Methane Measurements and Proxies

Gemma Miller and Rainer Roehe
GreenCow Respiration Chambers

- Six respiration chambers
- Six training pens
- Feed intake recording equipment
Extensive experimental records

Feed and productive efficiency

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

Chamber based measurements

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

Carcass and meat quality based measurements

- 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

**Nitrates**

- 20% decrease in Methane (g/kg DMI) for Coriander oil additive.

- Coriander silage reduces Methane by 8-9% compared to Control.

**Lipids**

- 7.5% reduction in Methane for Coriander oil additive.

- Methane reduction for Barley straw compared to Silage.

**Forage Type**

- Grass silage versus Red Clover silage shows a P < 0.05 difference in Methane (g/kg DMI).
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

- Complex (genetic) interactions
- Methane
- Rumen microbial composition
- Diet
- Feed conversion efficiency
- Meat fatty acid profiles & Animal health
## Variation in Methane Emissions g/day between Animals

<table>
<thead>
<tr>
<th></th>
<th>Forage</th>
<th>Concentrate</th>
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</thead>
<tbody>
<tr>
<td>A. Angus x</td>
<td>172–333 g/day</td>
<td>78–233 g/day</td>
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<tr>
<td>Limousin x</td>
<td>152–266 g/day</td>
<td>86–216 g/day</td>
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Large differences in methane emissions between animals

CV = 14% – 32%
Variation in Archaea:Bacteria Ratio between Animals using Samples collected on Slaughtered Animals

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<tr>
<td>A. Angus x</td>
<td>1.5 – 11.0</td>
<td>0.9 – 5.8</td>
</tr>
<tr>
<td>Limousin x</td>
<td>2.2 – 14.0</td>
<td>1.4 – 4.9</td>
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Extreme large differences in Archaea:Bacteria ratios between animals

CV = 35% – 50%
Roehe et al. (2016) PLOS Genetics
# Deep Sequencing of DNA from Rumen Microbes

<table>
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<tr>
<th>Metagenomic analysis</th>
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<td>Microbial community</td>
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<tr>
<td>Domain</td>
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<td>e.g. Archaea, Bacteria</td>
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</table>

- **Domain**: e.g. Archaea, Bacteria
- **Phylum**: e.g. Bacteroidetes, Proteobacteria
- **Genus**: e.g. Methano-brevibacter, Methanosphaera
- **Gene-centric**: Microbial genes, e.g. KEGG gene orthologues
Network of Rumen Microbial Genes

3970 microbial genes

20 genes explaining 81% of VAR in methane emissions

Methane emissions
Methane emissions & mcrA gene

\[ \text{mcrA} = \text{methyl-coenzyme M reductase alpha subunit} \]

Roehe et al. (2016) PLOS Genetics
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

Sampling rumen fluid in the abattoir or live animals

Determination of rumen microbial gene abundances

Prediction of feed efficiency
  - GEBV FCE

Prediction of methane emission
  - GEBV CH₄

Prediction of health traits
  - GEBV Health

GEBV FCE
GEBV CH₄
GEBV Health
Thank you very much!