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

Host Genetics and Microbiome

- Host (Animal) Genetics
- Rumen microbial gene abundances
- Diet
- Methane
- Complex (genetic) interactions

Feed efficiency
Microbes affecting Feed Efficiency (Symbiosis)

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

Feed (Forage)

Bacteria
Protozoa

Fungi

VFA (Energy)

Microbes (Protein)

Vitamins

10^{10} per g digesta

10^{6} per g digesta

10^{3} per g digesta

Diet

Animal

10^{6} per g digesta

10^{3} per g digesta
Deep Sequencing of DNA from Rumen Microbes

<table>
<thead>
<tr>
<th>Metagenomic analysis</th>
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</thead>
<tbody>
<tr>
<td>Microbial community</td>
</tr>
<tr>
<td>Gene- centric</td>
</tr>
</tbody>
</table>

- **Domain**
  - e.g. Archaea, Bacteria

- **Phylum**
  - e.g. Bacteroidetes, Proteobacteria

- **Genus**
  - e.g. Methanobrevibacter, Methanosphaera

- **Microbial genes**
  - e.g. KEGG gene orthologues
Microbial genes associated with FCE & CH$_4$

Methane emissions

Feed conversion ratio (FCR)

Roehe et al. (2016) PLOS Genetics
<table>
<thead>
<tr>
<th>Trait¹</th>
<th>Unit</th>
<th>Low</th>
<th>SD</th>
<th>High</th>
<th>SD</th>
<th>SE&lt;sub&gt;Diff&lt;/sub&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Mean</td>
<td></td>
<td>Mean</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DFI</td>
<td>kg/day</td>
<td>11.559&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1.279</td>
<td>11.919&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1.968</td>
<td>0.362</td>
</tr>
<tr>
<td>ADG</td>
<td>kg/day</td>
<td>1.653&lt;sup&gt;a&lt;/sup&gt;</td>
<td>0.389</td>
<td>1.780&lt;sup&gt;a&lt;/sup&gt;</td>
<td>0.430</td>
<td>0.089</td>
</tr>
<tr>
<td>FCR</td>
<td></td>
<td>6.626&lt;sup&gt;a&lt;/sup&gt;</td>
<td>0.741</td>
<td>8.871&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1.207</td>
<td>0.218</td>
</tr>
<tr>
<td>RFI</td>
<td></td>
<td>-0.328&lt;sup&gt;a&lt;/sup&gt;</td>
<td>0.682</td>
<td>0.431&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1.025</td>
<td>0.190</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Trait</th>
<th>Model factors (%)</th>
<th>Trait (%)</th>
<th>Microbial genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>DFI</td>
<td>50</td>
<td>72</td>
<td>23</td>
</tr>
<tr>
<td>ADG</td>
<td>64</td>
<td>55</td>
<td>166</td>
</tr>
<tr>
<td>FCR</td>
<td>61</td>
<td>68</td>
<td>167</td>
</tr>
<tr>
<td>RFI</td>
<td>40</td>
<td>73</td>
<td>12</td>
</tr>
</tbody>
</table>

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

Prediction of methane emission
- GEBV CH₄

Prediction of health/meat quality
- 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
Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse Bos Taurus Breeds and Basal Diets

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

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Microbiome
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Thank you very much!