Can rumen microbes improve prediction of metabolic traits in Dairy cows?

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Acknowledgements

Metagenomics Project
REMRUM Project

And With Special Thanks To
Background

• **Phenotype** = *Genes* + *Environment*

• For many traits this is not the case

• Rumen microbes form a key part of the engine!

• Feed utilization and methane
  – Completely dependent on rumen microbes
  – Produce VFAs: acetate, propionate and butyrate
Background

• Phenotype = Genes $\times$ Microbes $\times$ Environment

• Changing diet $E \rightarrow M$

• Rumen bacteria & archaea $h^2 G \rightarrow M$

• If $G$ & $M$ contribute to $P$

• One unit under natural selection

Zilber-Rosenberg and Rosenberg, 2008;
Bordenstein & Theis, 2015

Photo: Yokoyama & Cobos
Ketosis

• Metabolic disease

• High yielding dairy cows susceptible

• Severe NEB, mobilized fat exceeds capacity of liver

• Increased ketone bodies in milk, blood and urine
  – Biomarkers: Milk Acetone and BHB
  – Decreased ruminal propionate production

• Lowly heritable ($h^2 = 0.02 – 0.14$)
Research Questions

1) Do rumen microbes explain variation in Ketosis?

2) Can rumen microbial information improve prediction of Ketosis?
Rumen Samples

- Rumen Flora Scoop
- 16S rRNA gene amplicon sequencing & assembly
- Alignment & assembly: ‘bins’ 97% similarity = OTU
- OTU ~ relative counts of different **bacterial** and **archaeal** species
Data

• 277 lactating Holsteins 3 herds - E

• Milk metabolites NMR:
  – BetaHydroxyButyrate (BHB)
  – Acetone (ACE)

• Rumen Bacterial (4030) & Archaeal (203) OTU’s

• Illumina BovineSNP50 BeadChip > HD
Analysis

• Variance components estimation (DMU)

\[ Y = Xb + Zg + e \quad Y = Xb + Wm + e \]

• Microbial relationship matrix

\[ h^2 = \frac{V_g}{V_p} \quad m^2 = \frac{V_m}{V_p} \]

16S rRNA bacterial & archaeal abundance  intra-class correlation coefficient

Microbiability \((m^2)\)
## Results

<table>
<thead>
<tr>
<th></th>
<th>heritability</th>
<th>microbiability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acetone</td>
<td>0.10</td>
<td>0.15</td>
</tr>
<tr>
<td>BHB</td>
<td>0.03</td>
<td>0.15</td>
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Prediction reliabilities

• Five fold validation (20%)

• Reliability computed as correlation between:

\[ \text{MBLUP: } \frac{\text{corr}(cY; MV)}{m^2} \]
\[ \text{GBLUP: } \frac{\text{corr}(cY; \text{EBVs})}{h^2} \]
## Results

<table>
<thead>
<tr>
<th></th>
<th>G reliability</th>
<th>M reliability</th>
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</thead>
<tbody>
<tr>
<td>Acetone</td>
<td>0.25</td>
<td>0.35</td>
</tr>
<tr>
<td>BHB</td>
<td>0.02</td>
<td>0.55</td>
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Conclusions

• $m^2$ - a tool for identifying and quantify M contributions to complex phenotypes

• M explains more variation in Ace and BHB than G

• Prediction reliabilities of MBLUP exceeds GBULP

• Microbes - Correlation is not necessarily causation