

Methane Measurements and Proxies

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

GreenCow Respiration Chambers



- Six respiration chambers
- Six training pens
- Feed intake recording equipment

Extensive experimental records



Feed and
productive
efficiency



Chamber based
measurements



Carcass and
meat quality
based
measurements

- Feed intake (Hoko)
- Live-weight gain
- Feed efficiency & RFI
- US fat and muscle depth
- CH₄ – hood systems

- **Methane measurements**
- Feed intake
- Live-weight
- Rumen samples
- Faecal samples
- Feed characterisation

- EUROP grades
- VIA information
- Loin samples
 - Sensory
 - Fatty acid profiles
 - Vitamin E
 - Colour shelf life

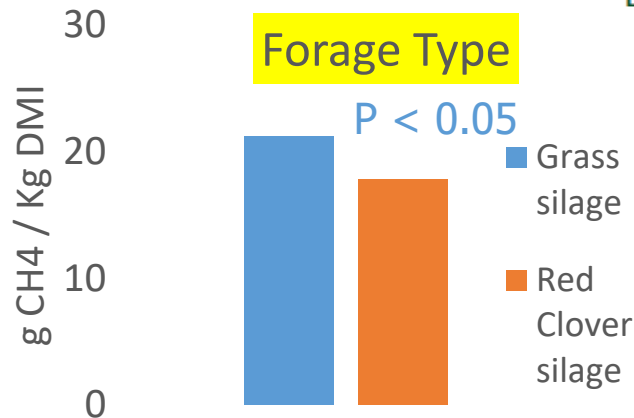
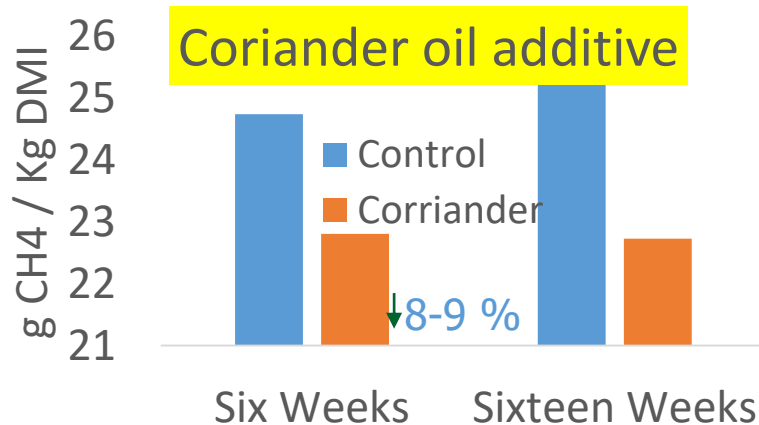
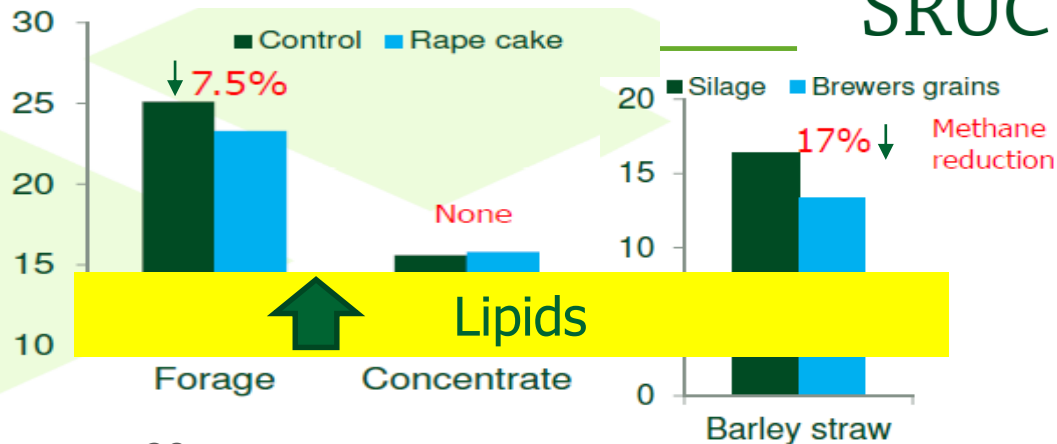
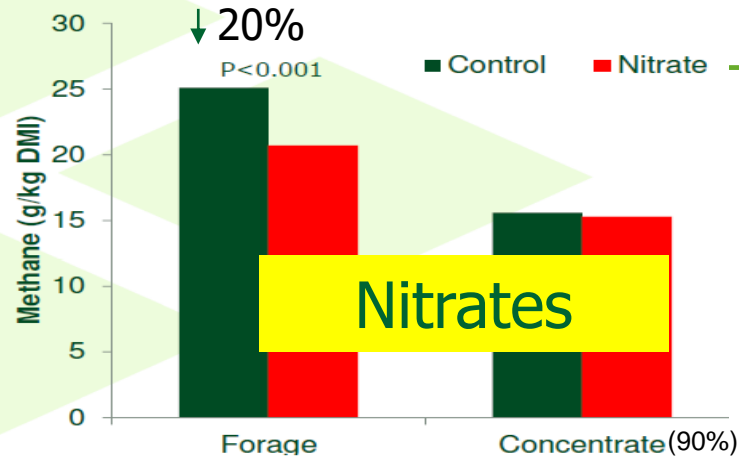
2011 – 2013 UK GHG Inventory



- Almost 500 animal data-points supplied by SRUC
- Cattle (cows and finishing animals) and sheep.
- Range of breeds and diets.
- Development of UK enteric methane emission factors.
- Moving from IPCC Tier 1 to Tier 2/3.



Dietary Manipulation



Proxy Measurements at SRUC

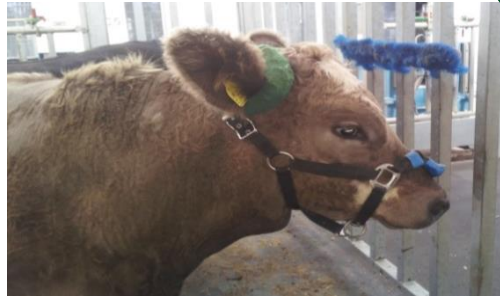
- Estimates or predicts individual animal methane production



Sniffer hoods



Methane gun



Methane Collars



SF6



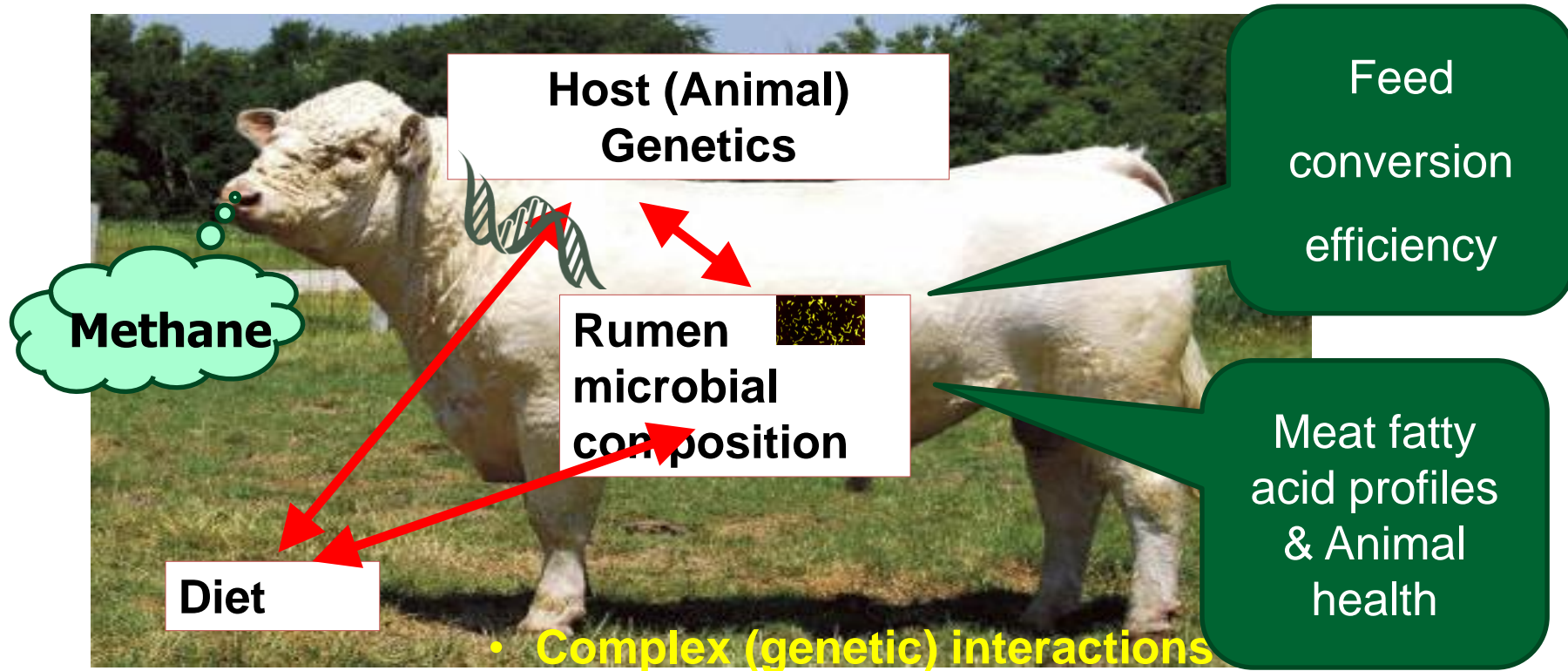
Rumen Microbiome

**SmartCow: SRUC's beef research facilities
to study associations of the rumen
microbiome with traits important for beef
production**

Rainer Roehe



Host Genetics and Microbiome



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



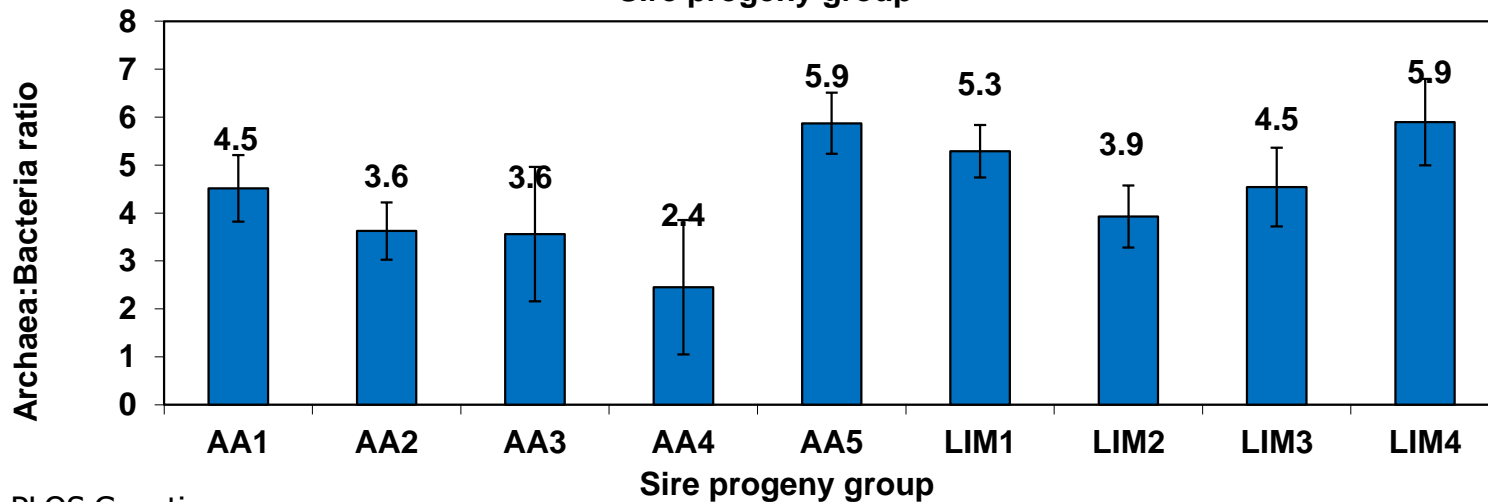
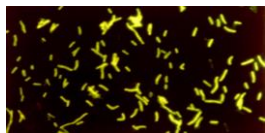
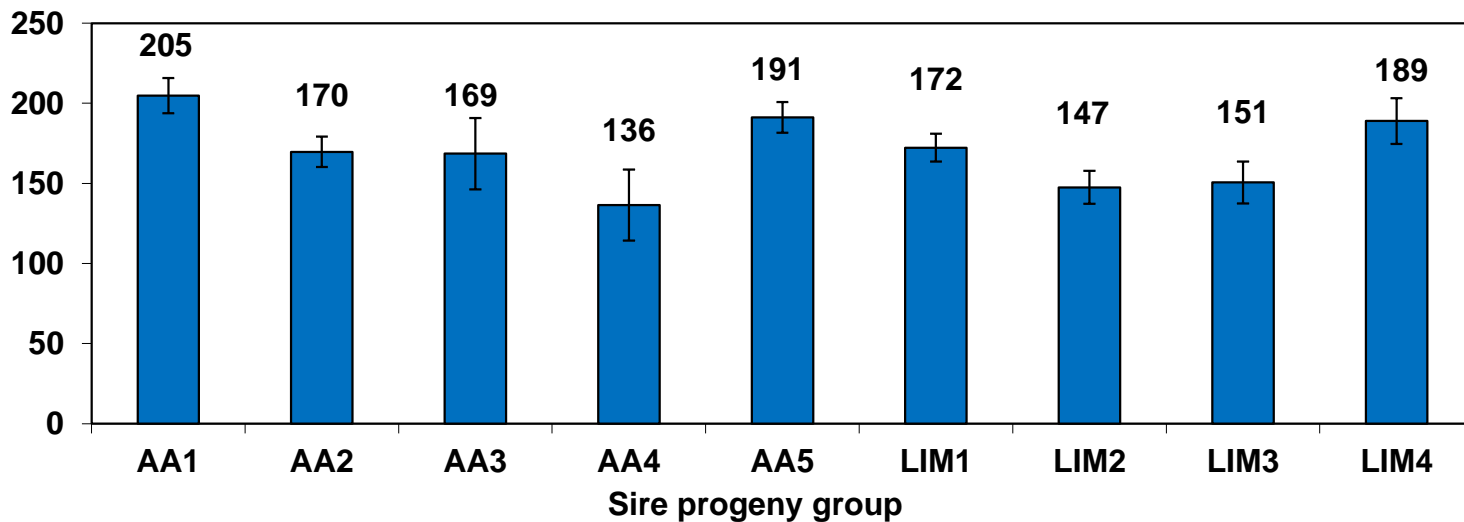
	Forage	Concentrate
A. Angus x	1.5 – 11.0	0.9 – 5.8
Limousin x	2.2 – 14.0	1.4 – 4.9

**Extreme large differences in
Archaea:Bacteria ratios between animals**

CV = 35% – 50%



Methane (g/day)



Deep Sequencing of DNA from Rumen Microbes

Metagenomic analysis

Microbial community

Gene-centric

Domain
e.g.
Archaea,
Bacteria

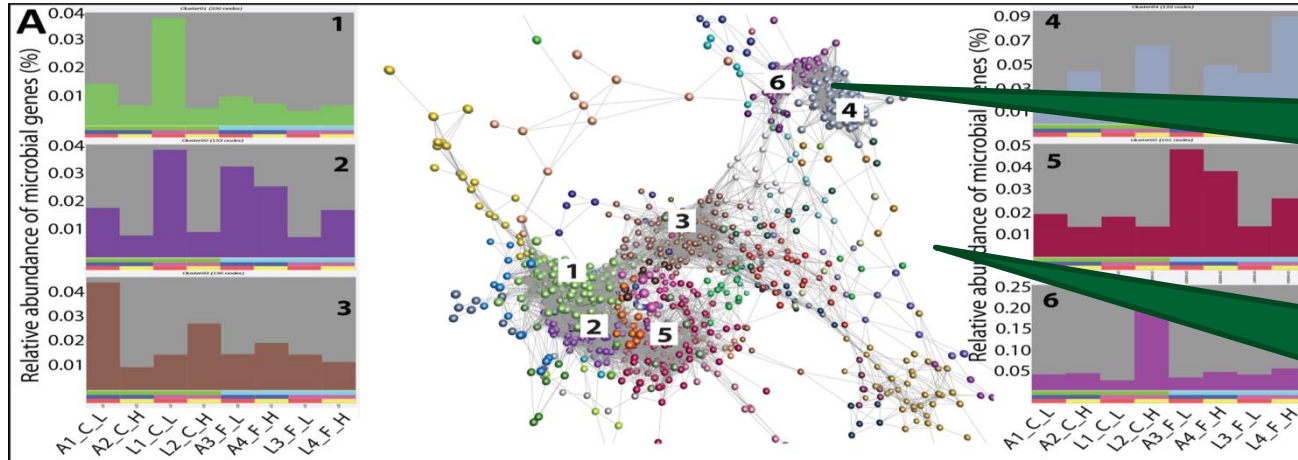
Phylum
e.g.
Bacteroidetes,
Proteobacteria

Genus
e.g.
Methano-
brevibacter,
Methanos-
phaera

Microbial genes,
e.g.
KEGG gene
orthologues

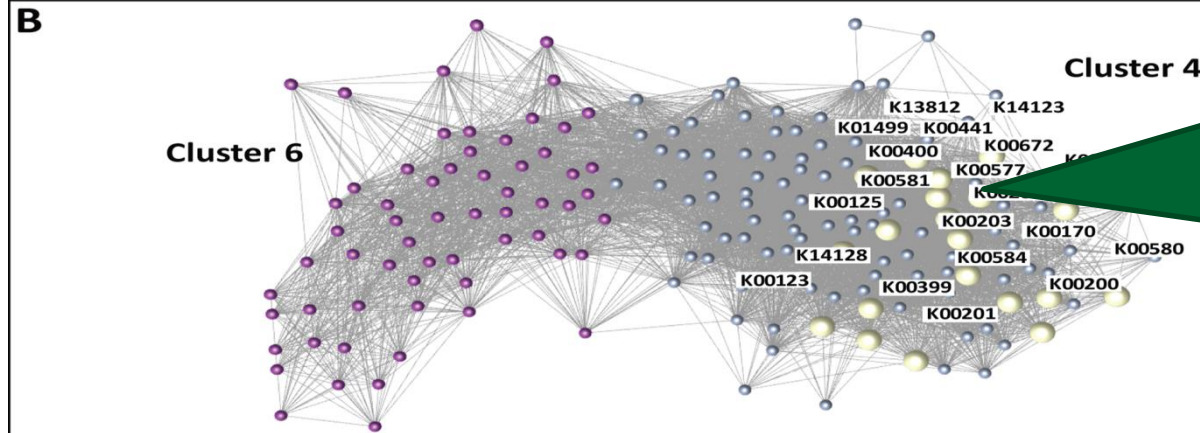
Proteins within
KEGG orthologues

Network of Rumen Microbial Genes



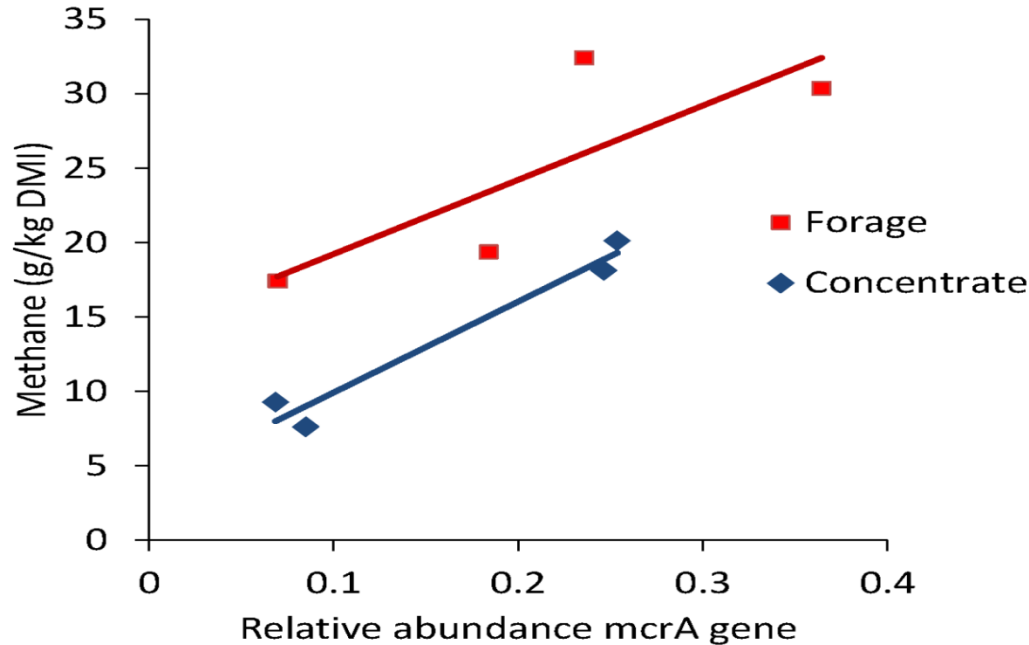
Methane emissions

3970 microbial genes



20 genes explaining
81% of VAR in
methane emissions

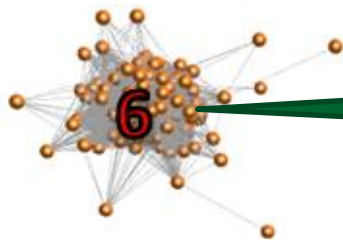
Methane emissions & mcrA gene



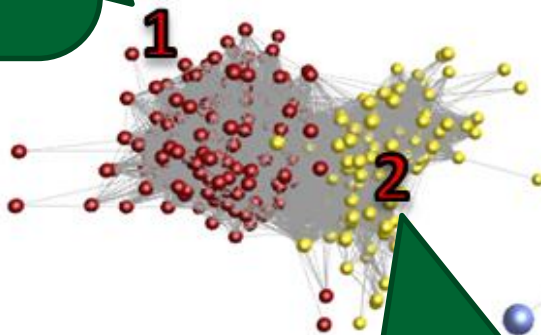
mcrA =methyl-coenzyme M reductase alpha subunit

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

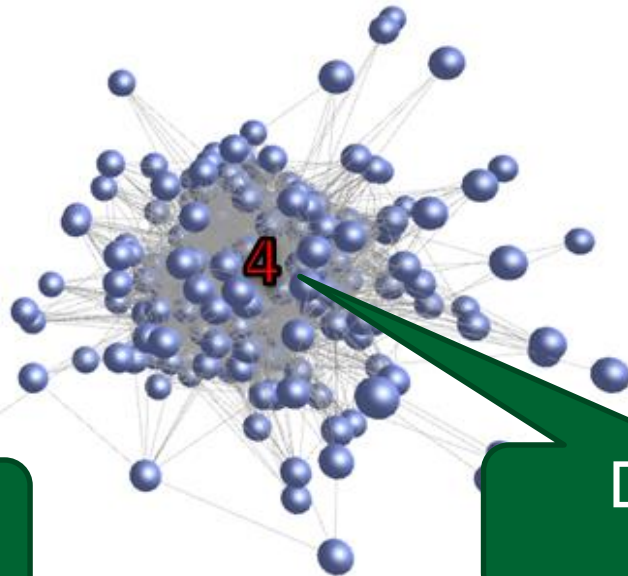
FCR (18)
ADG (18)
DFI (3)
RFI (3)



FCR (96)
ADG (92)

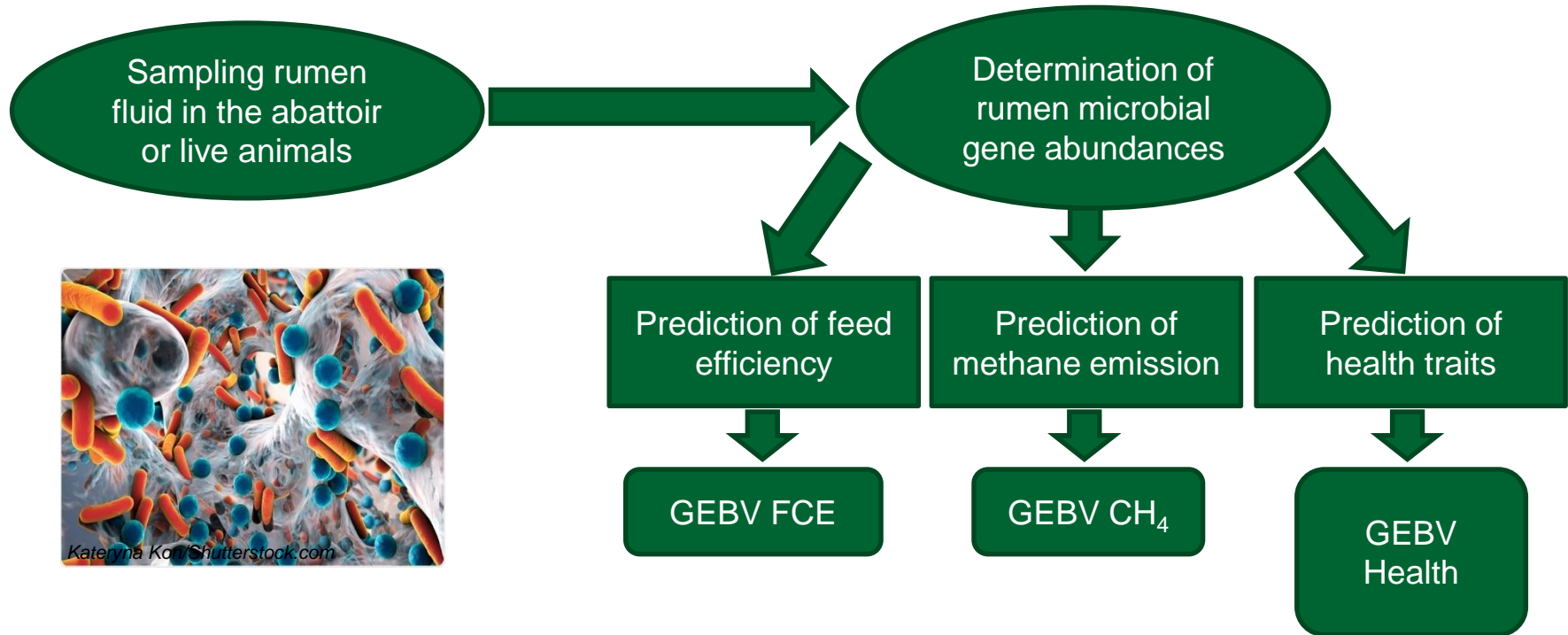


ADG (21)



DFI (14)
RFI (4)

Selection using rumen microbial information





Thank you very much!