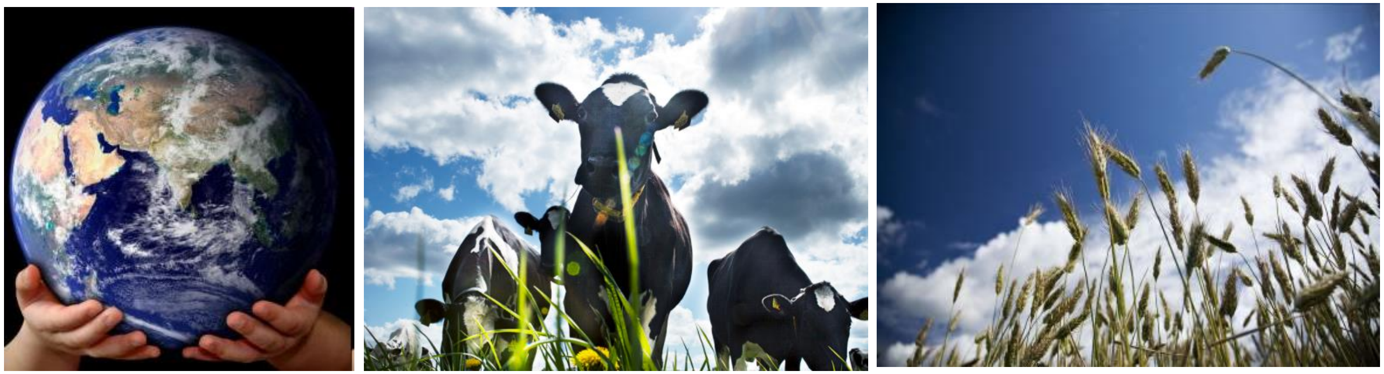
Can rumen microbes improve prediction of metabolic traits in Dairy cows?

Gareth F. Difford, G. Gebreyesus,
A.J. Buitenhuis, P. Løvendahl, J. Lassen, B. Guldbrandtsen & G. Sahana



gareth.difford@mbg.au.dk

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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** x **Microbes** x **Environment**
- Changing diet **E** ⟶ **M**
- Rumen bacteria & archaea h^2 **G** ⟶ **M**
- If **G** & **M** contribute to P
- One unit under natural selection

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

Photo: Yokoyama & Cobos

Ketosis

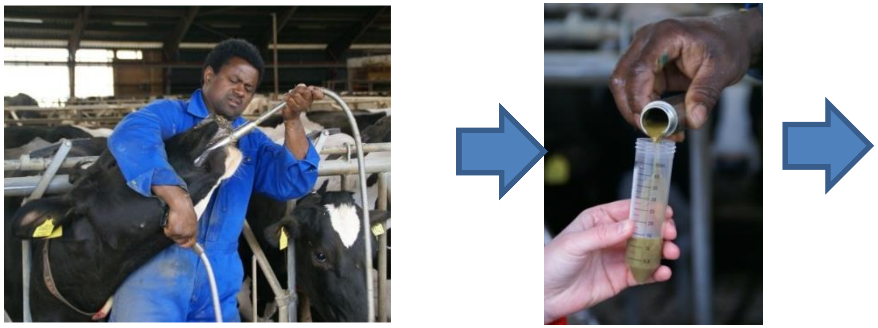
- Metabolic disease
- High yielding dairy cows susceptible
- Severe NEB, mobilized fat exceeds capacity of liver
- Increased ketone bodies in milk, blood and urine
  - Biomarkers: Milk Acetone and BHB
  - Decreased ruminal propionate production
- Lowly heritable ($h^2 = 0.02 – 0.14$)

Research Questions

1) Do rumen microbes explain variation in Ketosis?

2) Can rumen microbial information improve prediction of Ketosis?

Rumen Samples



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OTU        SampleA    SampleB    SampleC
OTU_1      0          12         8
OTU_2      1          22         0
OTU_3      6          0          2
```

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

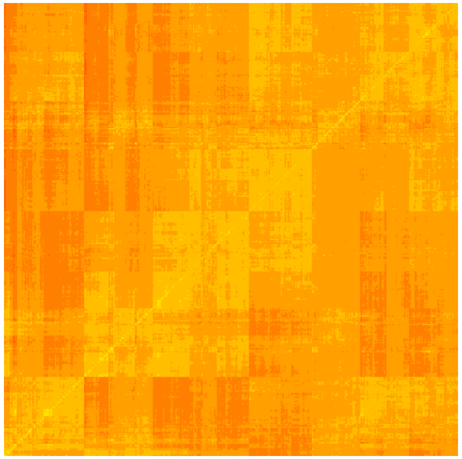
Data

- 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)



GBLUP ***MBLUP***

$$\boldsymbol{Y = Xb + Zg + e} \qquad \boldsymbol{Y = Xb + Wm + e}$$

- Microbial relationship matrix

- $h^2 = \frac{Vg}{Vp}$ $m^2 = \frac{Vm}{Vp}$

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

Microbiability (m^2)

Results

	heritability	microbiability
Acetone	0.10	0.15
BHB	0.03	0.15

Prediction reliabilties

- Five fold validation (20%)
- Reliability computed as correlation between:

MBLUP: corr(cY; MV)/m^2 GBLUP: corr(cY; EBVs)/h^2

Results

	G reliability	M reliability
Acetone	0.25	0.35
BHB	0.02	0.55

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