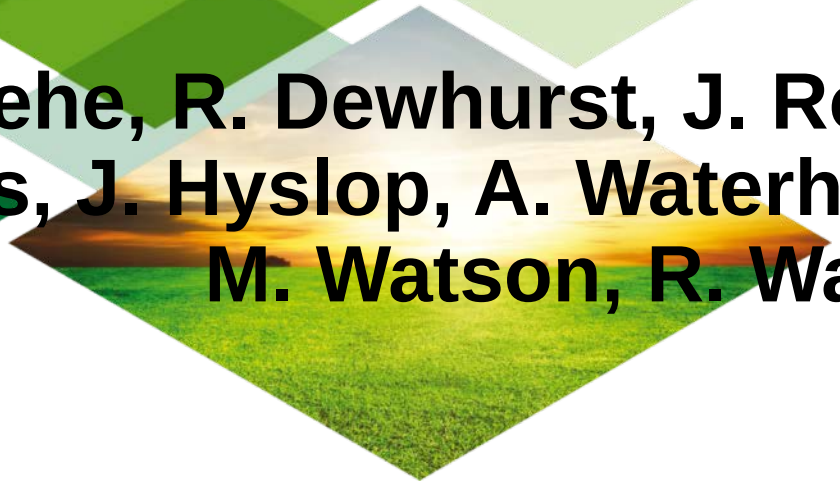
Novel selection criteria for rumen microbial genes to improve feed efficiency and methane mitigation

R. Roehe, R. Dewhurst, J. Rooke, N. McKain, D. Ross, J. Hyslop, A. Waterhouse, T. Freeman, M. Watson, R. Wallace

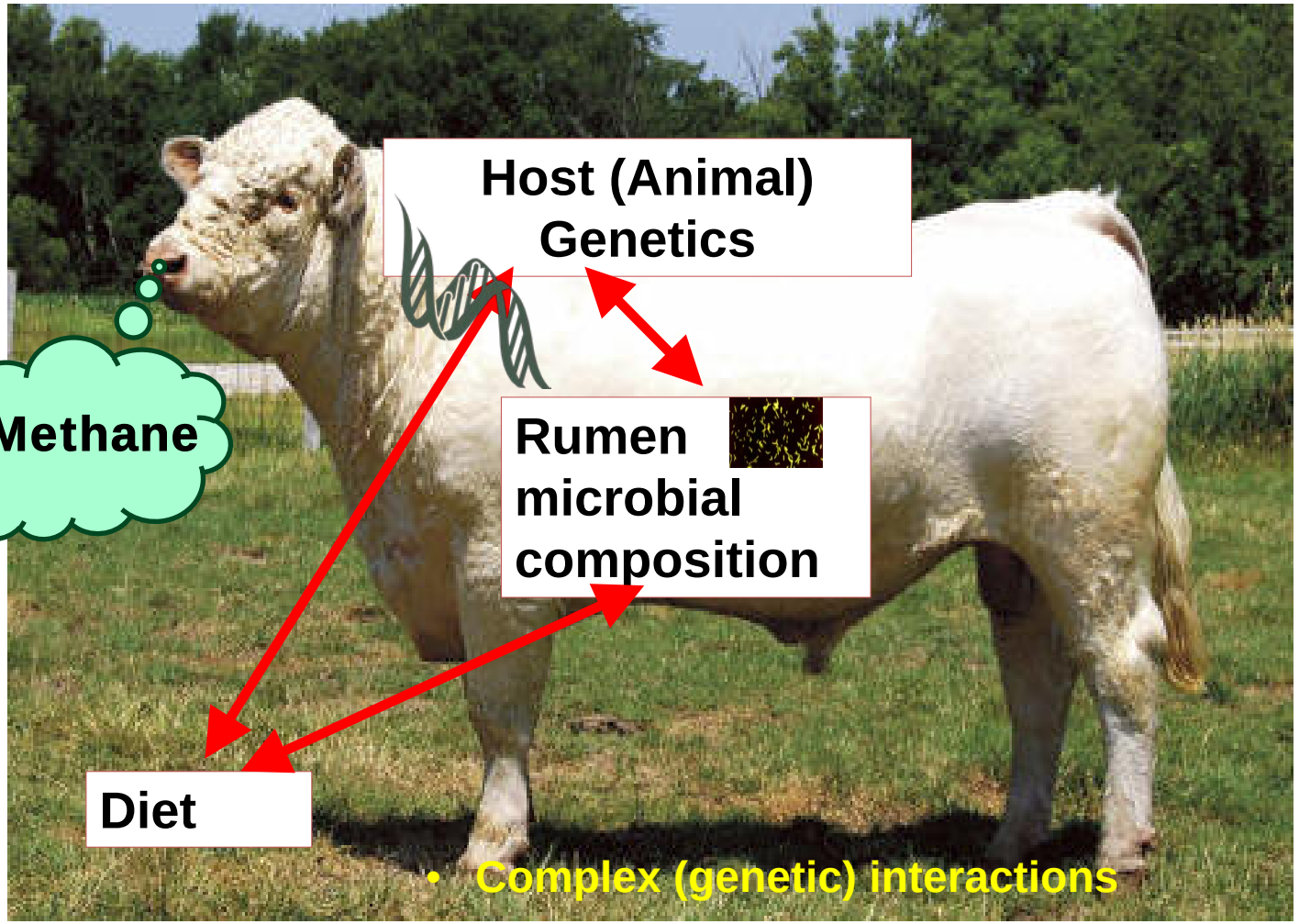


Leading the way in Agriculture and Rural Research, Education and Consulting

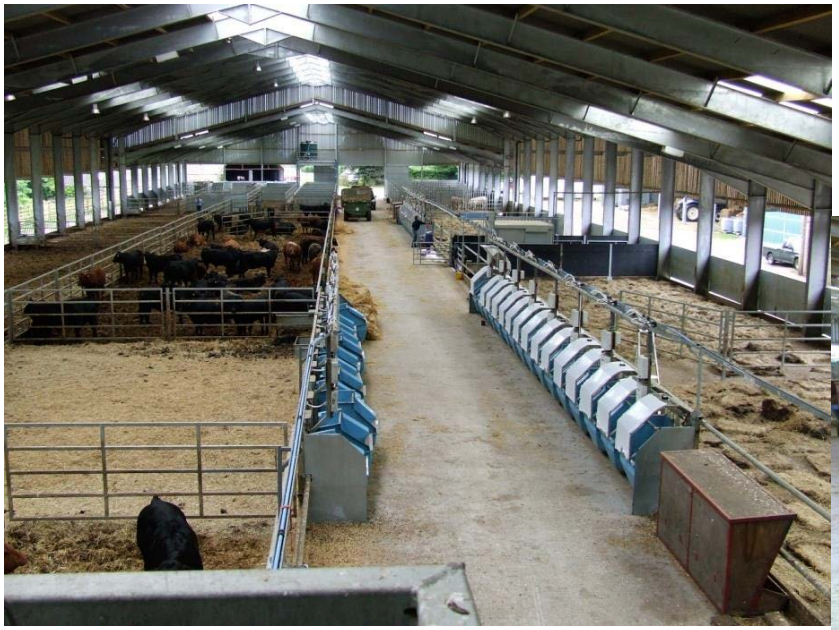
Host (animal) selection for feed efficiency and methane mitigation

- Feed conversion efficiency (FCE) in beef cattle
  - High economic impact (60 - 70% feed costs)
  - Use of limited resources
- 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



Recording feed intake & methane emissions

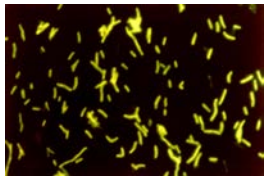


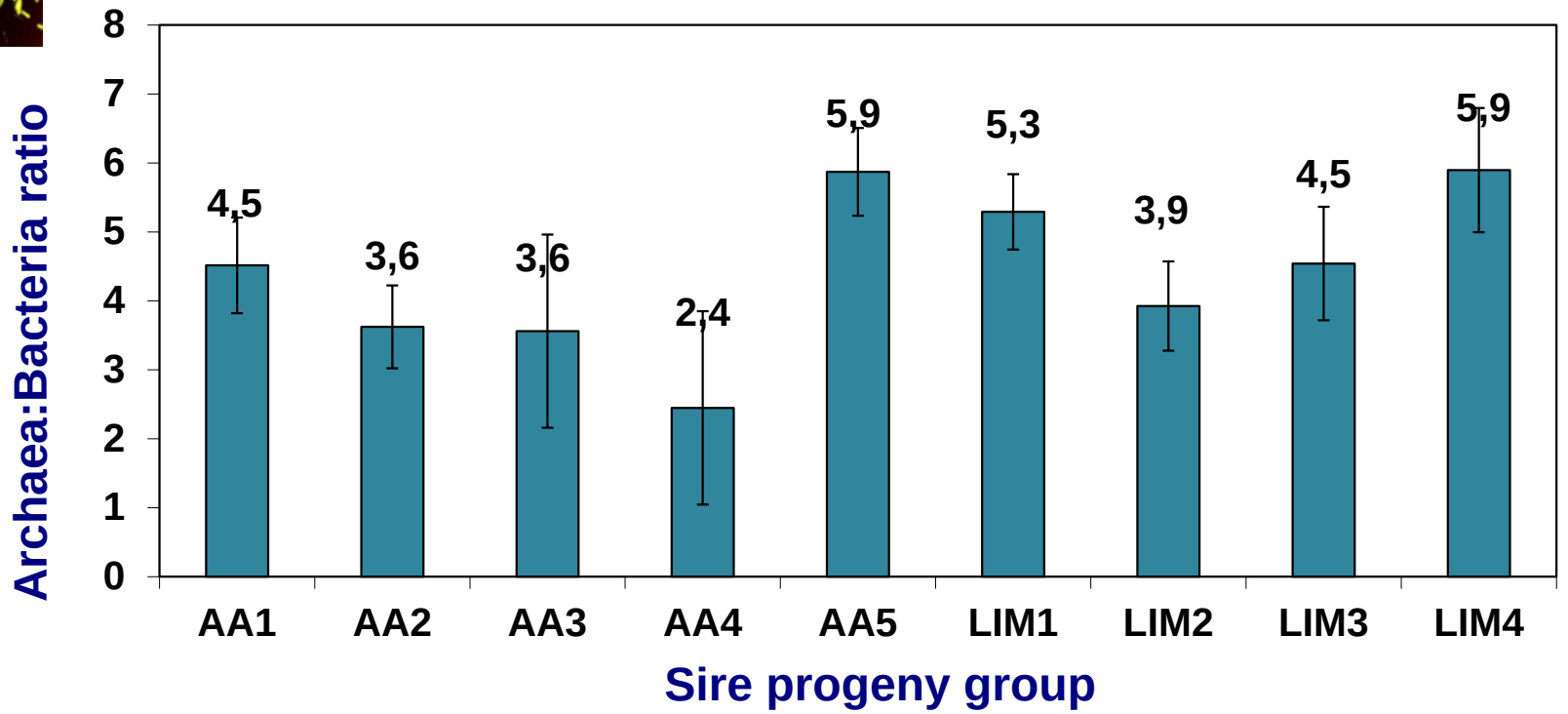
Individual feed intake

Individual methane emissions

SRUC Beef Research Centre, Easter Howgate

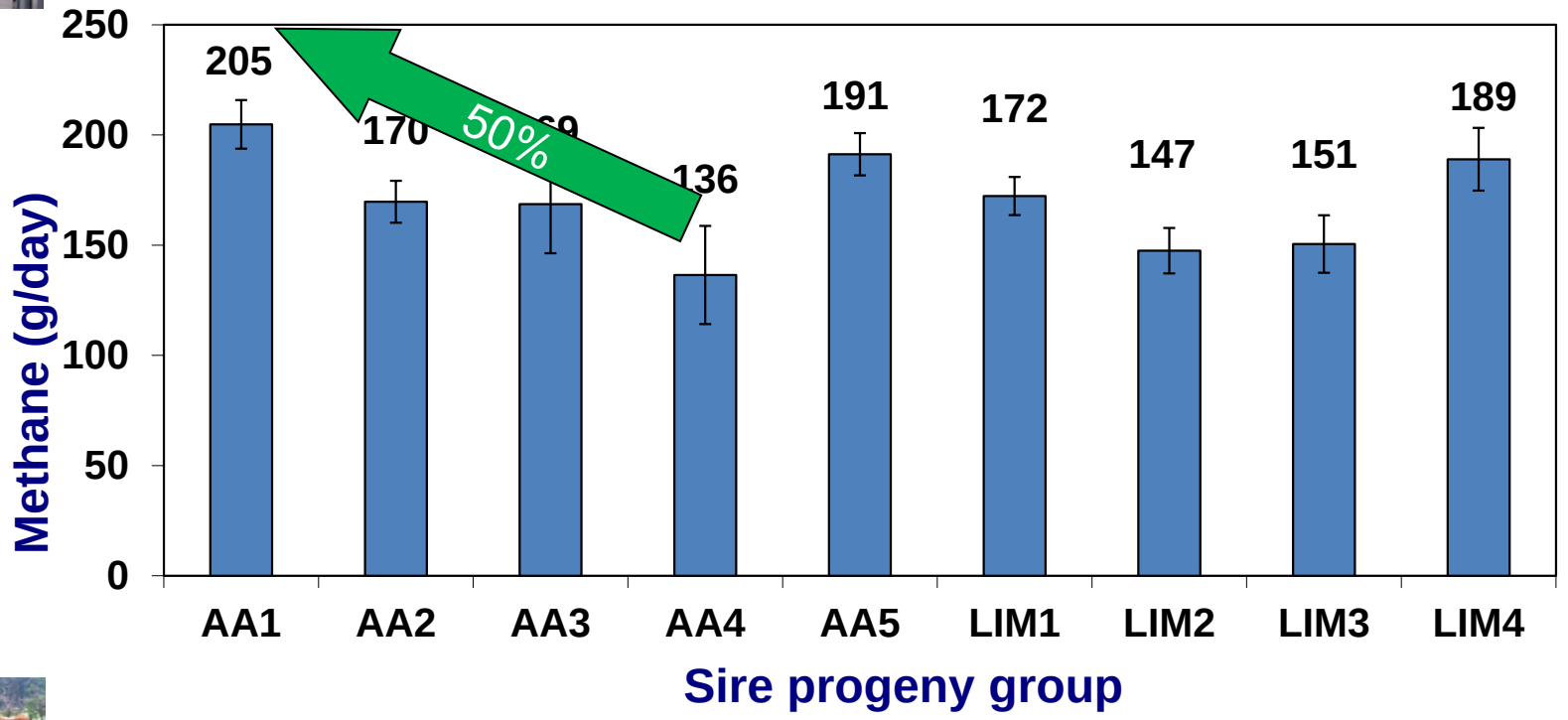
Host (Animal) genetics shapes microbial community (A:B ratio)



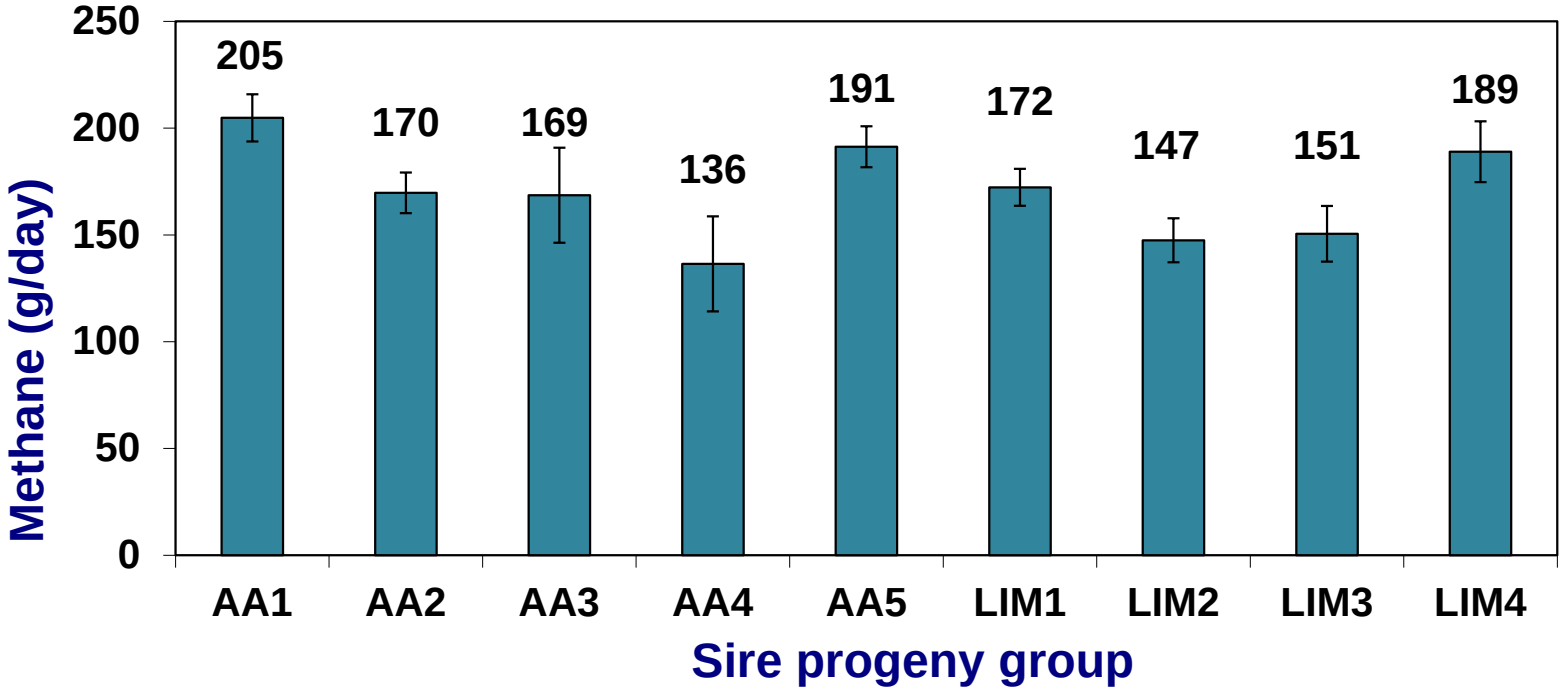


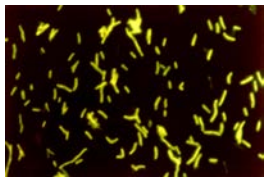
Roehe *et al.* (2016) PLOS Genetics

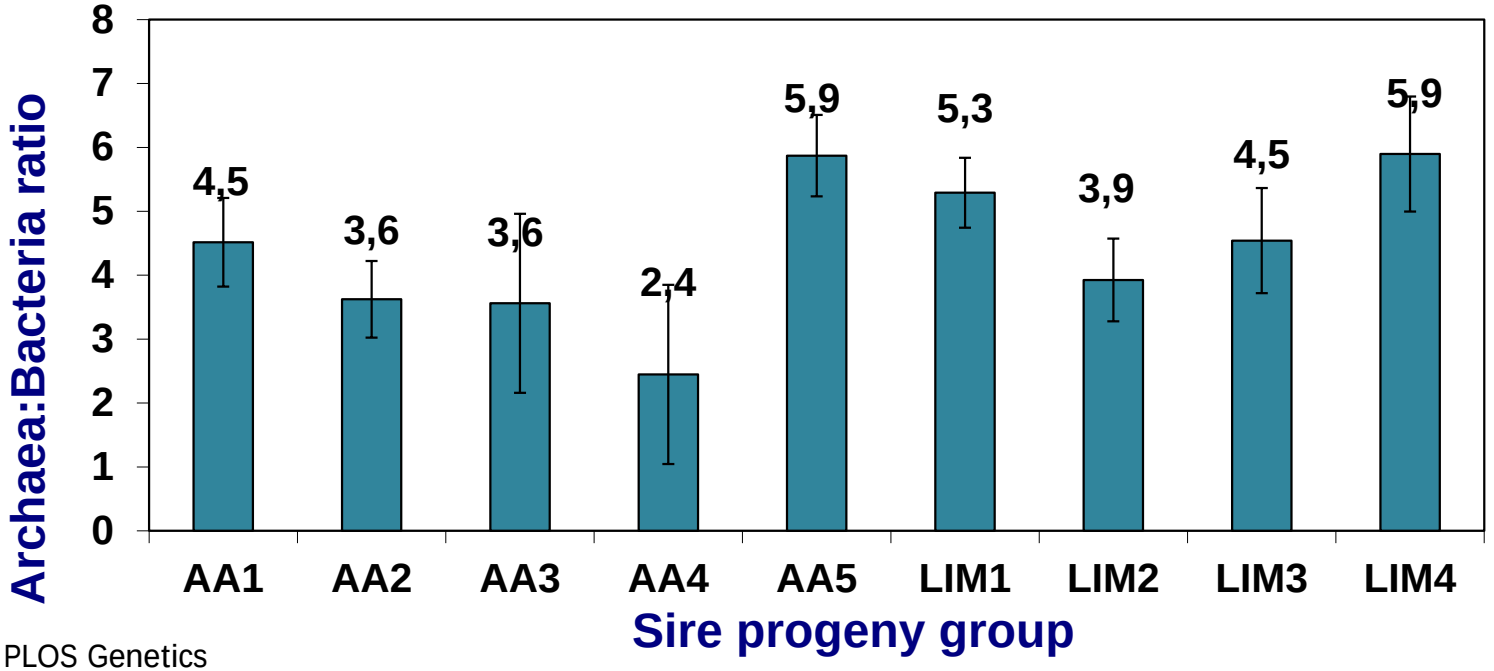
Host (animal) genetics affects methane emissions (g/day)



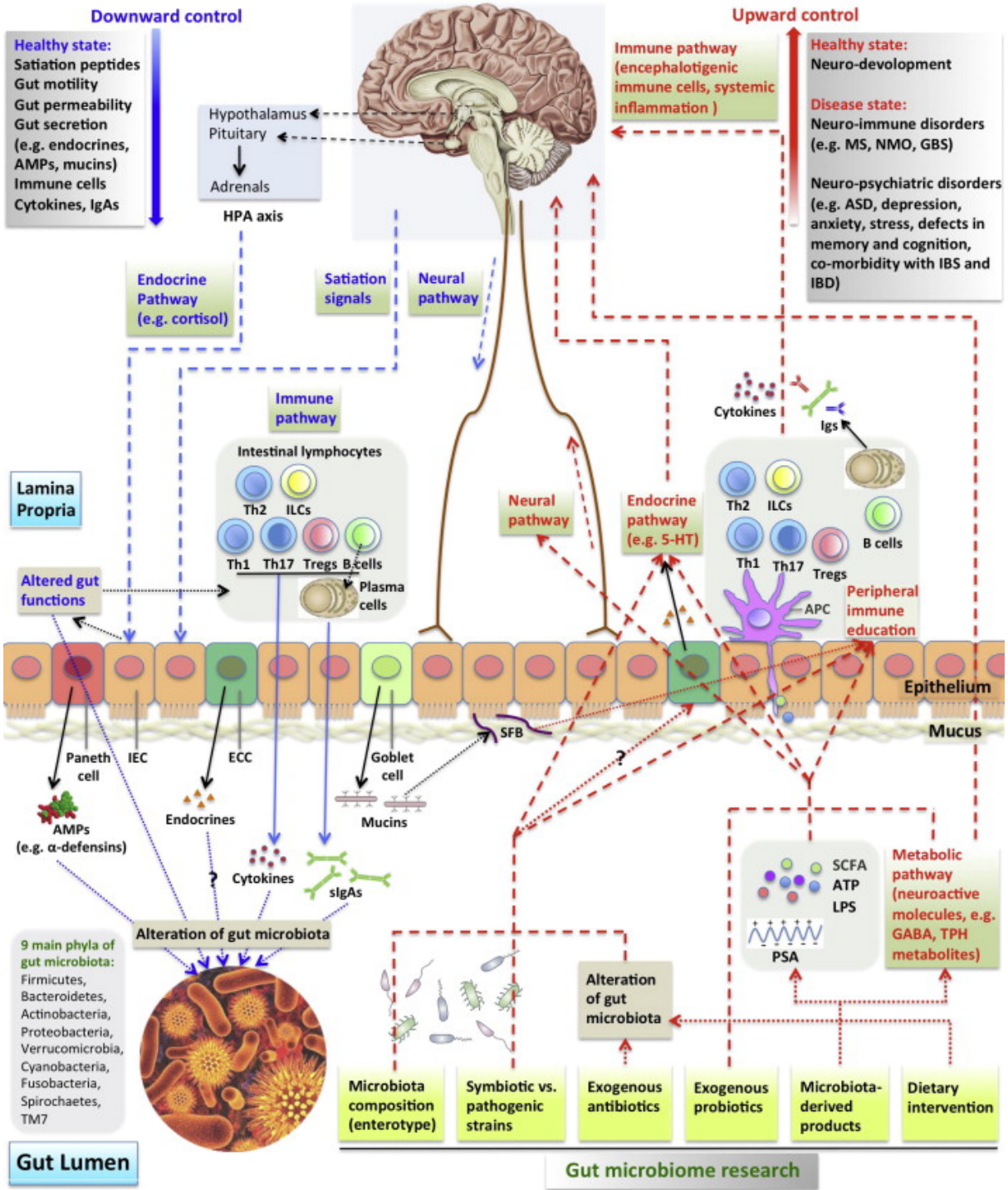
Roehe *et al.* (2016) PLOS Genetics







Roehe *et al.* (2016) PLOS Genetics



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.
Bacterioidetes,
Proteobacteria

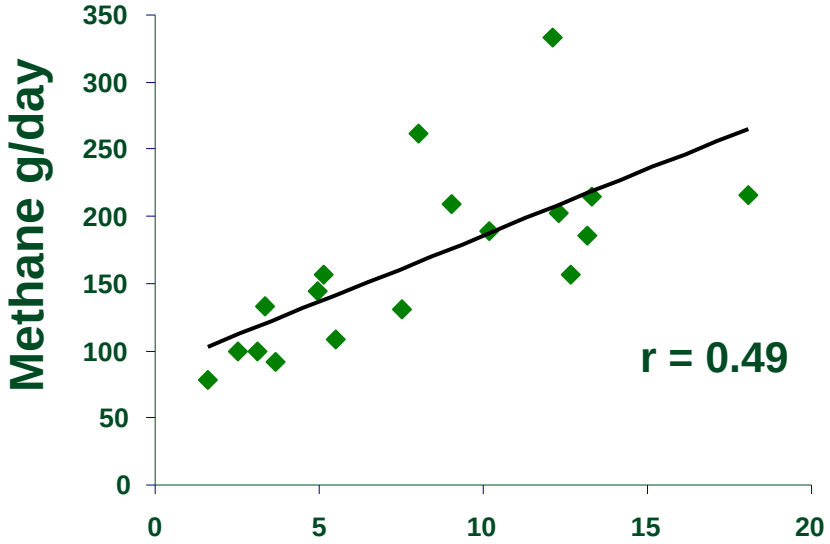
Genus
e.g.
Methano-
brevibacter,
Methano-
sphaera

Microbial enzyme genes
e.g.
KEGG gene ortholog

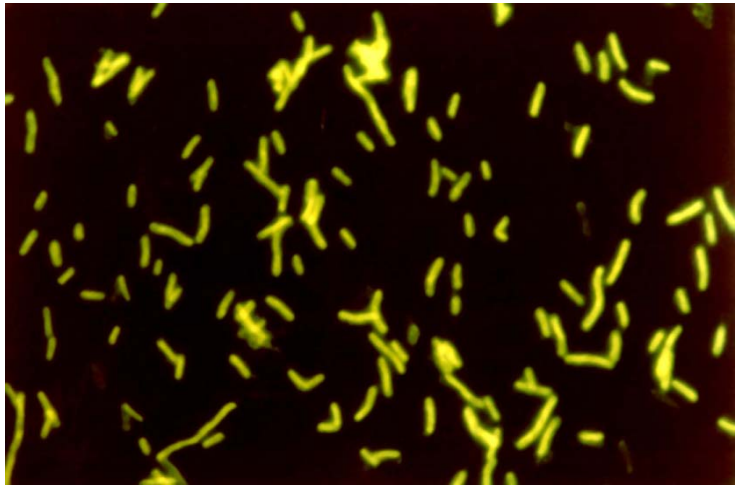
Proteins within KEGG ortholog

Predicting methane emissions by methanogenic archaea/bacteria ratio

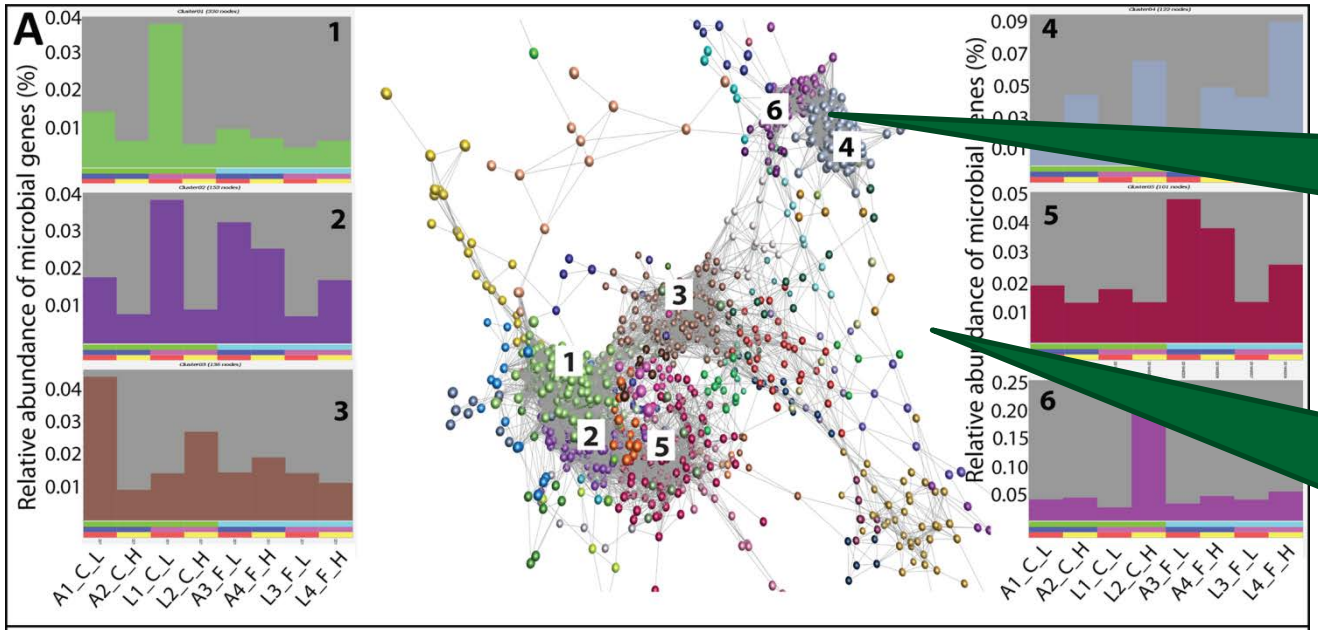
Microbial Kingdom

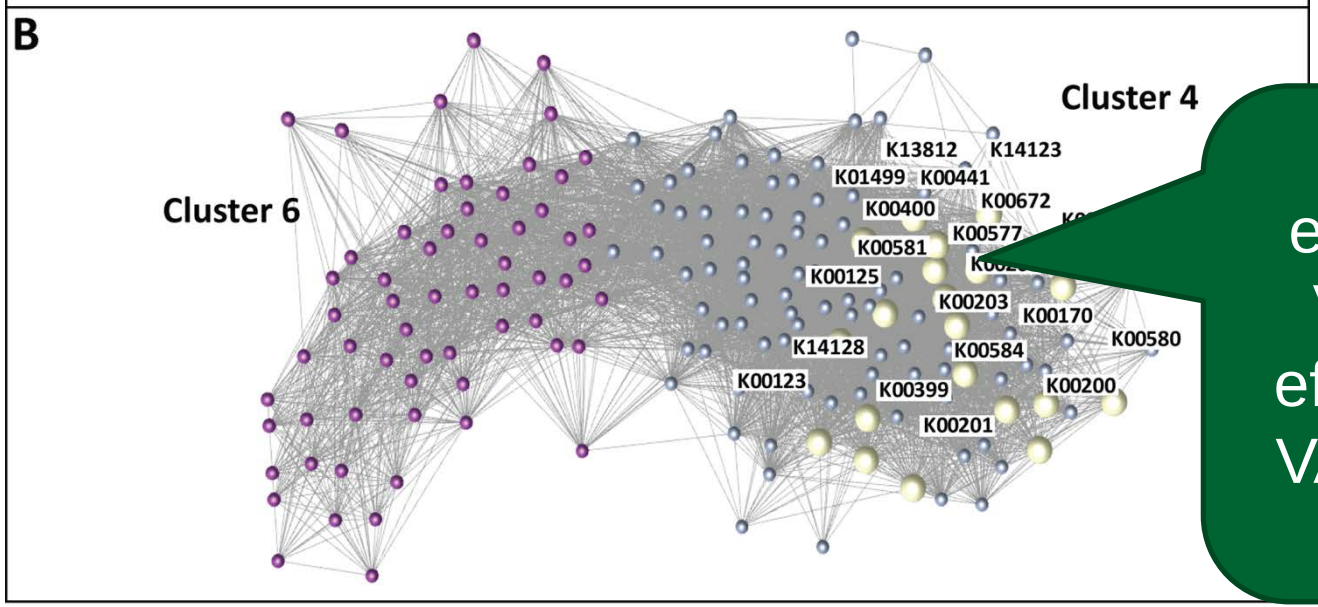


Rumen fluid samples
(both on live & slaughtered animals)



Network of rumen microbial genes



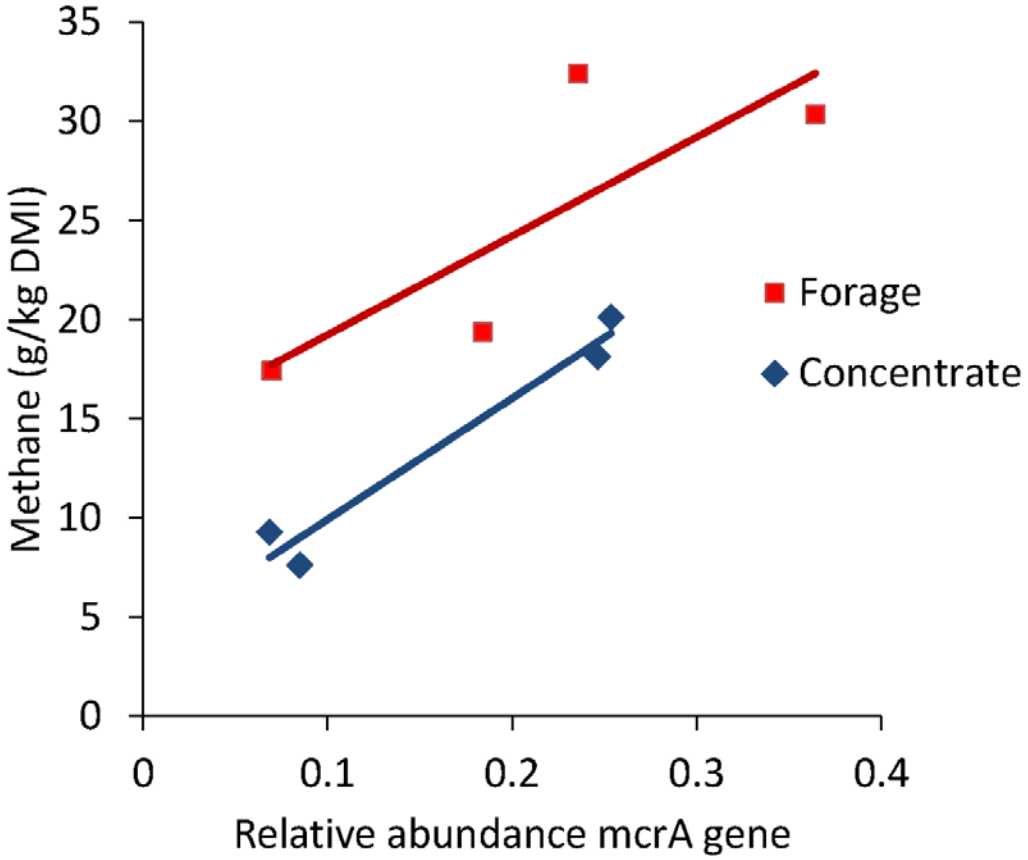


Methane emissions

3970 microbial genes

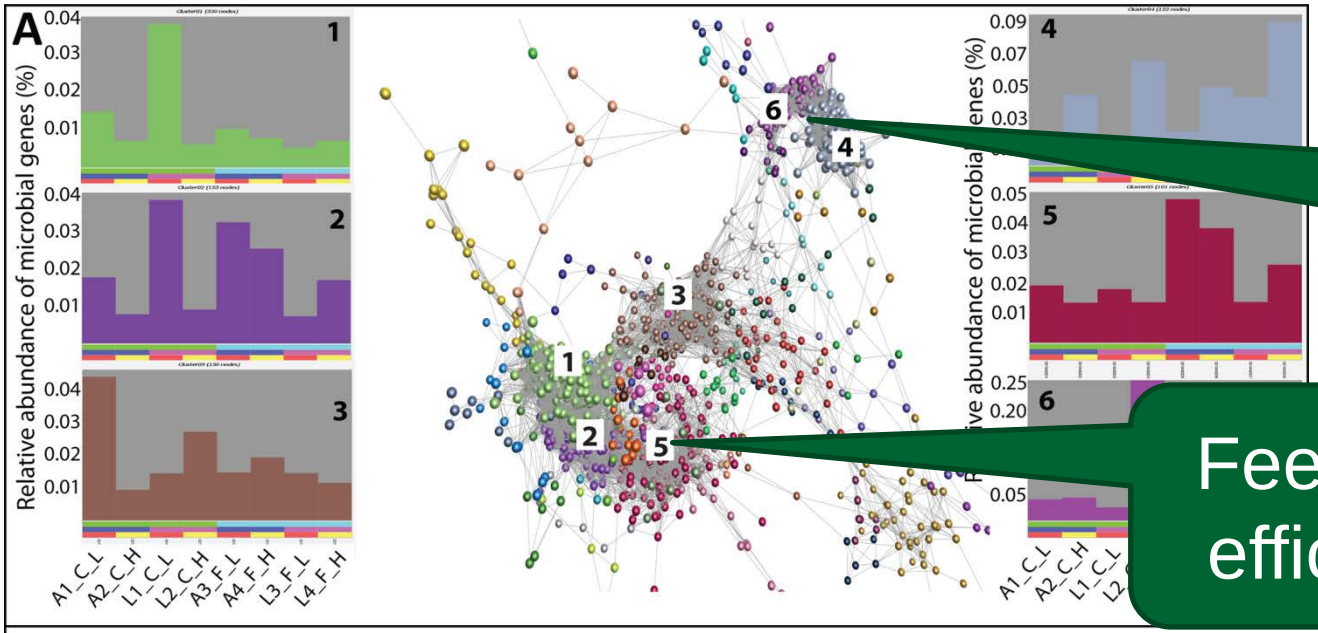
20 genes explaining 97% VAR in model effects & 81% of VAR in methane emissions

Methane emissions & mcrA gene



mcrA =methyl-coenzyme M reductase alpha subunit

Microbial genes associated with FCE



Methane emissions

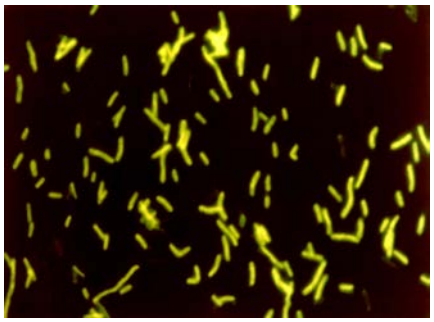
Feed conversion efficiency (FCE)

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

Selection using rumen microbial information

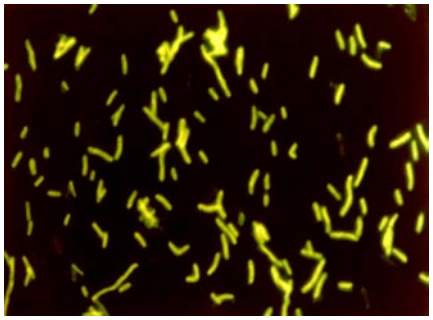
Conclusions

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



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 showed metabolic background**



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

Acknowledgements

The research is funded by:

**The Scottish Government (RESAS) and
Biotechnology and Biological Sciences Research Council (BBSRC)**

Aligned research is sponsored through:

**Department for Environment, Food and Rural Affairs (Defra),
English Beef and Lamb Executive Ltd. (EBLEX)
and Quality Meat Scotland (QMS)**

Other collaborators: