SRUC

Metagenomic Information from Rumen Contents to Improve Feed Efficiency and Mitigate Methane Emissions

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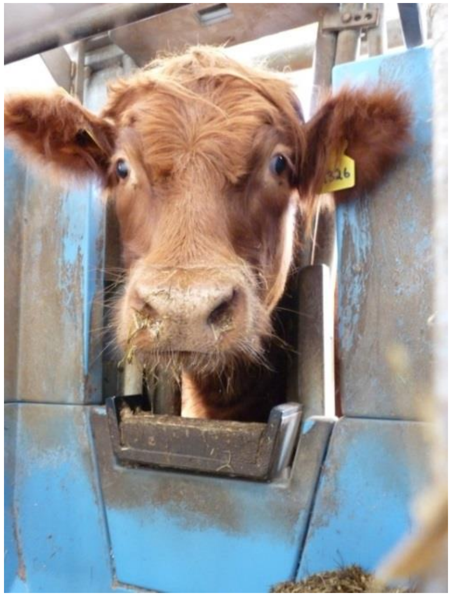
Leading the way in Agriculture and Rural Research, Education and Consulting

Host (Animal) Selection for Feed Efficiency and Methane Mitigation

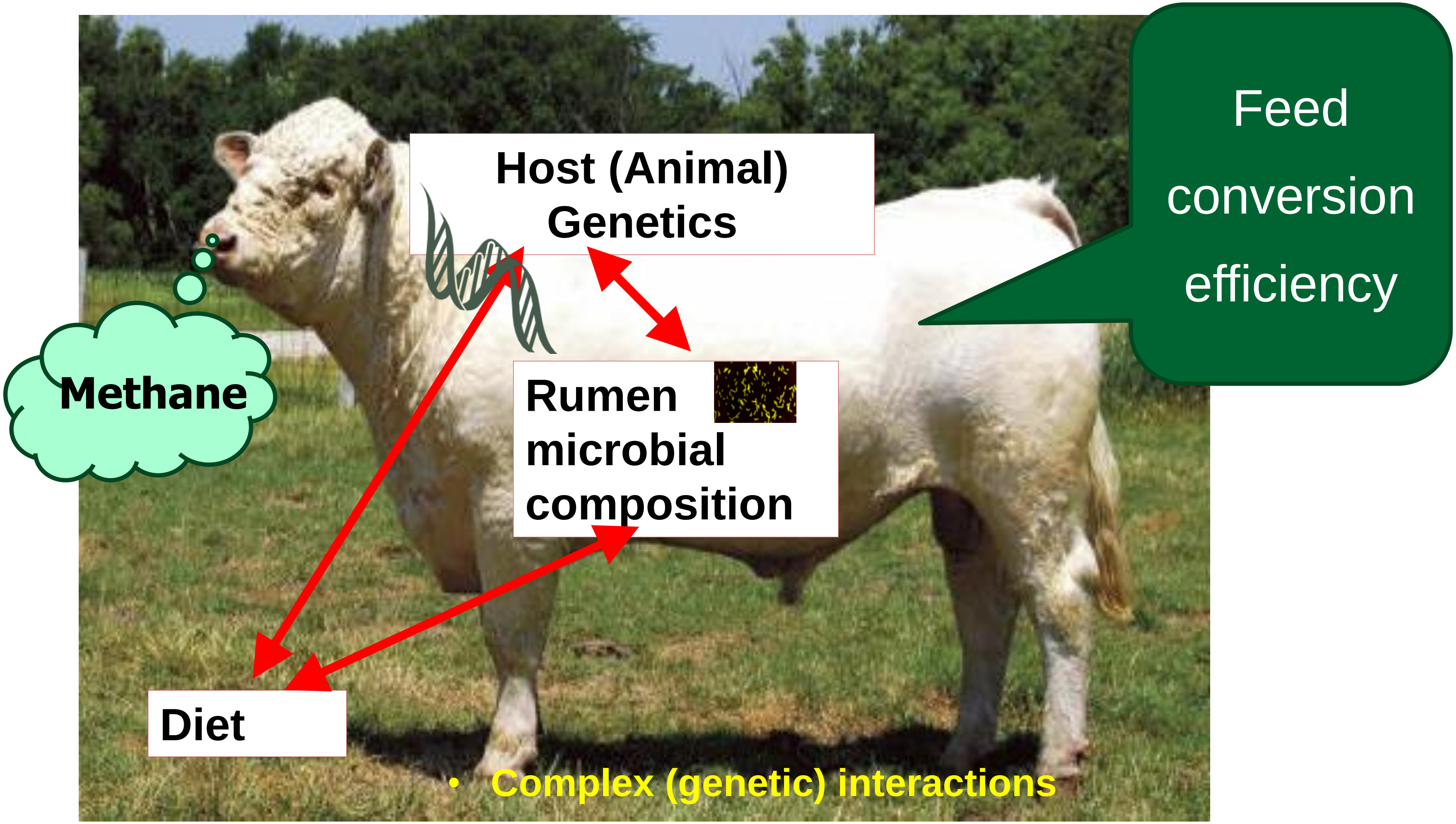
- Feed conversion efficiency (FCE) in beef cattle
  - High economic impact
  - Use of limited resources
  - Brazil second largest beef producer

- Methane
  - 7.1 billion tonnes $CO_{2\text{-eq}}$ per annum (Gerber et al., 2013)
  - ~40% from enteric methane

- Host (Animal) Genetics
  - FCE & Methane emissions
  - Rumen microbiome information
  - Best selection criteria



Host Genetics and Microbiome



Feed conversion efficiency

Host (Animal) Genetics

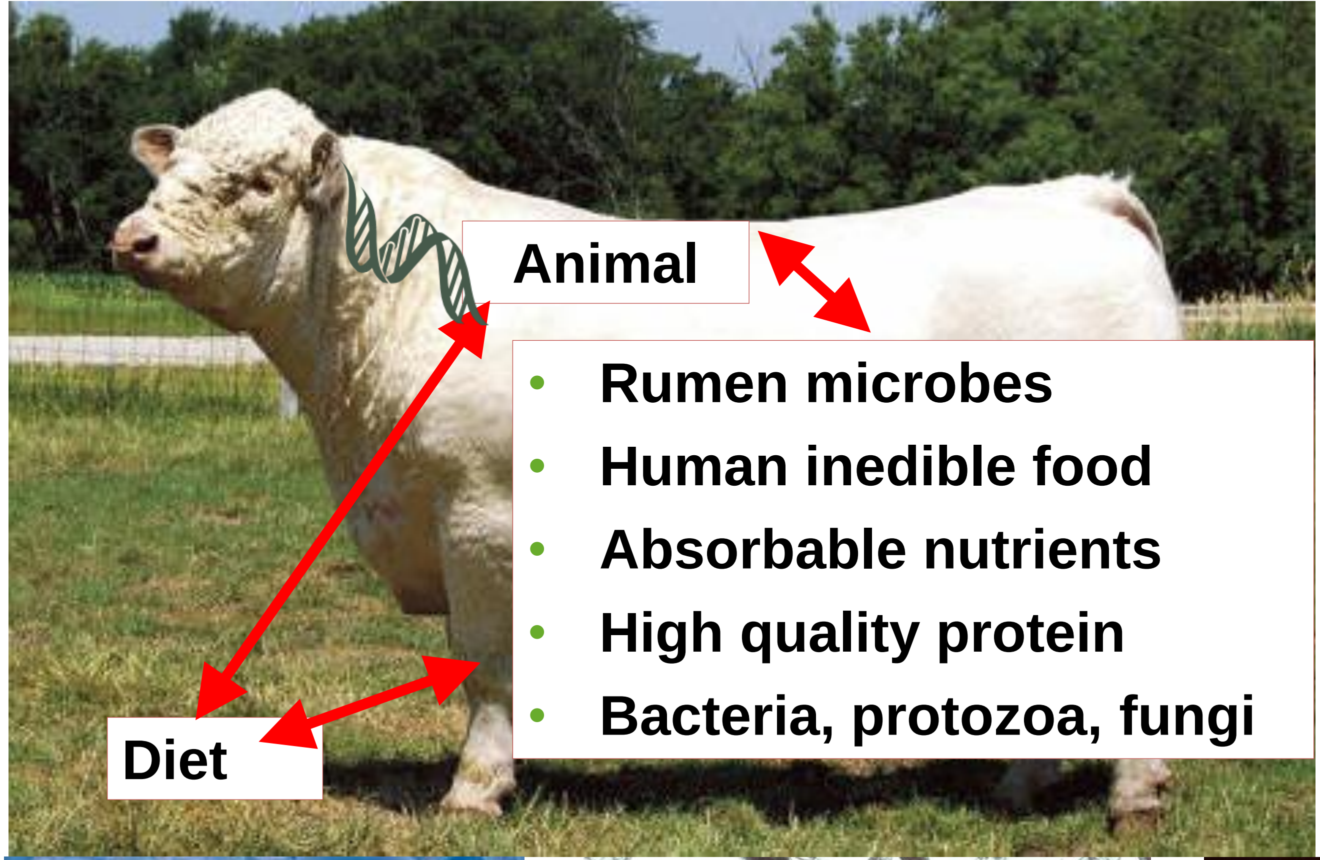
Methane

Rumen microbial composition

Diet

- Complex (genetic) interactions

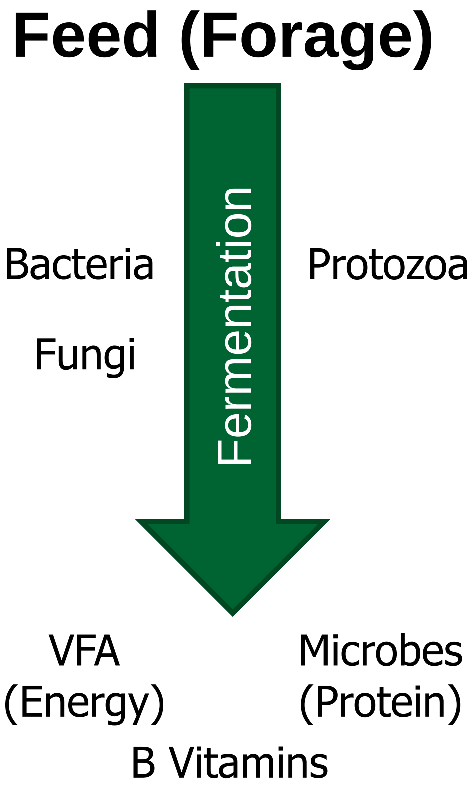
Microbes affecting Feed Efficiency (Symbiotic Relationship)



Animal

Diet

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



Feed (Forage)

Fermentation

Bacteria

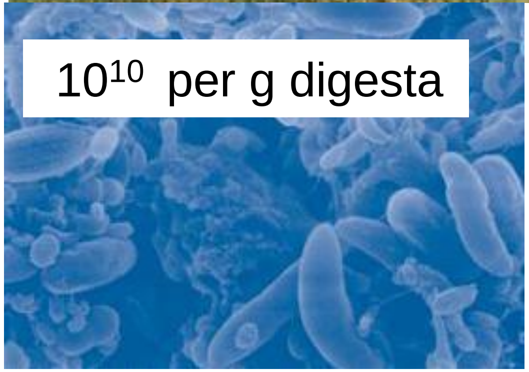
Protozoa

Fungi

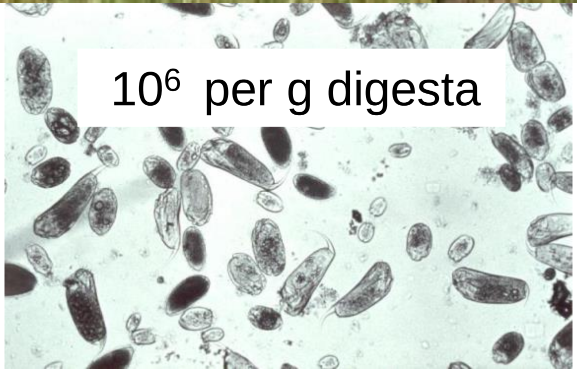
VFA
(Energy)

Microbes
(Protein)

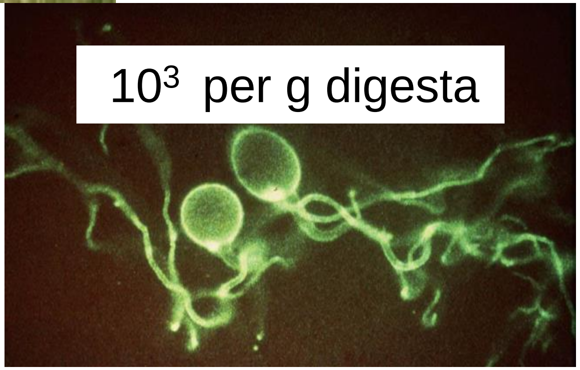
B Vitamins



10^{10} per g digesta

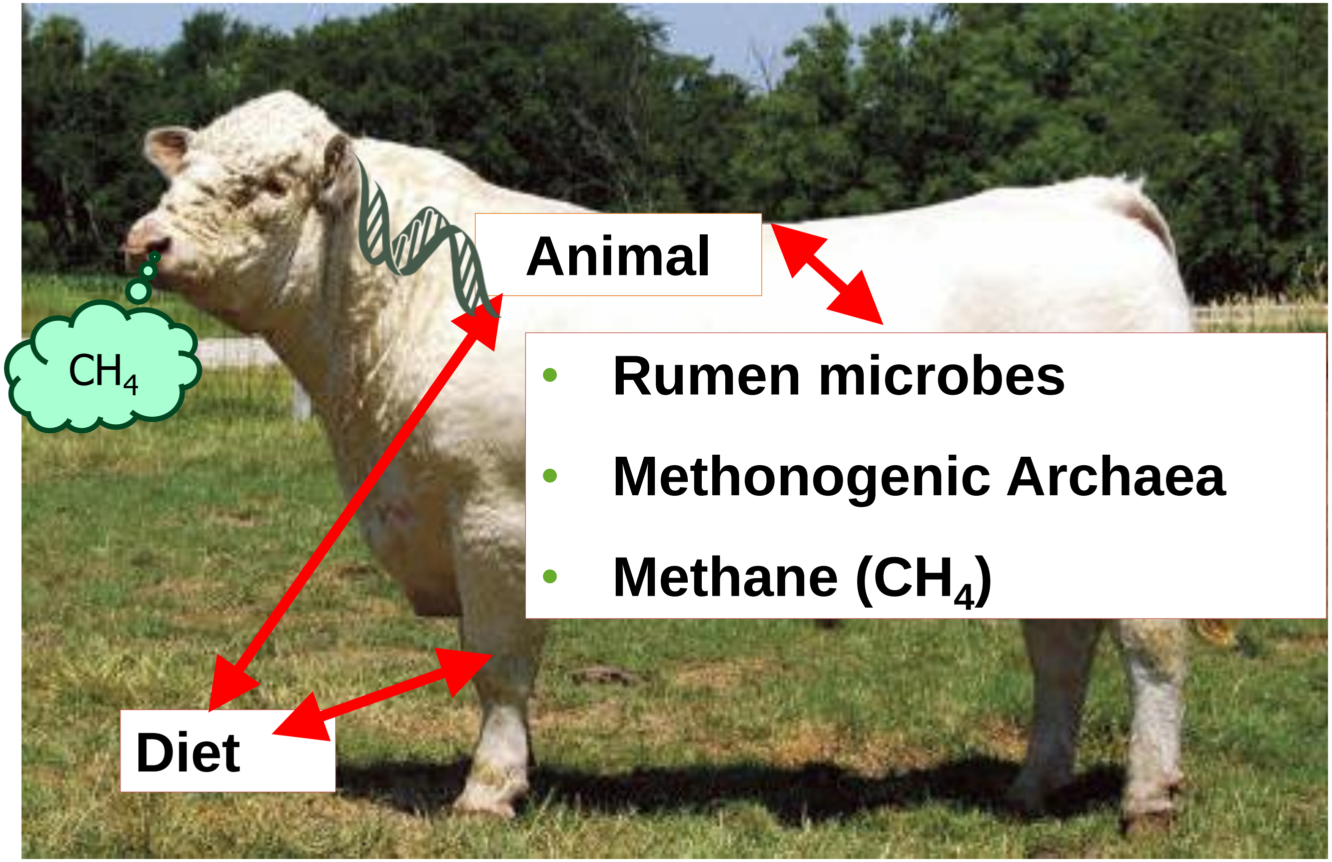


10^{6} per g digesta



10^{3} per g digesta

Microbes affecting Methane Emissions



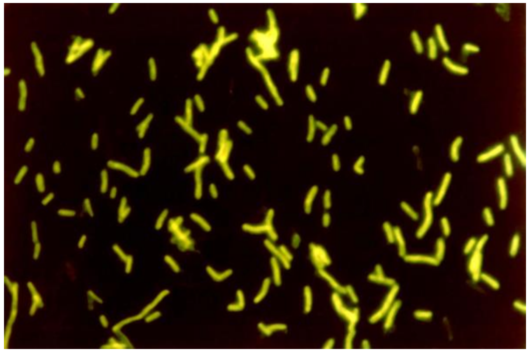
CH_4

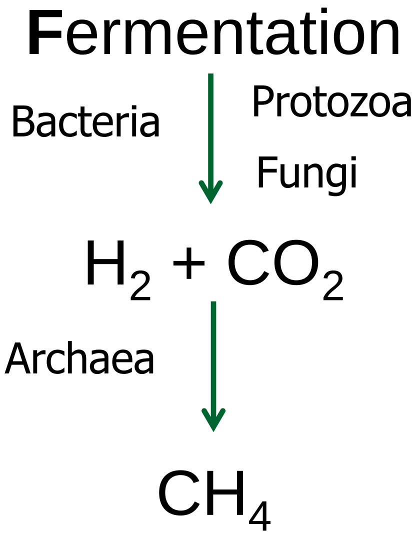
Animal

- **Rumen microbes**
- **Methonogenic Archaea**
- **Methane (CH_4)**

Diet

10^8 per g digesta





Fermentation

Bacteria

Protozoa

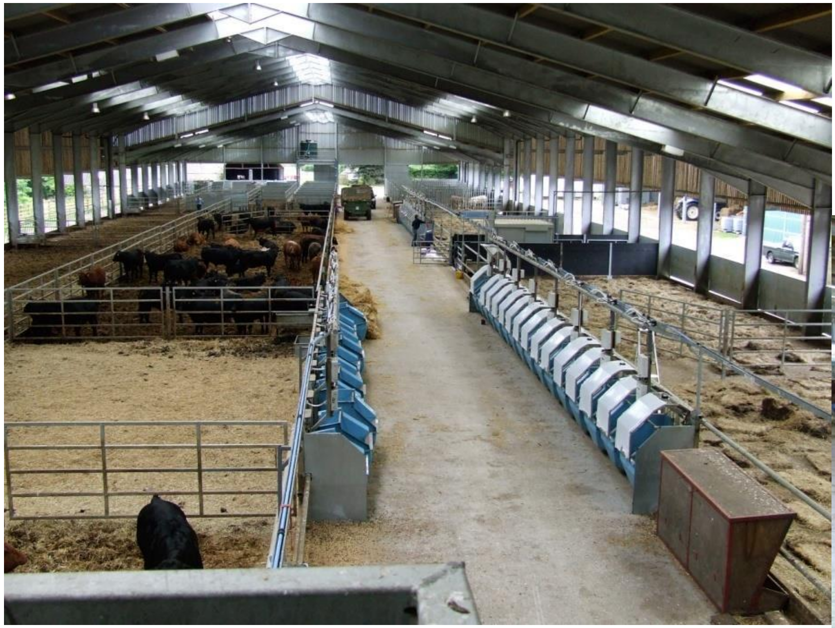
Fungi

$H_2 + CO_2$

Archaea

CH_4

Recording Feed Intake & Methane Emissions

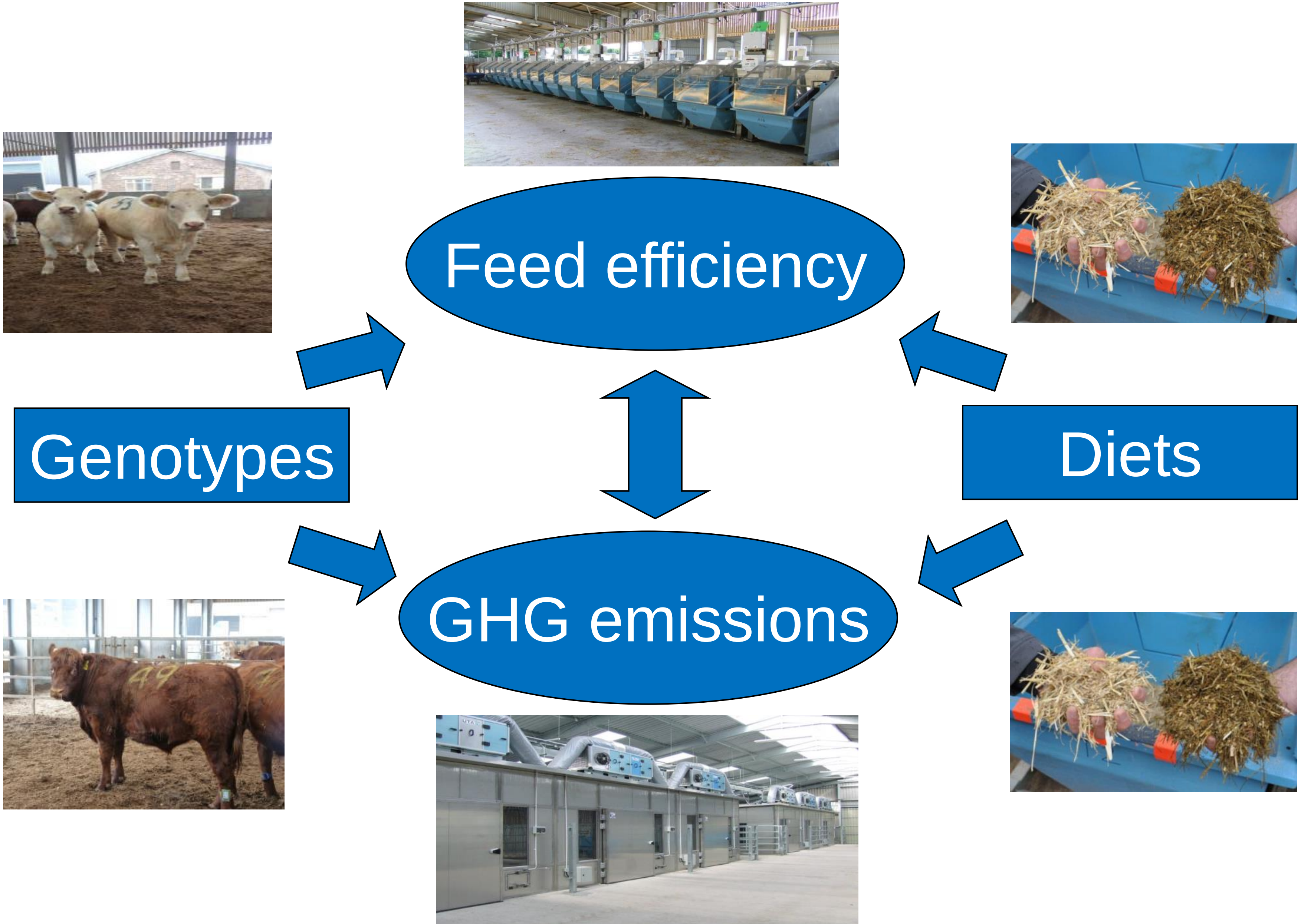


Individual feed intake

Individual methane emissions

SRUC Beef Research Centre, Easter Howgate

Experimental Beef Trials



Feed efficiency

Genotypes

Diets

GHG emissions

Variation in Methane Emissions g/day between Animals

	Forage	Concentrate
A. Angus x	172–333 g/day	78–233 g/day
Limousin x	152–266 g/day	86-216 g/day

Large differences in methane emissions between animals

CV = 14% – 32%

Variation in Methane Emissions (g/DMI) between Animals

	Forage	Concentrate
A. Angus x	15.9–31.4 g/DMI	7.6–18.1 g/DMI
Limousin x	14.4–30.4 g/DMI	9.3–22.8 g/DMI

Large differences in methane emissions between animals

CV = 18% – 29%

Variation in Archaea:Bacteria Ratio between Animals using Samples collected on Slaughtered Animals

	Forage	Concentrate
A. Angus x	1.5 – 11.0	0.9 – 5.8
Limousin x	2.2 – 14.0	1.4 – 4.9

Extreme large differences in Archaea:Bacteria ratios between animals

CV = 35% – 50%

Variation in Archaea:Bacteria Ratio between Animals using Samples collected on Live Animals

	Forage	Concentrate
A. Angus x	3.1 – 17.1	0.7 – 8.5
Limousin x	2.1 – 9.4	1.0 – 6.7

Extreme large differences in Archaea:Bacteria ratios between animals

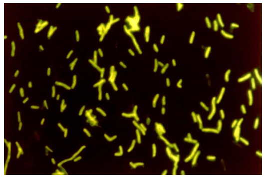
CV = 39% – 65%

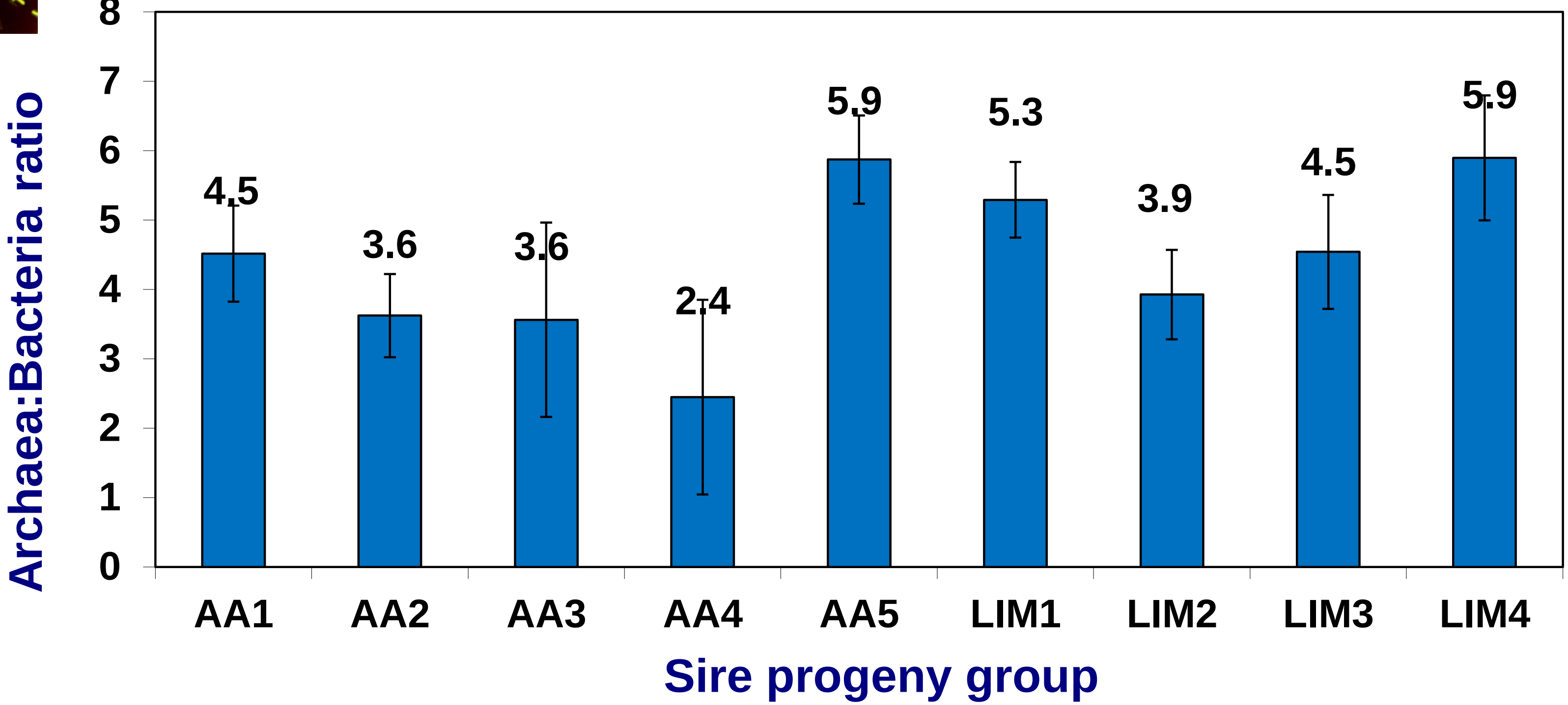
Effect of Breed & Diet Type on Methane Emissions g/day

A. Angus x	184 g/day	Forage	205 g/day
Limousin x	164 g/day	Concentrate	142 g/day
	SE = 5.7		SE = 5.7

Rooke *et al.* (2014); Roehe *et al.* (2016)

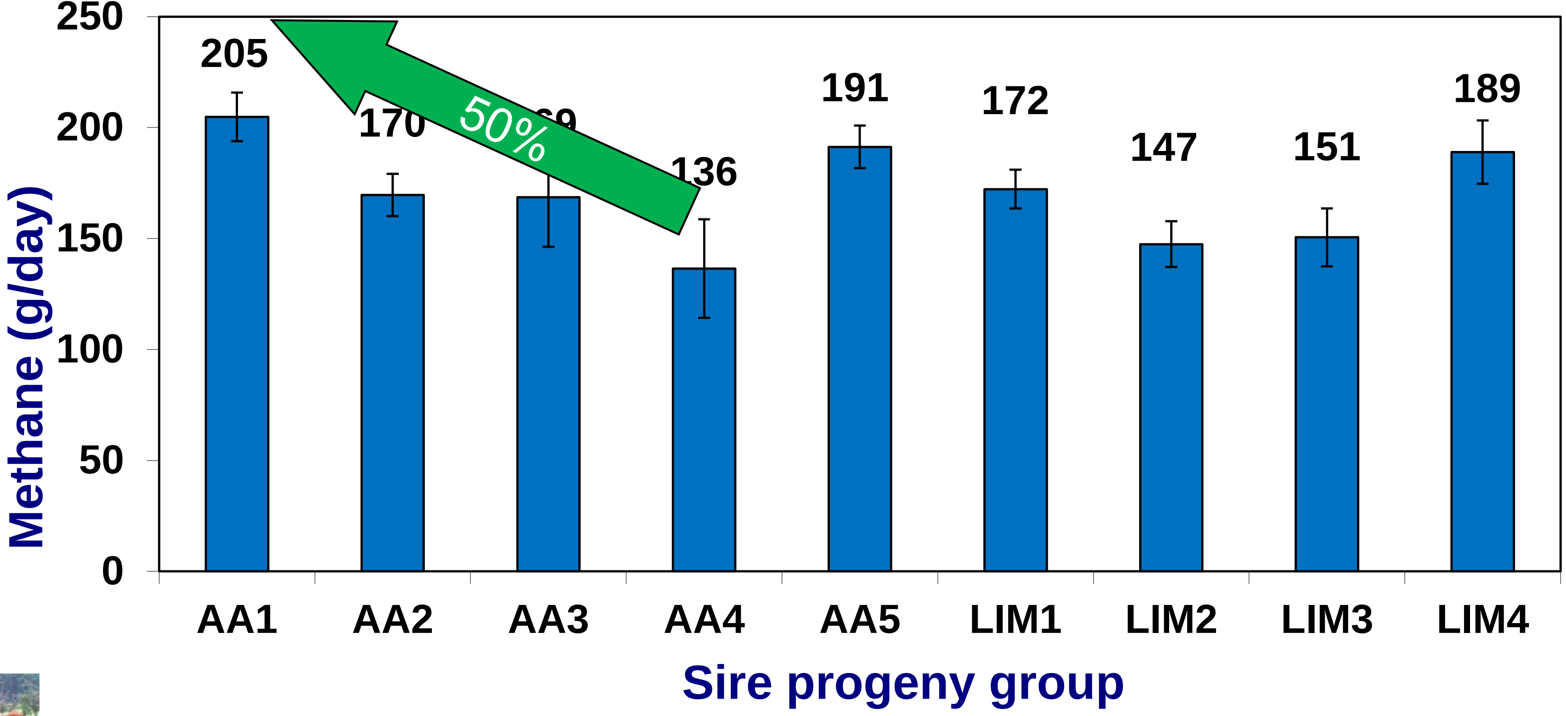
Host (Animal) Genetics shapes the Microbial Community (A:B ratio)



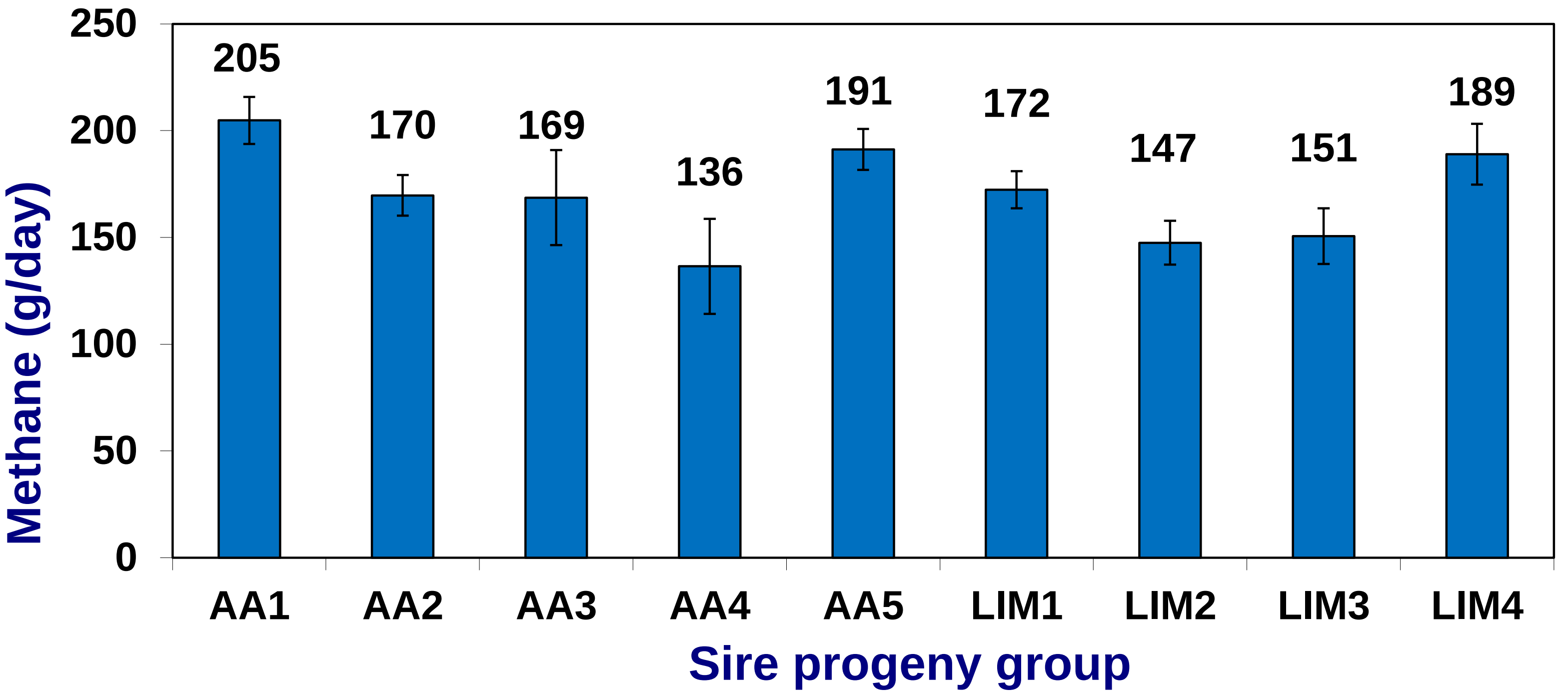


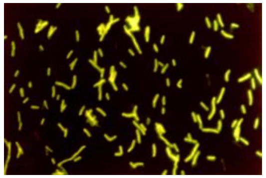
Roehe *et al.* (2016) PLOS Genetics

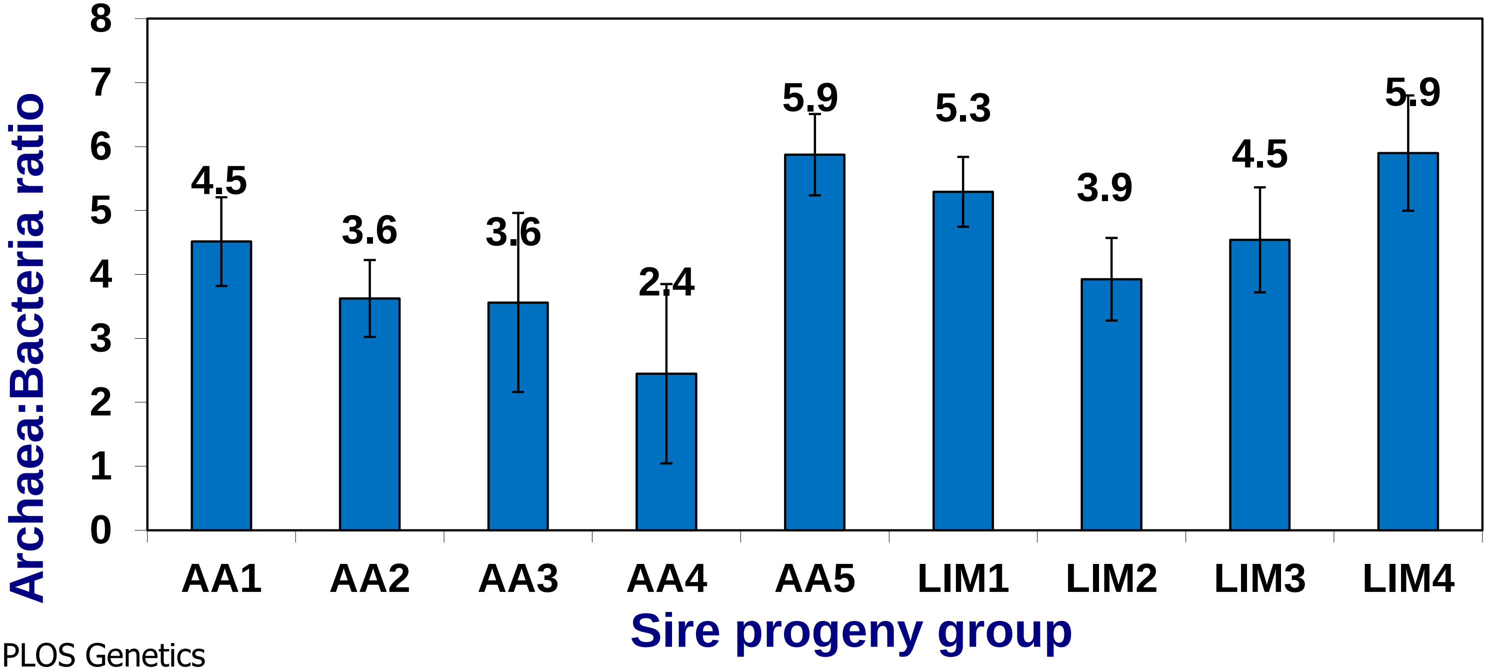
Host (Animal) Genetics affects Methane Emissions (g/day)



Roehe *et al.* (2016) PLOS Genetics





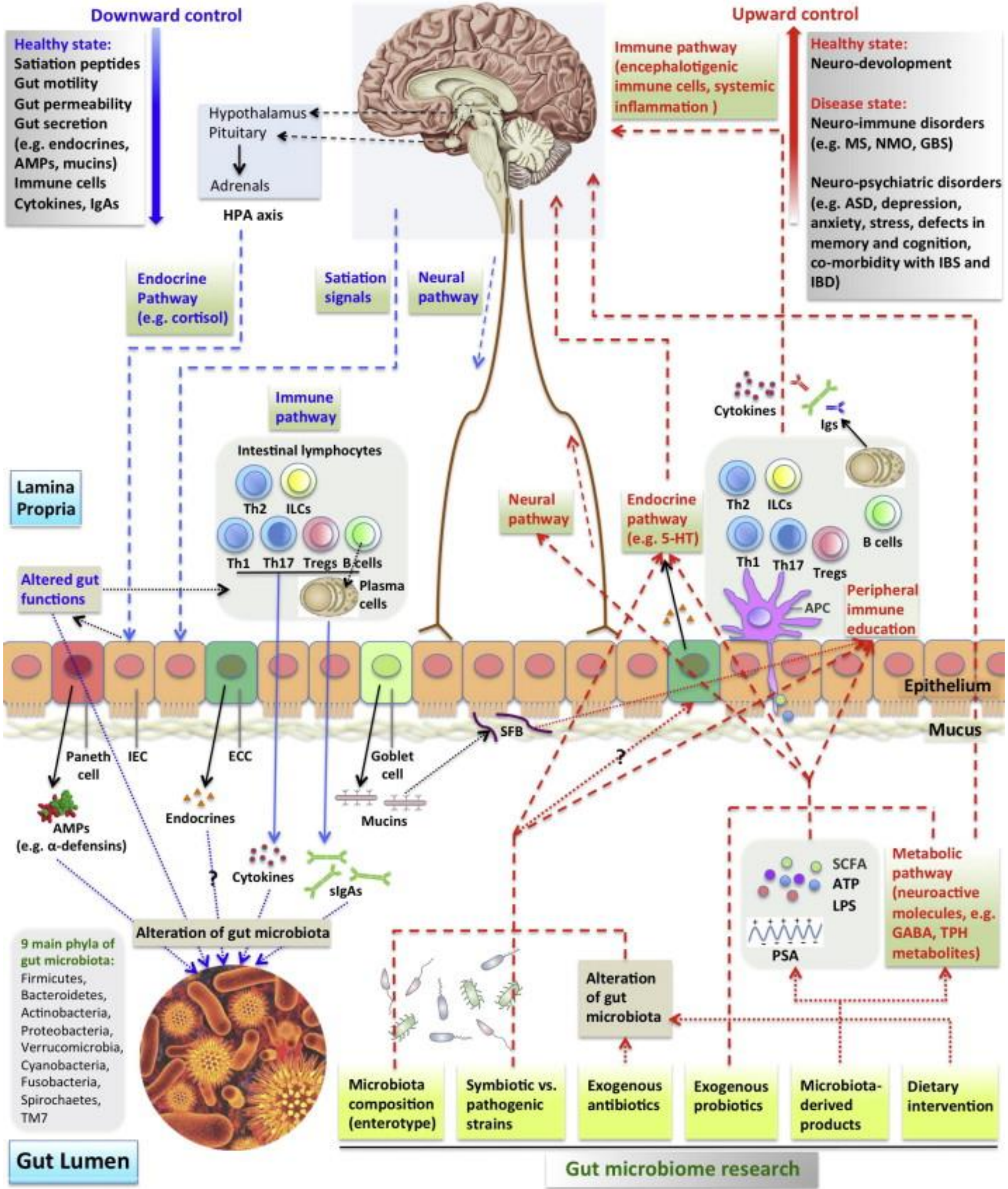


Roehe *et al.* (2016) PLOS Genetics

Biological Mechanisms

– Host Genetics and Microbiome Interactions –

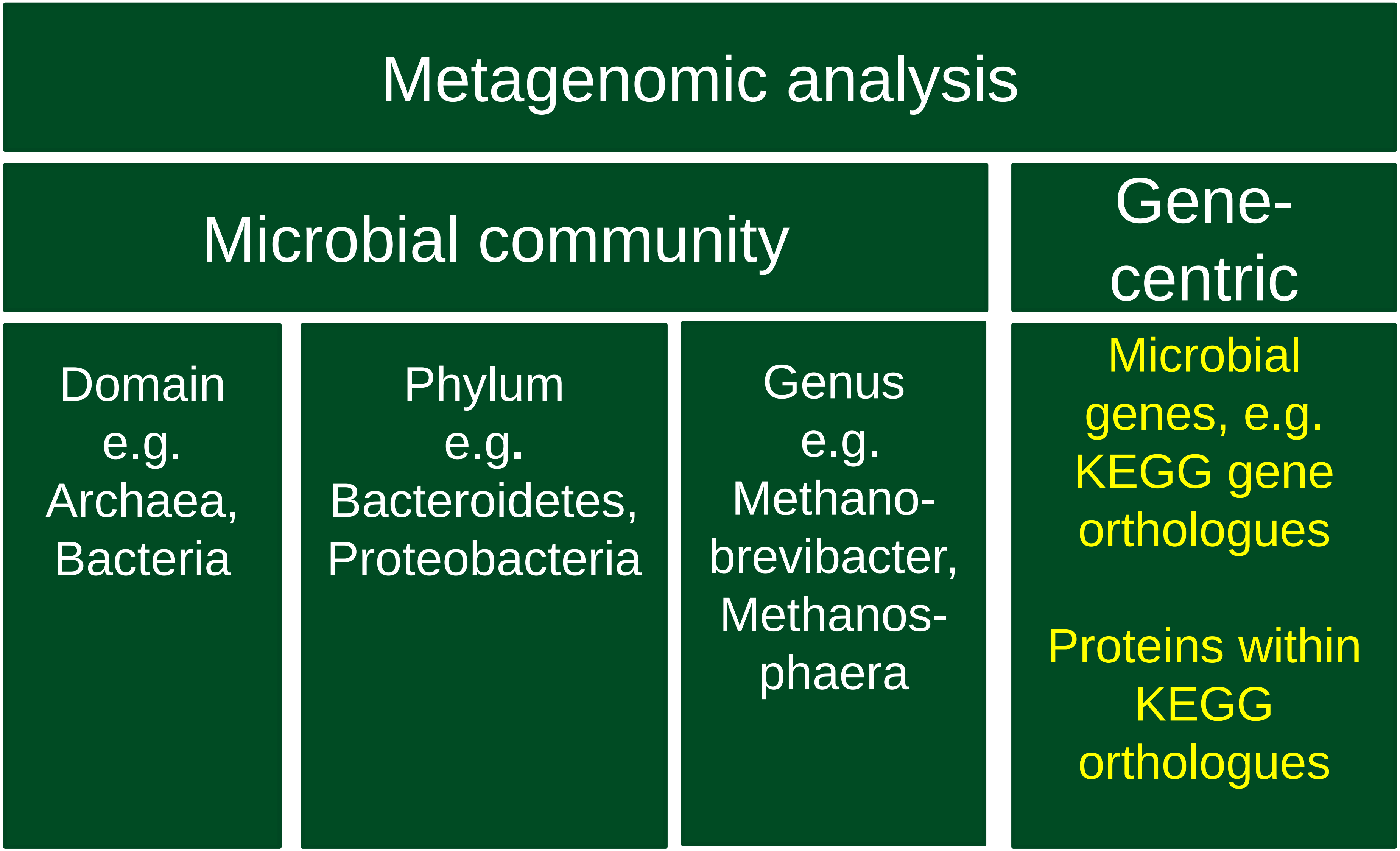
- Rumen pH influences microbial community
  - Saliva contains bicarbonate
  - Large variation in saliva production (av. 150 l/day)
  - Differences in short chain fatty acids absorption
  - Passage rate of protons
- Variation in physical size & structure of the rumen
- Rumen contractions and passage rate of digesta
- Microbiome-gut-brain axis
  - Stress
  - Immune system
  - ‘Fucose sensing’, gut microbiome and host epithelia cell cross-talk



Microbiome-Gut-Brain Axis

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

Deep Sequencing of DNA from Rumen Microbes



Metagenomic analysis

Microbial community

Gene-centric

Domain
e.g.
Archaea,
Bacteria

Phylum
e.g.
Bacteroidetes,
Proteobacteria

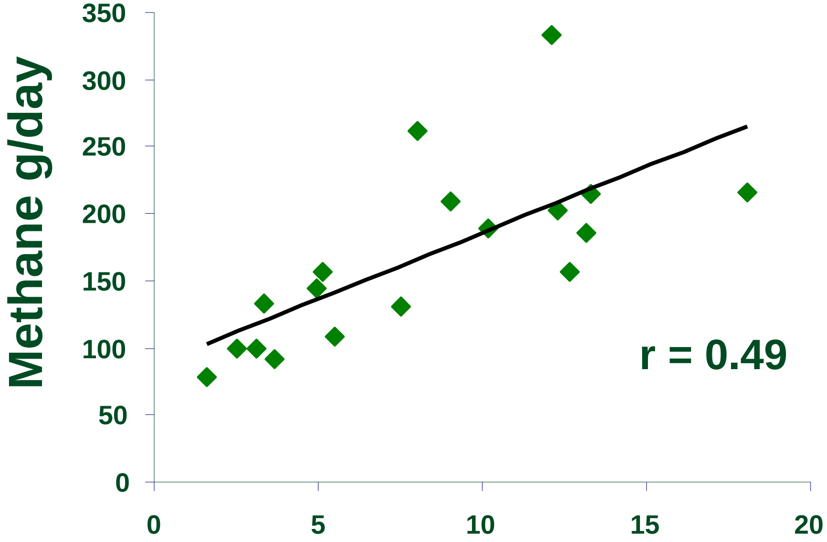
Genus
e.g.
Methanobrevibacter,
Methanosphaera

Microbial genes, e.g. KEGG gene orthologues

Proteins within KEGG orthologues

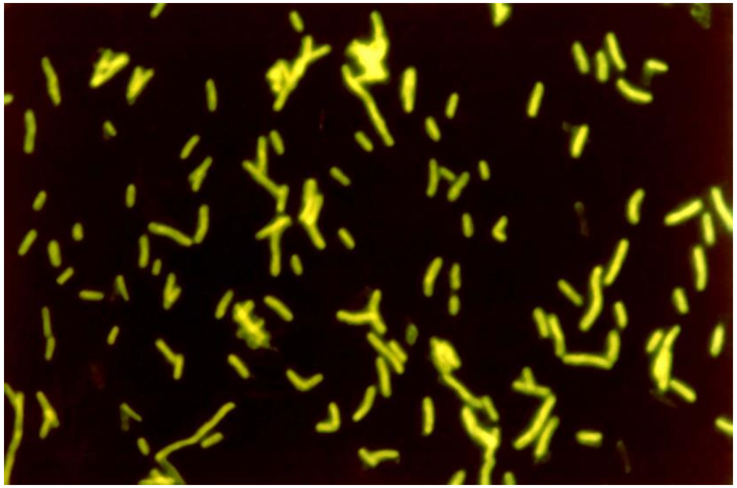
Predicting Methane Emissions by Methanogenic Archaea : Bacteria Ratio

Microbial Kingdom



Archaea/bacteria ratio post mortem

Rumen fluid samples
(both on live & slaughtered animals)



Wallace *et al.* (2014) Scientific Reports

Prediction of Methane by Genera

Methane			
Genus	Estimate	VIP	R^2
Methanosphaera	0.360	1.15	0.84
VadinCA11	0.279	1.07	0.77
Methanobrevibacter	0.190	1.05	0.92
Moryella	0.098	0.98	0.77
Megasphaera	-0.092	0.90	0.83
Desulfovibrio	-0.027	0.81	0.98

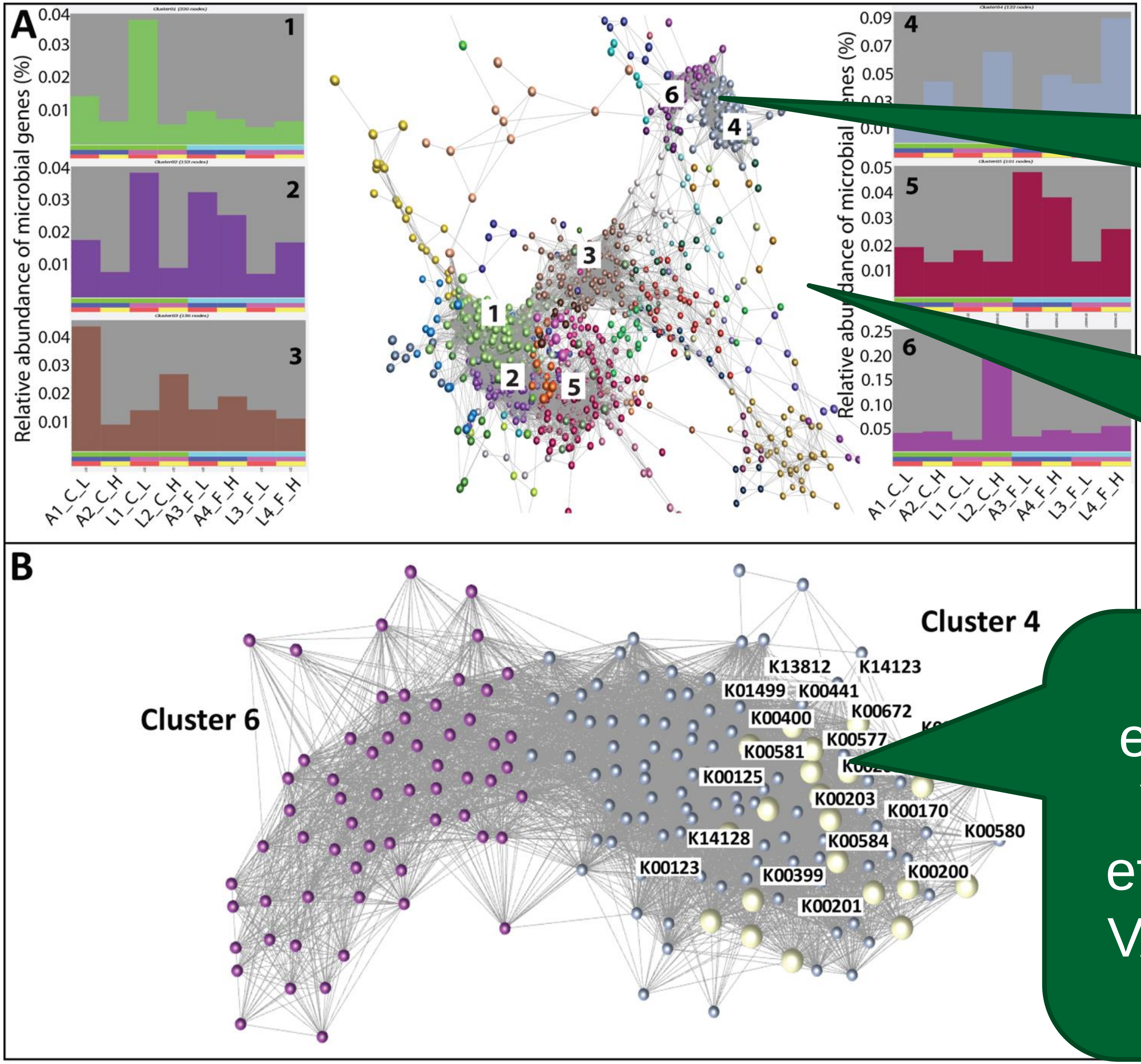
PLS model explains 89.7% of the variation in model effects and 84.5% of the variation in methane

Prediction of Feed Conversion Ratio by Genera

Feed conversion ratio			
Genus	Estimate	VIP	R^2
Sphaerochaeta	0.224	1.09	0.82
Ruminobacter	0.206	1.06	0.84
Succiniclasticum	0.360	1.04	0.80
Dialister	0.277	1.01	0.73
Clostridium	0.156	0.95	0.83
Bifidobacterium	0.074	0.83	0.66

PLS model explains 86.9% of the variation in model effects and 73.6% of the variation in FCR

Network of Rumen Microbial Genes

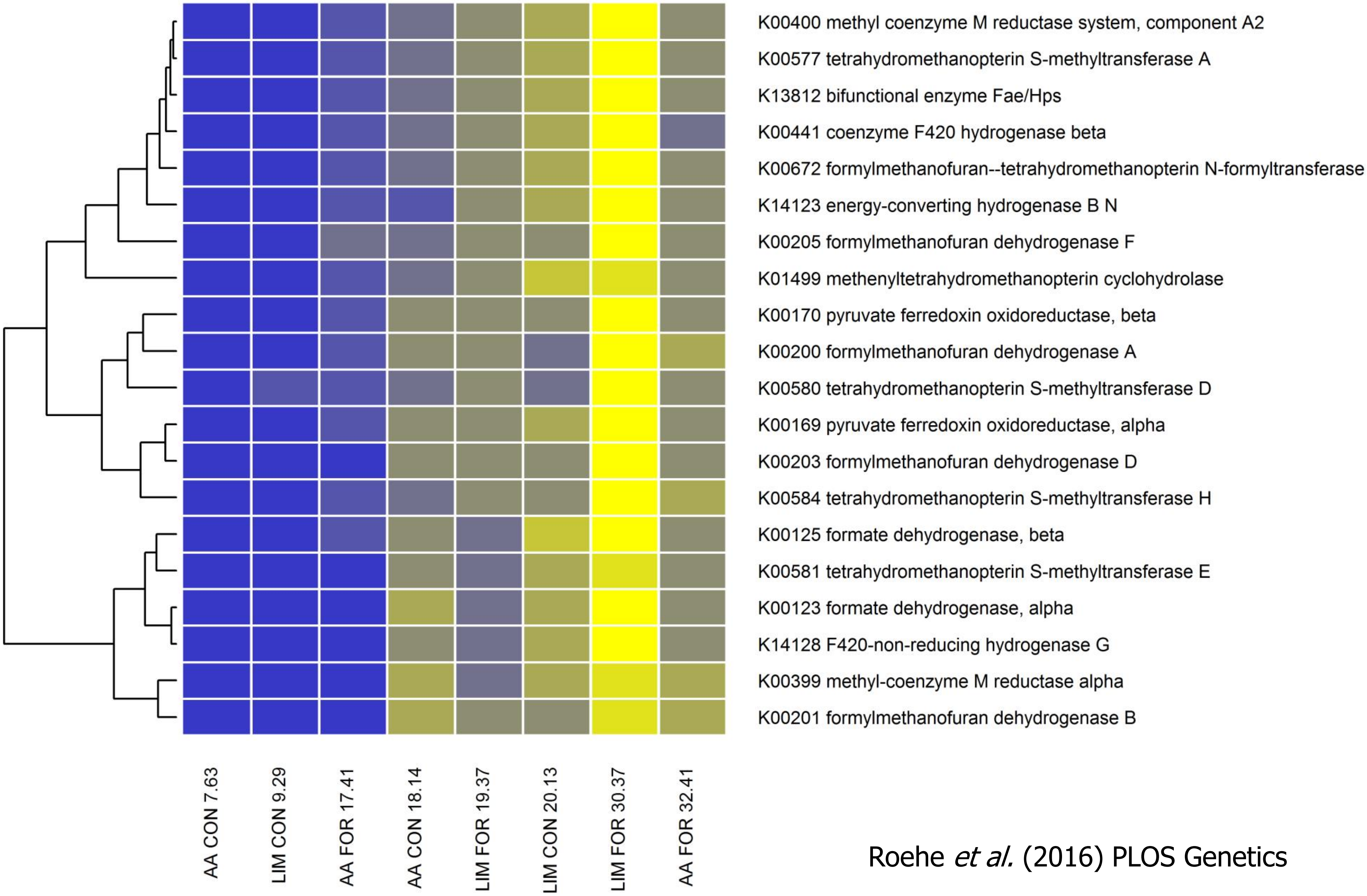


Methane emissions

3970 microbial genes

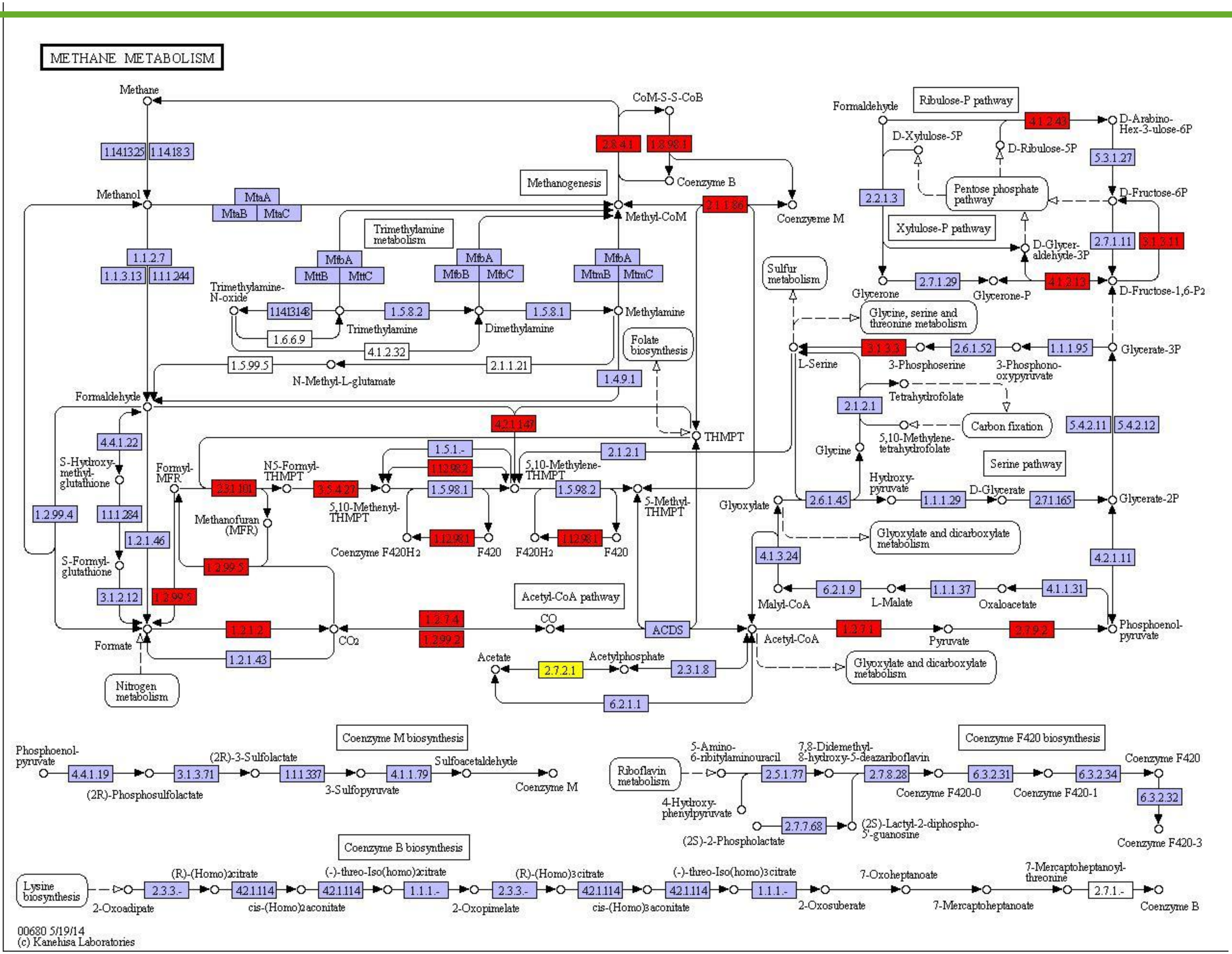
20 genes explaining 97% VAR in model effects & 81% of VAR in methane emissions

Microbial Genes associated with Methane



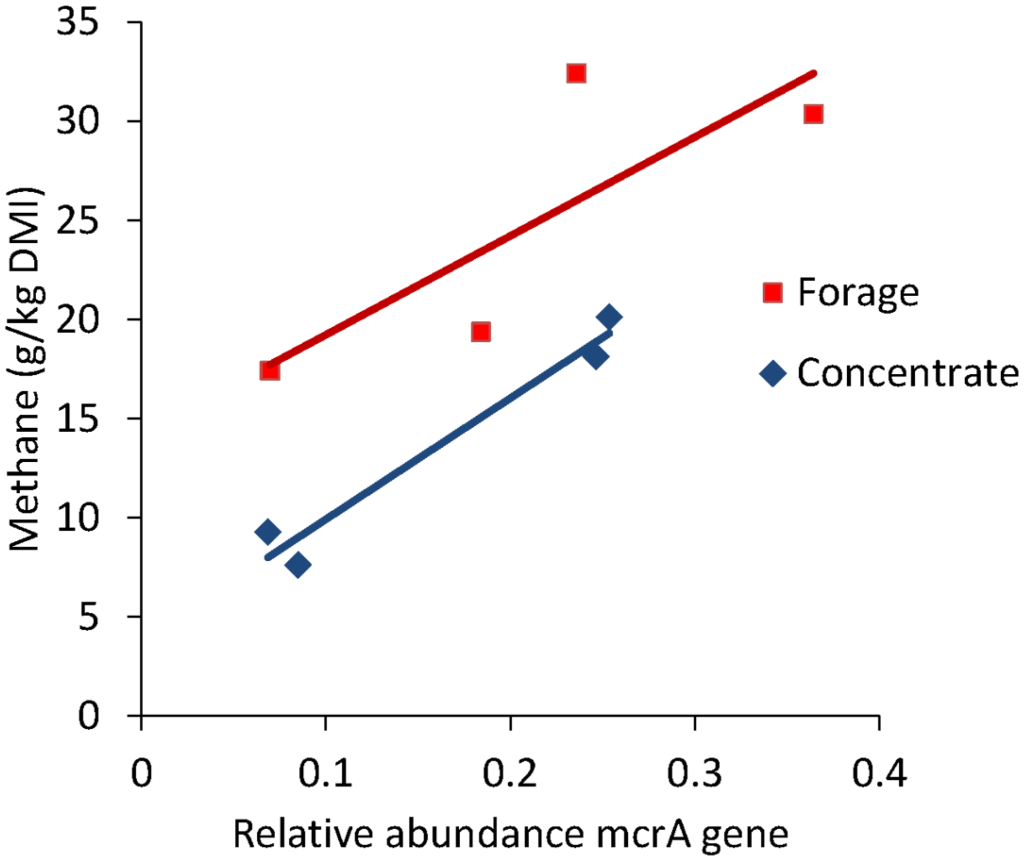
Roehe *et al.* (2016) PLOS Genetics

Microbial Genes in the Methane Metabolism



Wallace *et al.* (2015) BMC Genomics

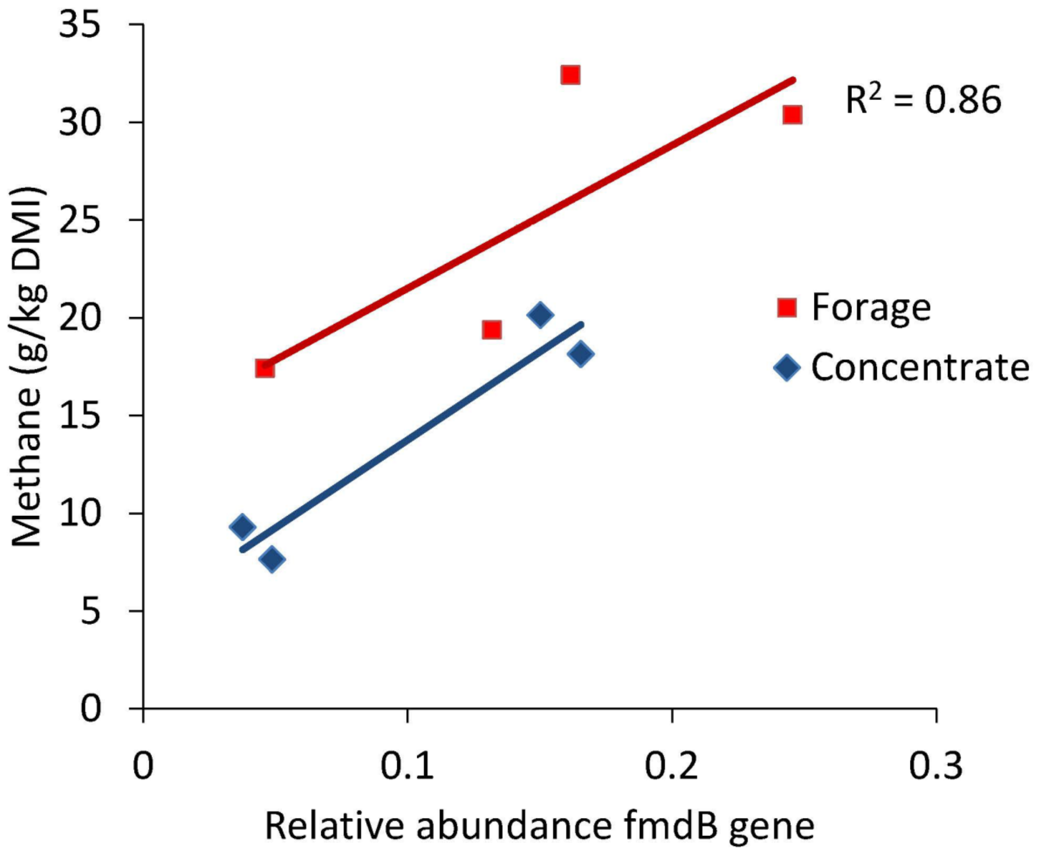
Methane Emissions & mcrA Gene



mcrA =methyl-coenzyme M reductase alpha subunit

Roehe *et al.* (2016) PLOS Genetics

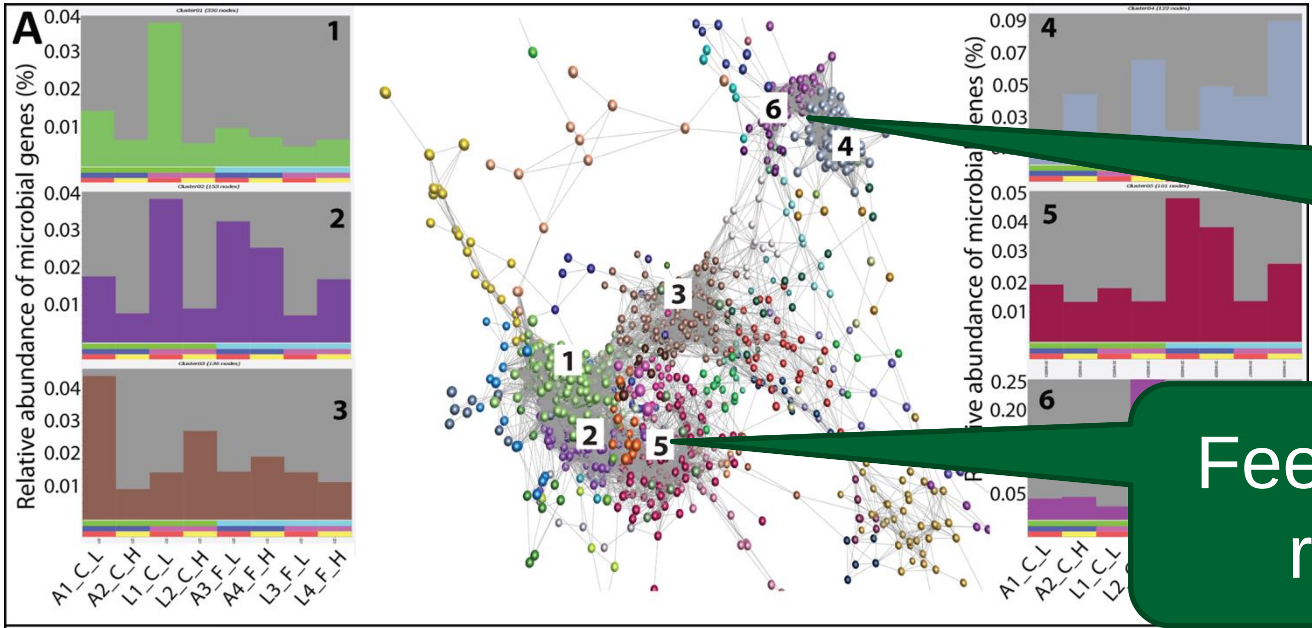
Methane Emissions & fmdB Gene



fmdB =formylmethanofuran dehydrogenase subunit B

Roehe *et al.* (2016) PLOS Genetics

Microbial Genes associated with FCR

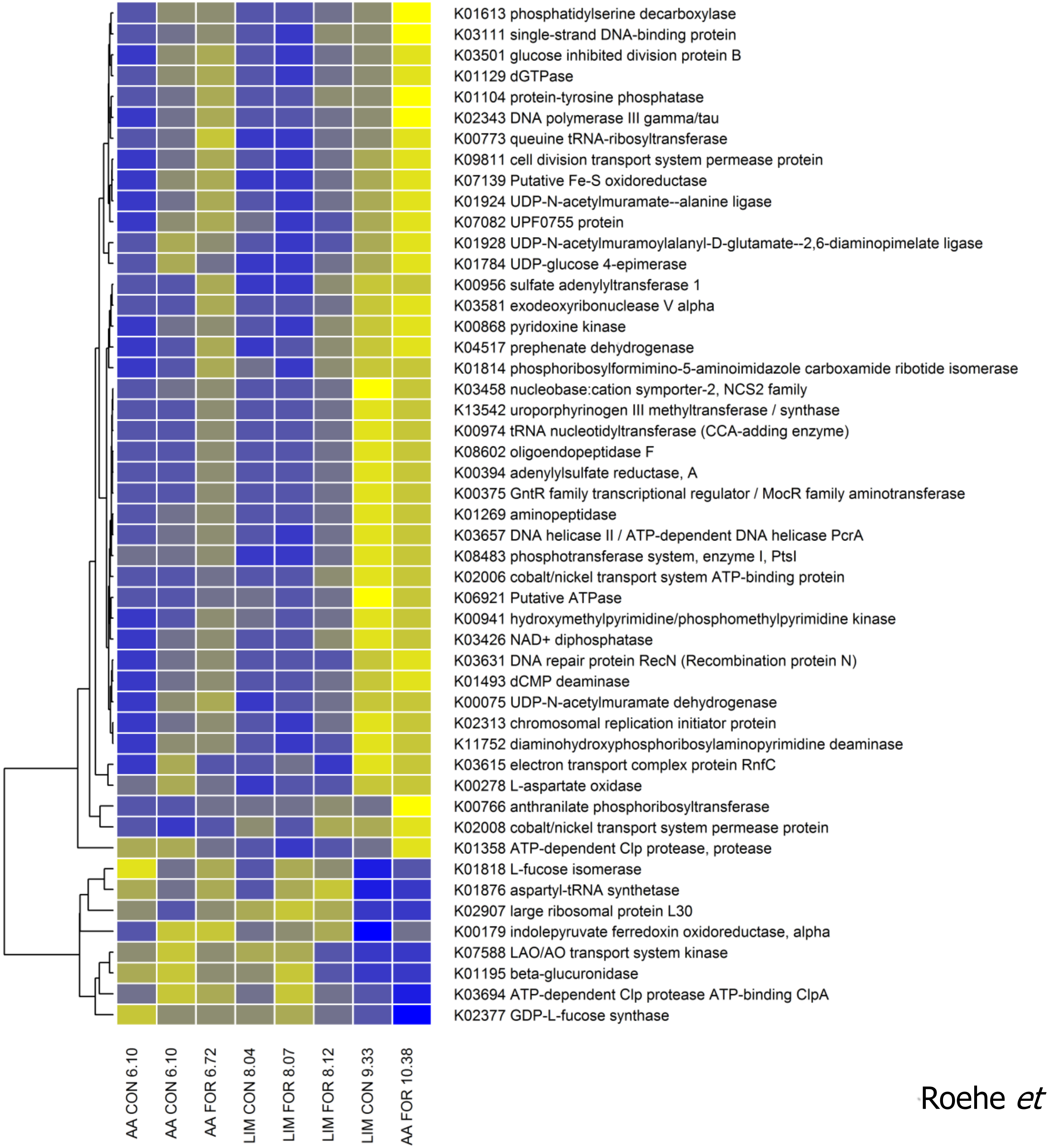


Methane emissions

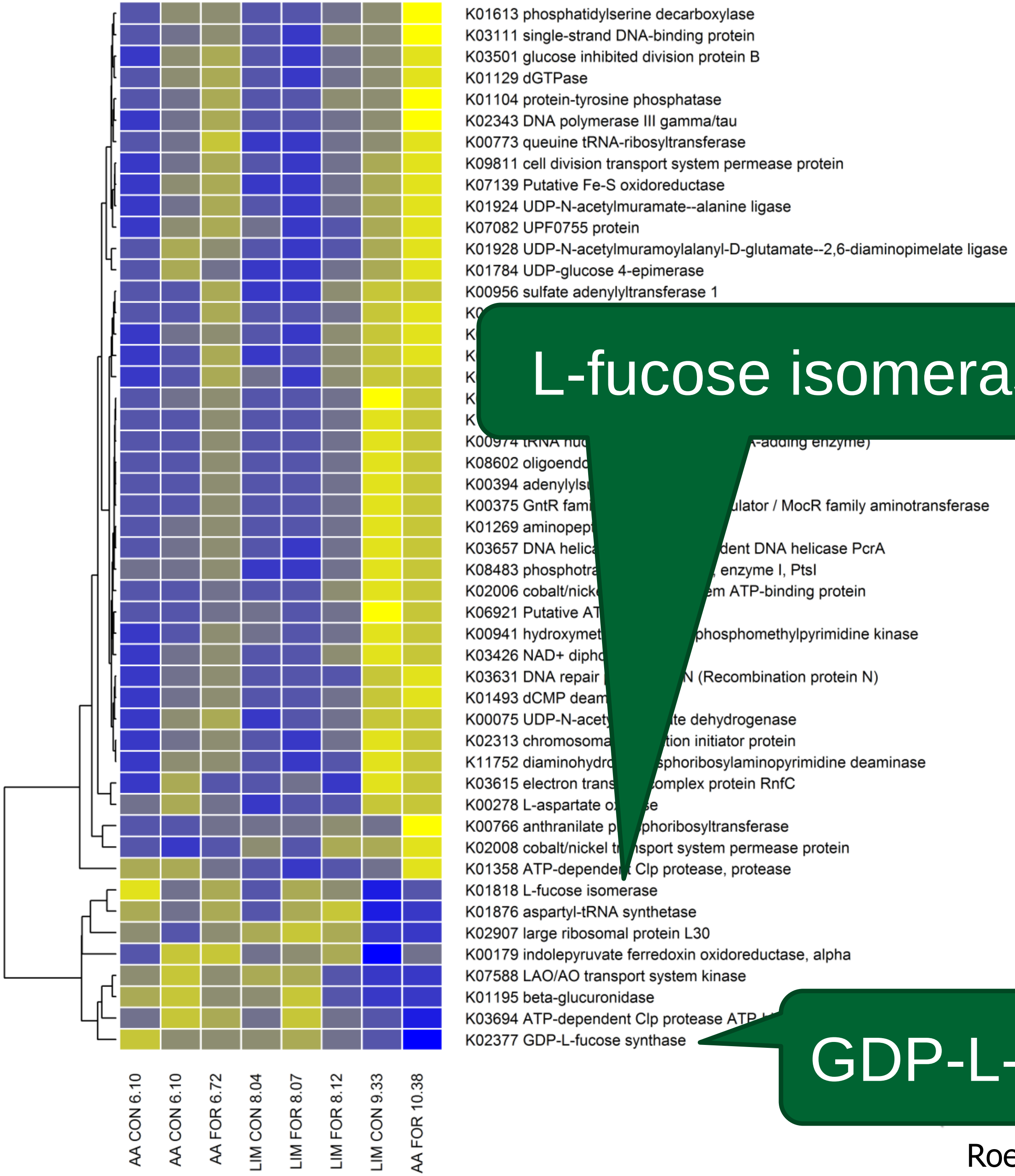
Feed conversion ratio (FCR)

- **49 microbial genes** significantly associated with **feed conversion ratio** explaining **81% of the variation in model effects & 88% of the variation in FCR.**
- Microbial genes are related to known metabolic pathways, e.g. degradation of amino acids and proteins, protein and vitamin synthesis

Microbial genes associated with feed conversion ratio



Roehe *et al.* (2016) PLOS Genetics



L-fucose isomerase

Microbial genes associated with feed conversion ratio

GDP-L-fucose synthase

Roehe *et al.* (2016) PLOS Genetics

‘Fucose Sensing’

- **Fucose**
  - **Component of innate immunity glycoproteins (mucins)**
  - **Intestinal mucosa**
  - **Saliva glands**
  - **Integrity of the mucosal barrier**
- **Bacterial demand for fucose**
  - **Degradation mucins**
- **FucR: L-fucose operon activator**
  - **Controls bacterial signalling for host mucins production**
  - **Controls bacterial demands for fucose with supply**
- **Cross-talk of microbiome & host**

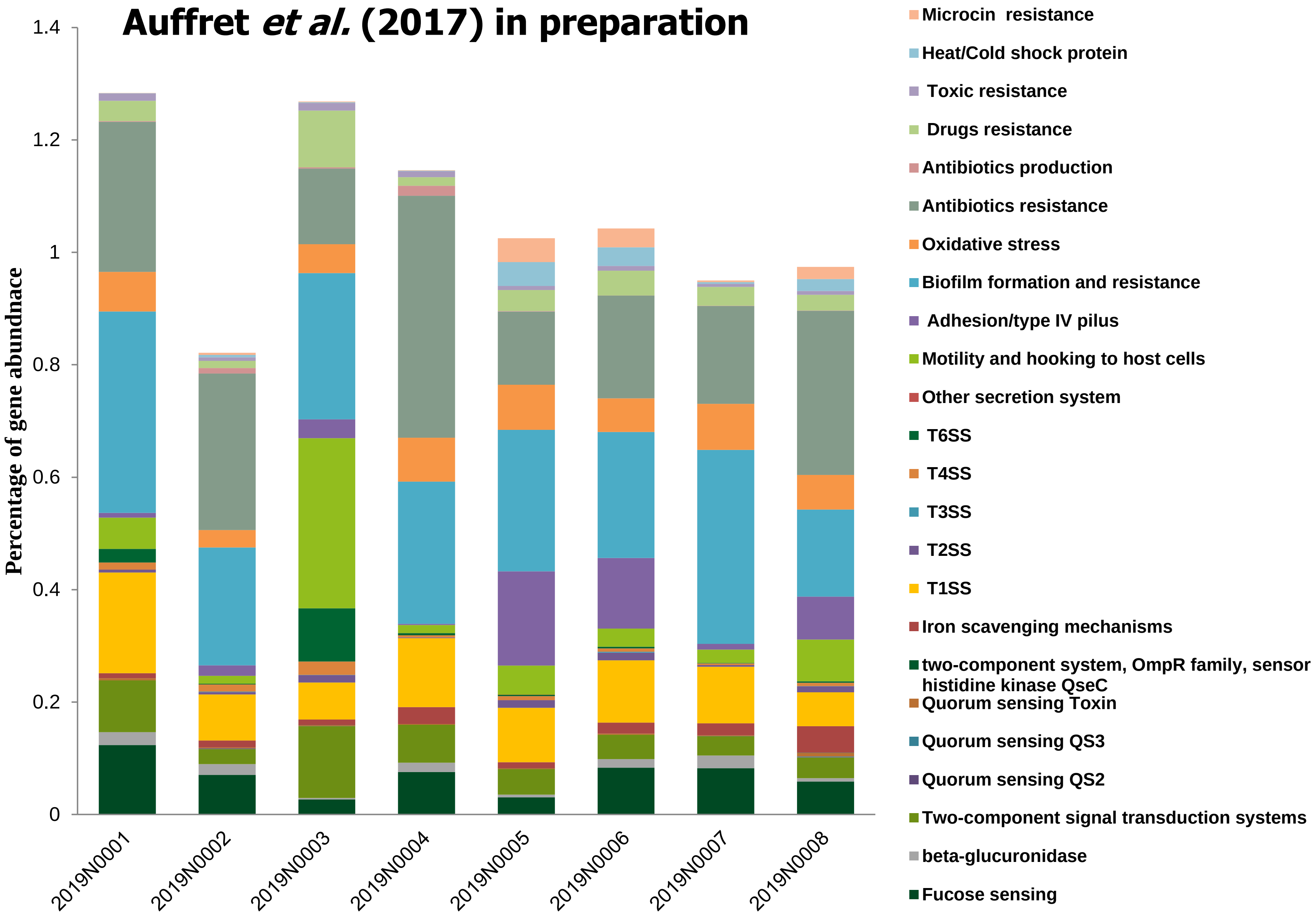
Conclusions Microbial Selection Criteria

- **Microbial information highly informative**
  - **Relative abundance of <u>microbial community</u>**
    - **Deviation from normal distribution**
    - **More restricted numbers**
    - **No unique biological (functional) background**

  - **Relative abundance of <u>microbial genes</u>**
    - **Most microbial genes normally distributed**
    - **Many thousands of microbial genes**
    - **Many proteins within KEGG orthologues**
    - **Known biological (functional) background**

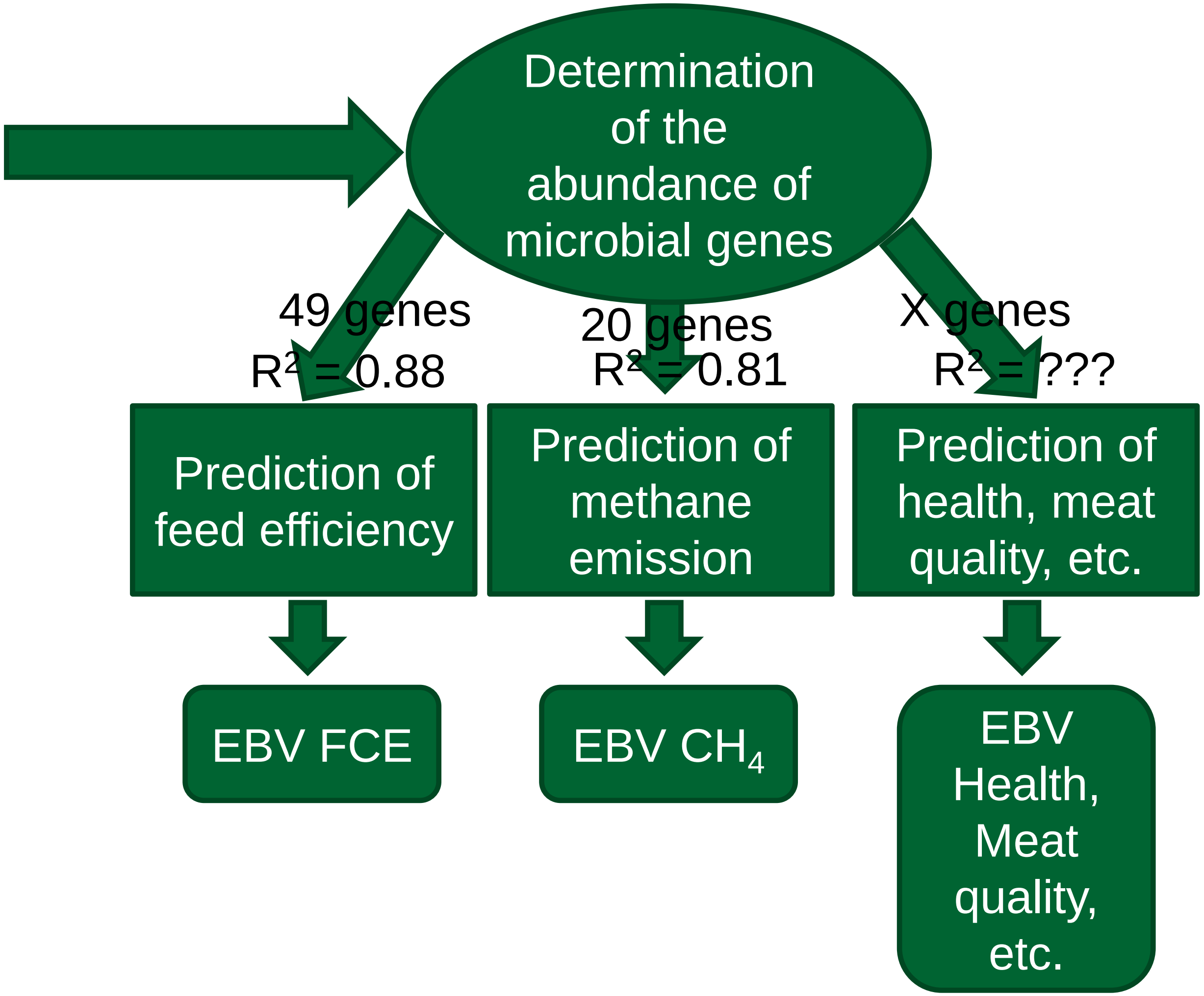
- **Combination of taxa & microbial genes BEST!**

Microbial Genes associated with Antimicrobial Resistance



Selection using Rumen Microbial Information

Sampling rumen fluid in the abattoir or live animals



Determination of the abundance of microbial genes

49 genes $R^2 = 0.88$

20 genes $R^2 = 0.81$

X genes $R^2 = ???$

Prediction of feed efficiency

Prediction of methane emission

Prediction of health, meat quality, etc.

EBV FCE

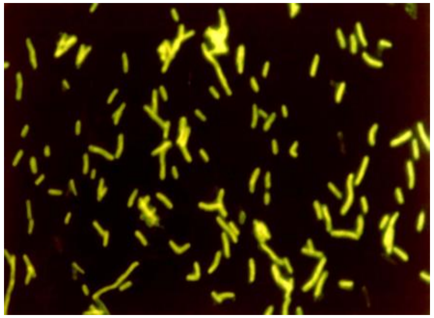
EBV CH_4

EBV Health, Meat quality, etc.

Conclusions

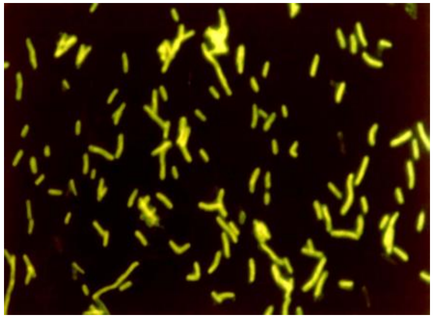
- Host (animal) genetic effect
  - Microbial community & microbial genes
  - Methane emissions
- Selection criterion
  - Abundance of microbial genes associated with feed conversion efficiency and methane emissions
  - Development of a microbial gene microarray

- Abundance of microbial genes
  - Health & meat quality
  - Susceptibility to heat stress
  - Biomarker for animal welfare, etc.



Conclusions

- Advantages of this selection strategy
  - Genetic improvement of difficult and costly to measure traits via abundances of microbial genes
  - Highly cost-effective
  - Microbial genes have functional background



- New era of breeding for animals (hosts) providing the best environment for efficient rumen microbes can begin!

Outlook & Recommendation

- Brazilian meat production is expected to continue its **fast growth** in the coming decade, according to the FAO.
- Based FAO outlook to 2024, beef production in Brazil will increase due to:
  - **Increasing domestic and international demand**
  - **Lower projected feed costs**
  - **Improved animal genetics**
  - **Better Health and Nutrition**

Recommendation **Use of Microbial Gene Information**

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