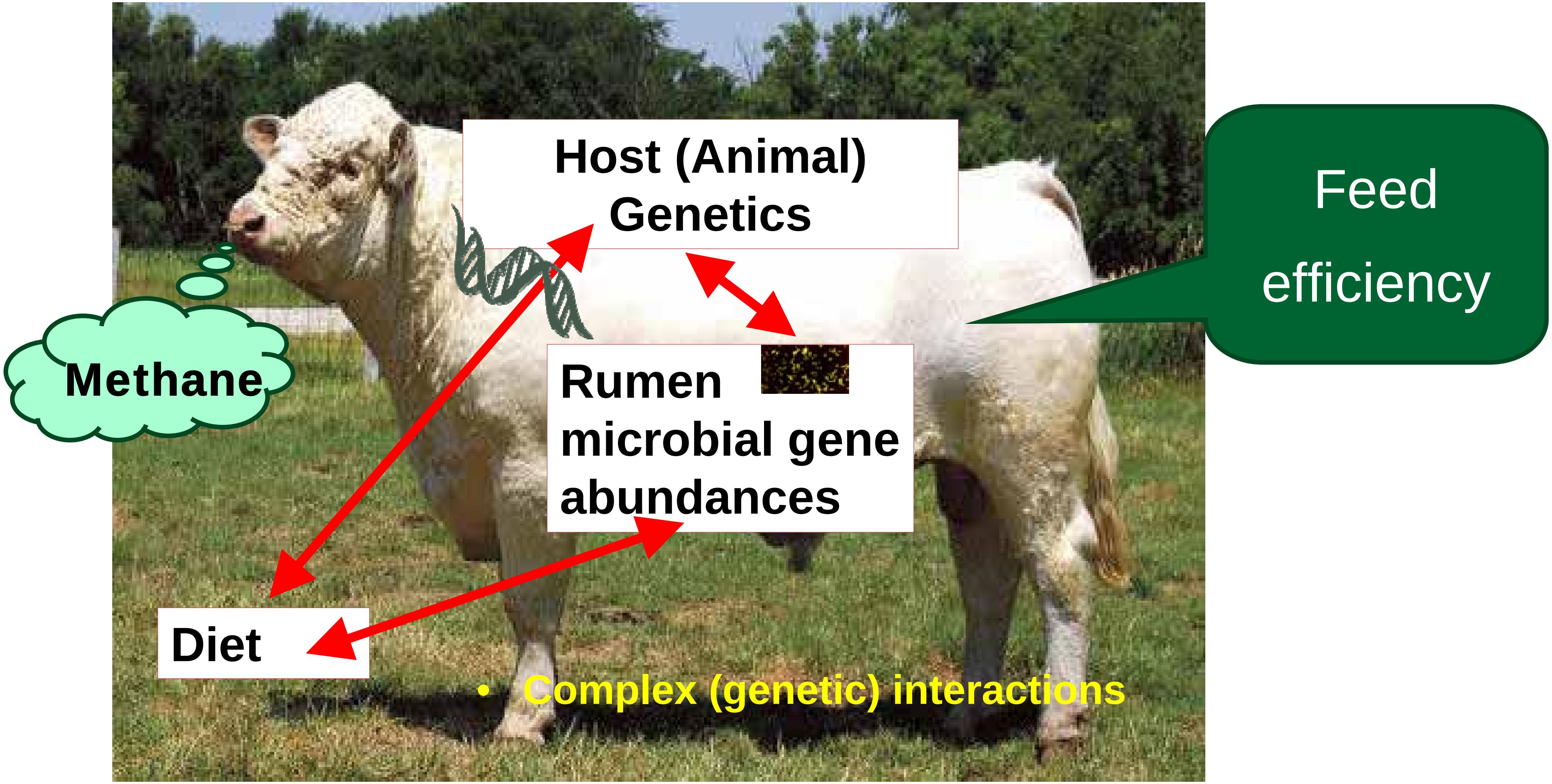
SRUC

The potential of using rumen microbial gene abundances to improve feed efficiency in beef cattle

R. Roehe, M.D. Auffret, A.J. Southwell, C-A. Duthie, J.A. Rooke, R.J. Wallace, T.C. Freeman, T.J. Snelling, R.D. Stewart, M. Watson, R.J. Dewhurst

Leading the way in Agriculture and Rural Research, Education and Consulting

Host Genetics and Microbiome



Host (Animal) Genetics

Rumen microbial gene abundances

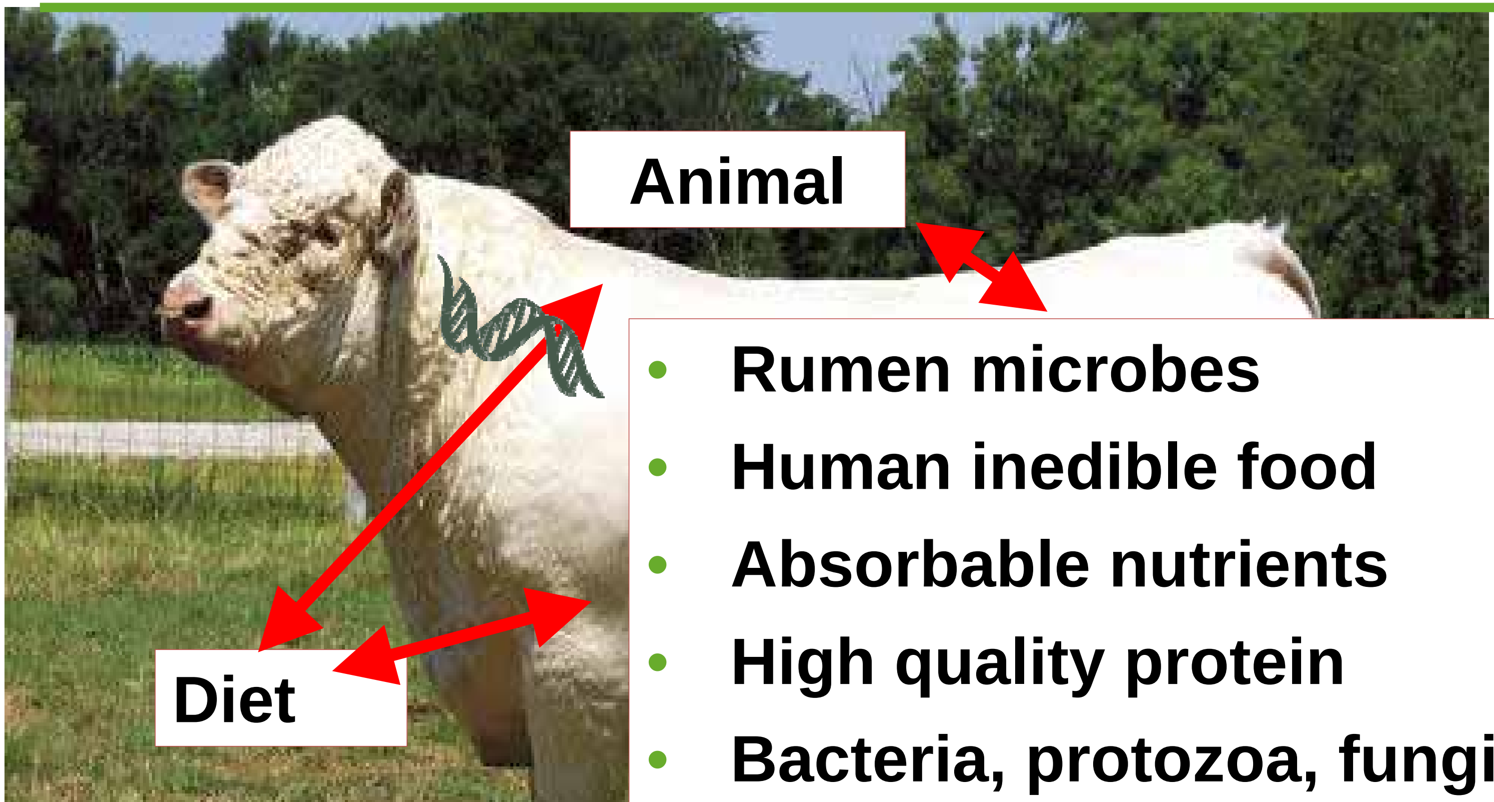
Diet

Methane

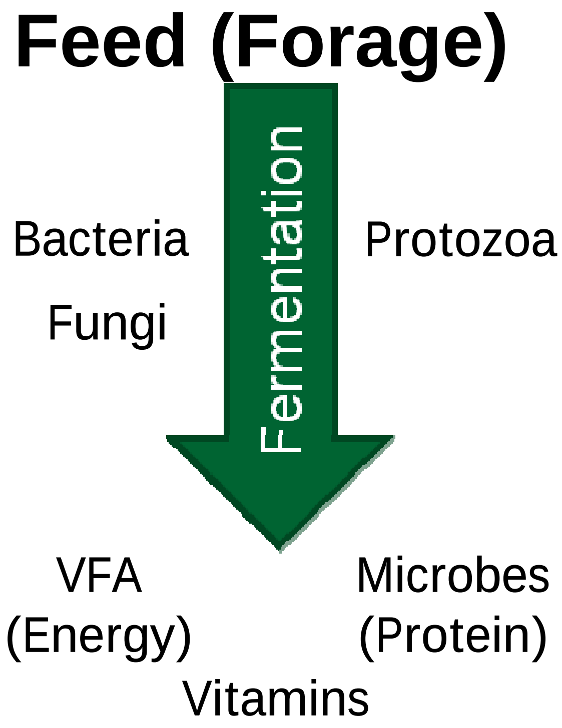
Feed efficiency

- Complex (genetic) interactions

Microbes affecting Feed Efficiency (Symbiosis)



- **Rumen microbes**
- **Human inedible food**
- **Absorbable nutrients**
- **High quality protein**
- **Bacteria, protozoa, fungi**



Feed (Forage)

Bacteria

Fungi

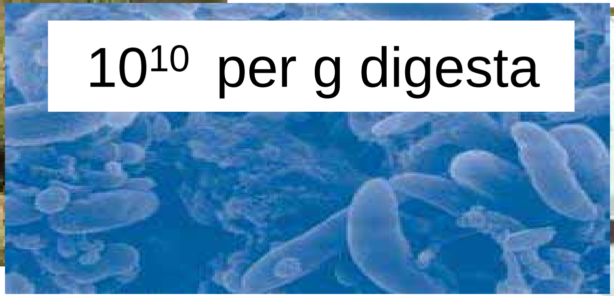
Fermentation

Protozoa

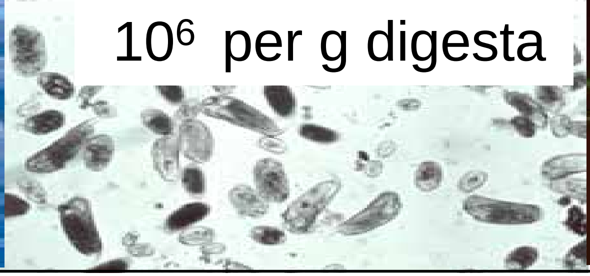
VFA (Energy)

Microbes (Protein)

Vitamins



10^{10} per g digesta



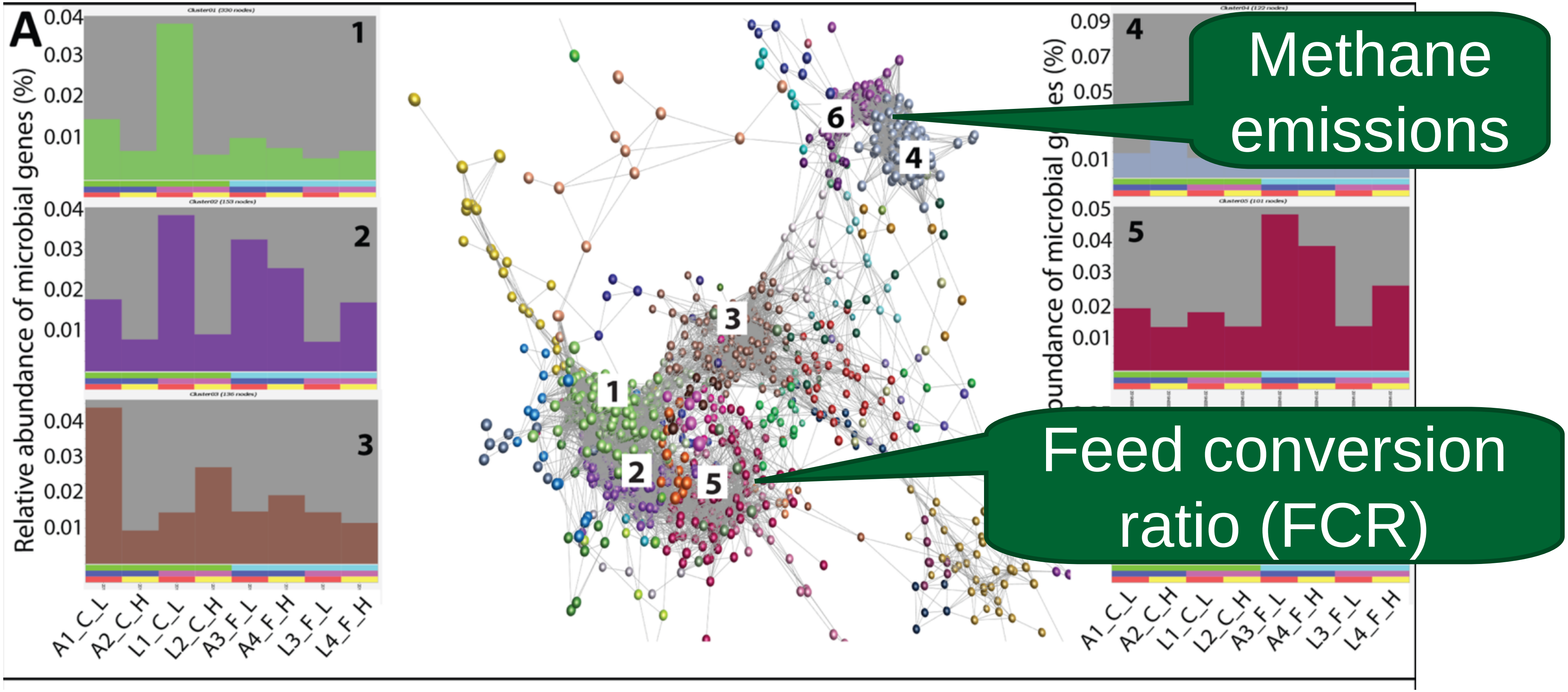
10^{6} per g digesta

10^{3} per g digesta

Deep Sequencing of DNA from Rumen Microbes

<table>
<tr><td colspan="4">Metagenomic analysis</td></tr>
<tr><td colspan="3">Microbial community</td><td>Gene- centric</td></tr>
<tr><td>Domain
e.g.
Archaea,
Bacteria</td><td>Phylum
e.g.
Bacteroidetes,
Proteobacteria</td><td>Genus
e.g.
Methano-
brevibacter,
Methanos-
phaera</td><td>Microbial genes,
e.g.
KEGG gene
orthologues</td></tr>
</table>

Microbial genes associated with FCE & CH_4



Methane emissions

Feed conversion ratio (FCR)

Roehe *et al.* (2016) PLOS Genetics

Selection of Animals for low and high FCR

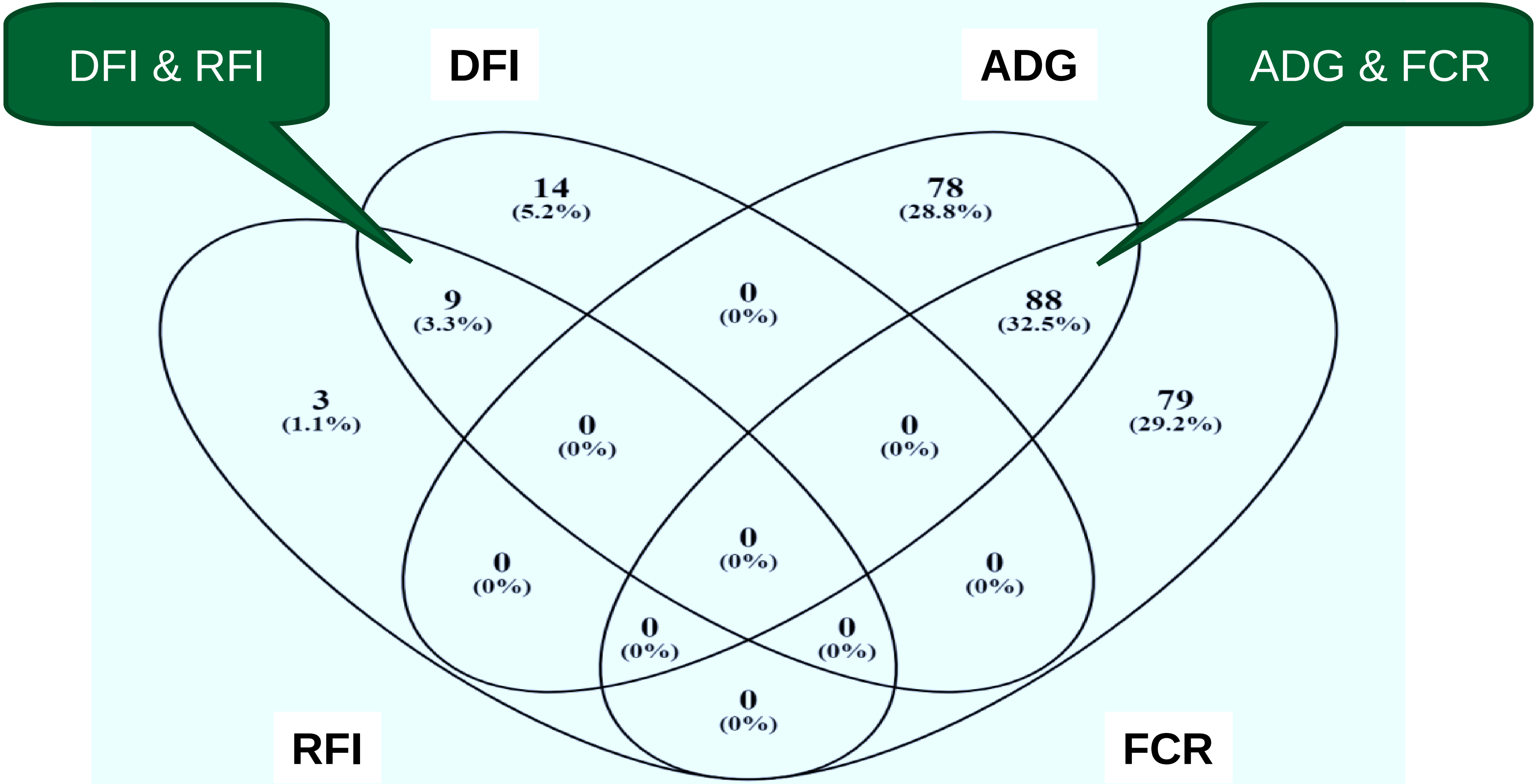
		FCR				
		Low		High		
Trait[1]	Unit	Mean	SD	Mean	SD	**SE_{Diff}**
DFI	kg/day	11.559^{a}	1.279	11.919^{a}	1.968	**0.362**
ADG	kg/day	1.653^{a}	0.389	1.780^{a}	0.430	**0.089**
FCR		6.626^{a}	0.741	8.871^{b}	1.207	**0.218**
RFI		-0.328^{a}	0.682	0.431^{b}	1.025	**0.190**

DFI = daily feed intake; ADG = average daily gain; FCR = feed conversion ratio;
RFI = residual feed intake

PLS analysis to predict traits associated with feed efficiency based on RMGA

	Variation explained in:		Number of:
Trait	Model factors (%)	Trait (%)	Microbial genes
DFI	50	72	23
ADG	64	55	166
FCR	61	68	167
RFI	40	73	12

DFI = daily feed intake; ADG = average daily gain; FCR = feed conversion ratio; RFI = residual feed intake

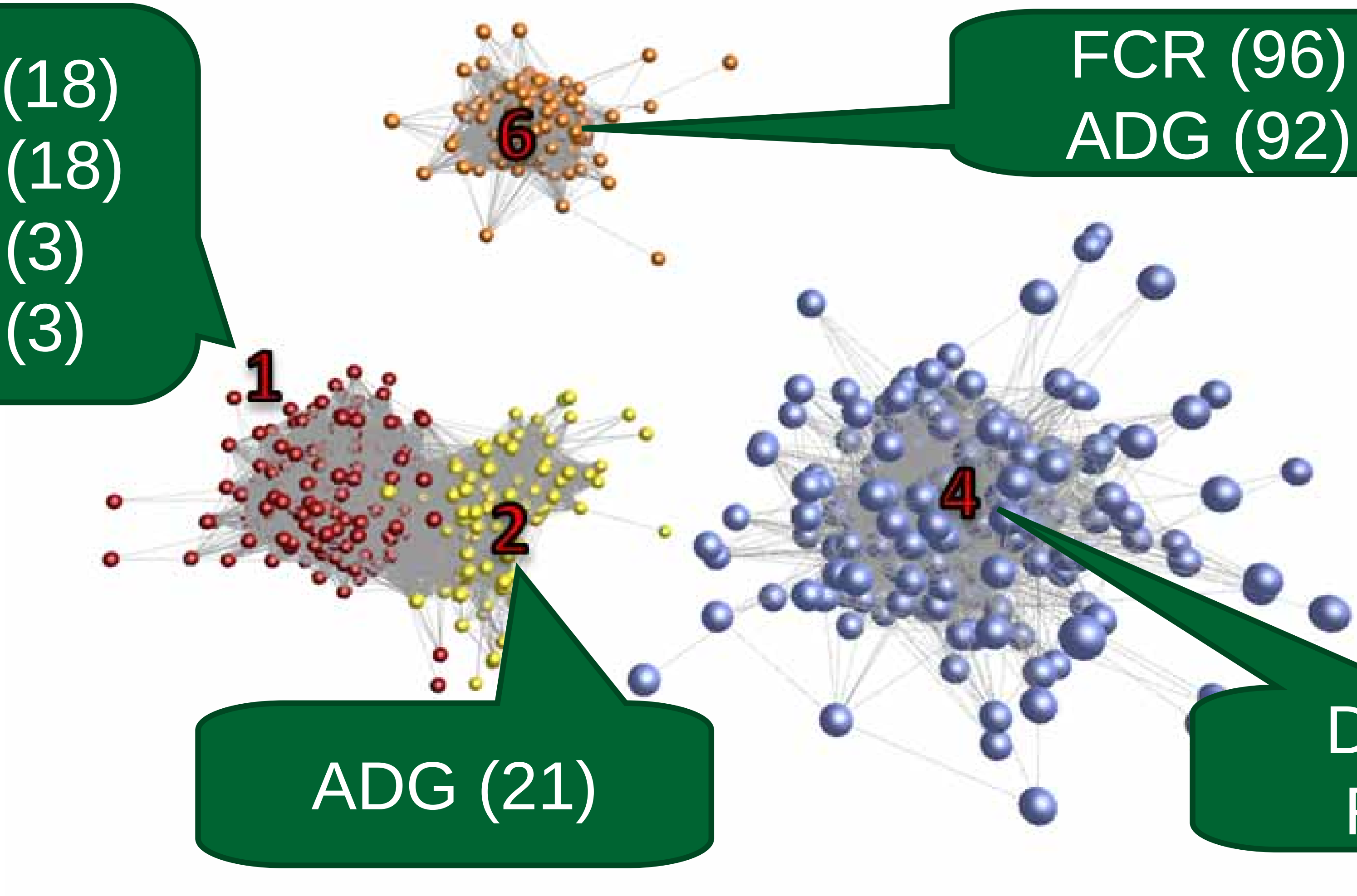


DFI & RFI

ADG & FCR

Distribution of different and equal microbial genes affecting the efficiency traits

Considering only the clusters including most microbial genes affecting the FE traits



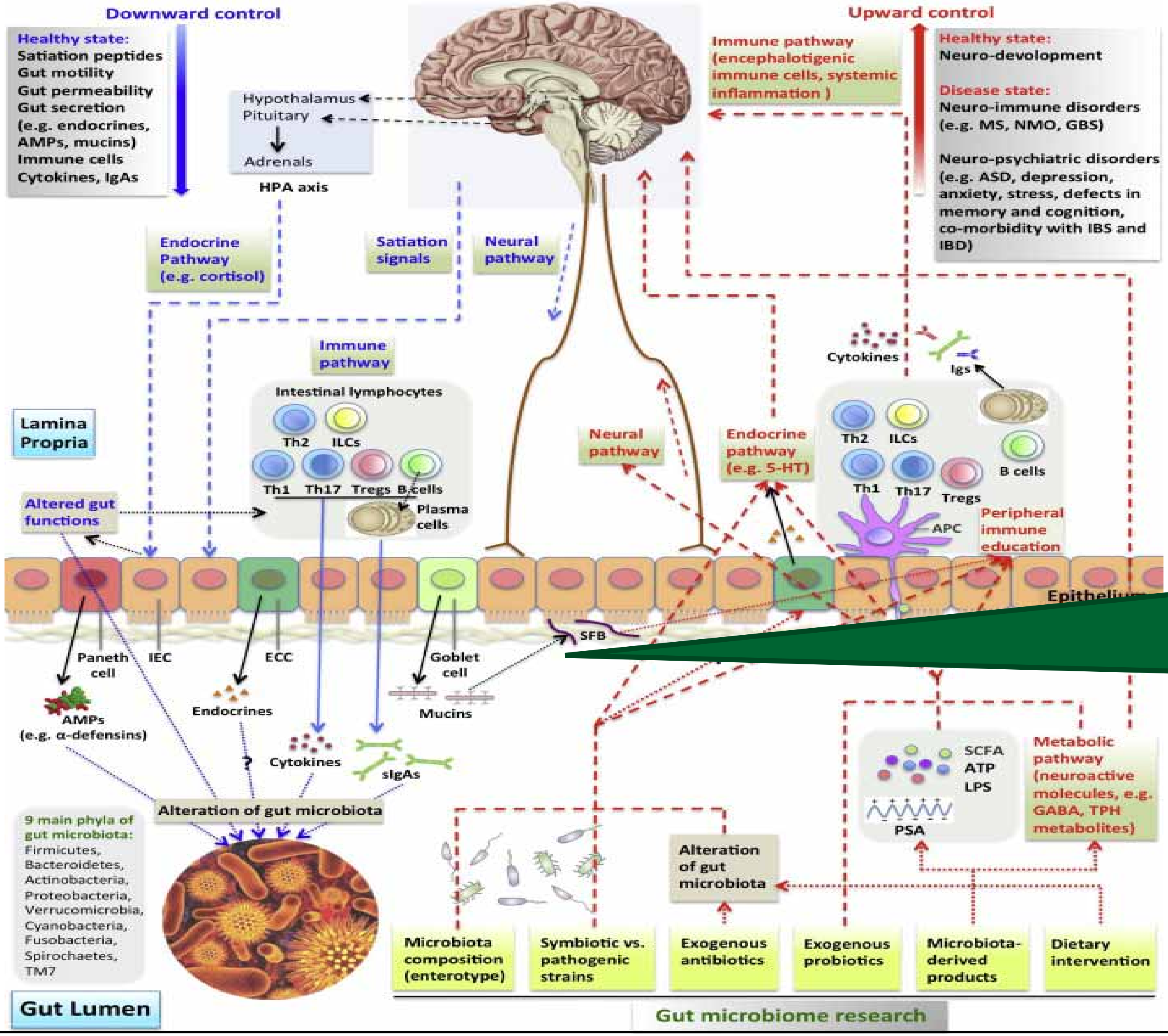
FCR (18)
ADG (18)
DFI (3)
RFI (3)

FCR (96)
ADG (92)

ADG (21)

DFI (14)
RFI (4)

Microbiome-Gut-Brain Axis



L-fucose isomerase & GDP-L-fucose synthase

Wang & Kasper (2014)
Brain, Behavior, and Immunity

Selection using rumen microbial information

Sampling rumen fluid in the abattoir or live animals

Determination of the RMGA

Prediction of feed efficiency

Prediction of methane emission

Prediction of health/ meat quality

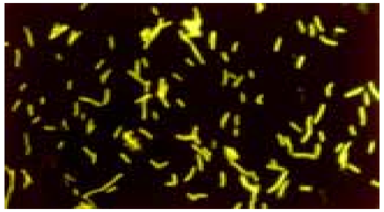
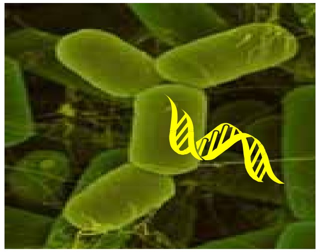
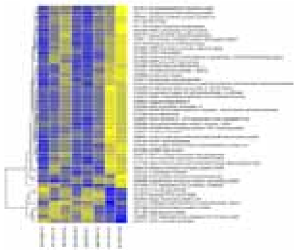
GEBV FCE

GEBV CH_4

GEBV Health, Meat quality

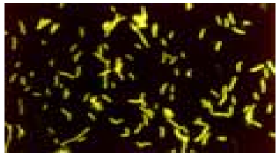
Conclusions rumen microbial selection criteria

- Relative rumen microbial gene abundances (RMGA)
  - Informative for prediction of DFI, FCR, RFI
  - RMGA normally distributed
  - Many thousand of microbial genes
  - Known biological (functional) background

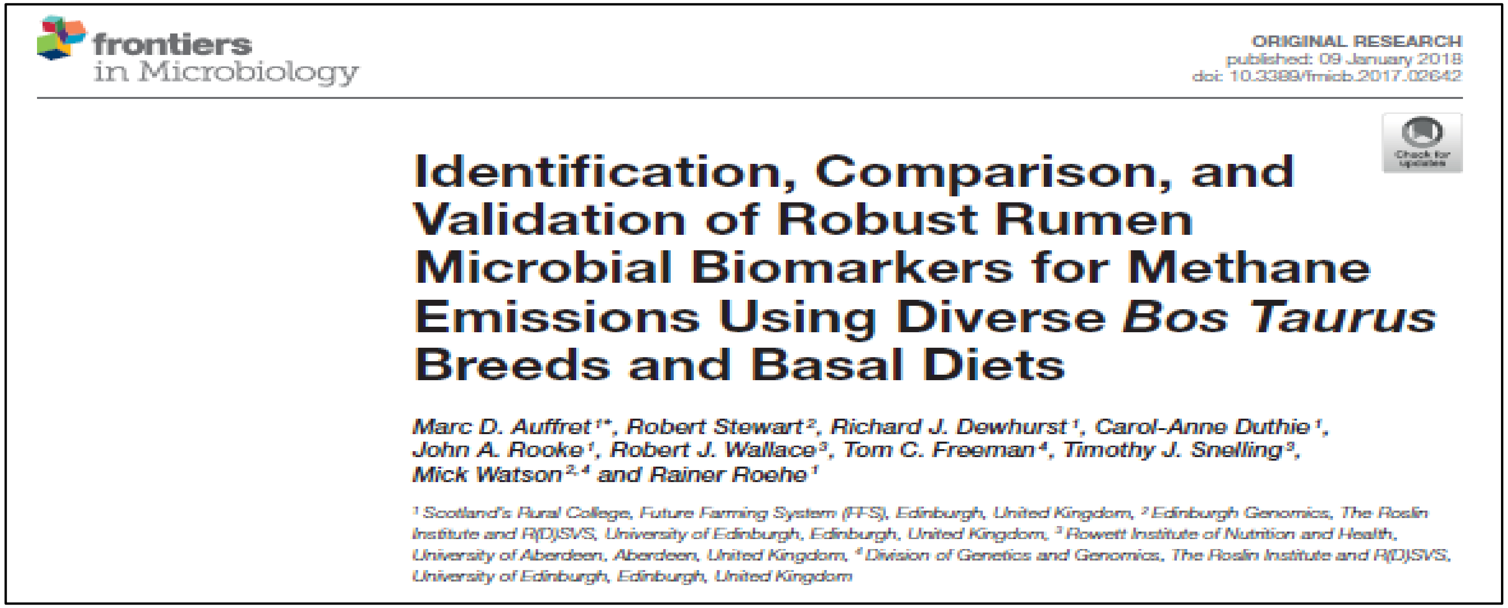




Conclusions

- Advantages of the selection strategy
  - Genetic improvement of difficult and costly to measure traits via abundances of microbial genes
  - Cost-effective
  - Microbial genes showed metabolic background



- RMGA as a new phenotype to breed animals (hosts) providing the best environment for efficient and highly symbiotic rumen microbes to improve many difficult and costly to measure traits



frontiers in Microbiology

ORIGINAL RESEARCH
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Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse *Bos Taurus* Breeds and Basal Diets

Marc D. Auffret[1]*, Robert Stewart[2], Richard J. Dewhurst[1], Carol-Anne Duthie[1], John A. Rooke[1], Robert J. Wallace[3], Tom C. Freeman[4], Timothy J. Snelling[3], Mick Watson[2,4] and Rainer Roehe[1]

[1] Scotland's Rural College, Future Farming System (FFS), Edinburgh, United Kingdom, [2] Edinburgh Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom, [3] Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, United Kingdom, [4] Division of Genetics and Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom

Auffret *et al. Microbiome* (2017) 5:159
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Microbiome

RESEARCH Open Access

The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle

Marc D. Auffret[1*], Richard J. Dewhurst[1], Carol-Anne Duthie[1], John A. Rooke[1], R. John Wallace[2], Tom C. Freeman[3], Robert Stewart[4], Mick Watson[3,4] and Rainer Roehe[1]

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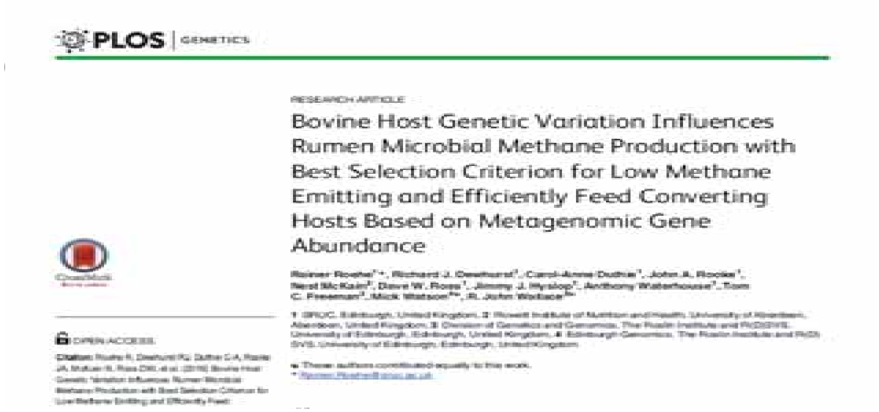

PLOS | GENETICS

RESEARCH ARTICLE

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

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Thank you very much!