Microbiability: – new insights into (genetic) modelling methane emissions of cattle

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Acknowledgements

REMRUM Project

EGS ABG

AARHUS UNIVERSITY

WAGENINGEN UR

METHAGENE

And With Special Thanks To

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Background

- **Phenotype** = **Genes** + **Environment**
- Something missing?
- 120x microbial cells vs cow cells
- Densest population on earth
- Cow = Bioreactor

Less than 1% are culturable

- Next generation sequencing technologies
- Culture independent
- Microbiomics
  - cow + microbes = holobiont
- Metagenomics
  - genome + metagenome = hologenome

Holobiont theory of evolution

- P = G + E → P = G x M x E
- If G & M contribute to P
- One unit under natural selection

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

- E.g Corals, insects and plants

  Shapira, 2016

- No evidence in livestock species (yet)

Background

- Mutualism coevolved ~ 50 million years
  - Rumen microbes not found elsewhere or distinct
- Feed utilization and methane
  - Completely dependent on rumen microbes

Photo: Yokoyama & Cobos

Ignoring M = results in suboptimal response to G & E

Is a cow a holobiont?

G x M

- Rumen microbes in new born calves = vertical transmission, means unknown (Guzman et al 2015)
- Breeds differ (Paz et al 2016)
- Rumen transfaunation = cow specificity & horizontal transmission (Weimer et al 2010)
- Metagenomic prediction of CH_4 dairy cattle (Ross et al*, 2013)*

Objectives

Broad: Can we tell if cows are holobionts?

$$\boldsymbol{Y = Xb + Za + Wm + e}$$

Specific: 1) Is there a link between G x M?

2) Is there a link between M and CH4?

3) Can we quantify this?

Rumen Samples

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

- 750 lactating Holsteins (6 herds) - E
- Phenotypes:
  - Methane Production(**CH4**)
  - Energy Corrected Milk (**ECM**)
  - Body Weight (**BW**)

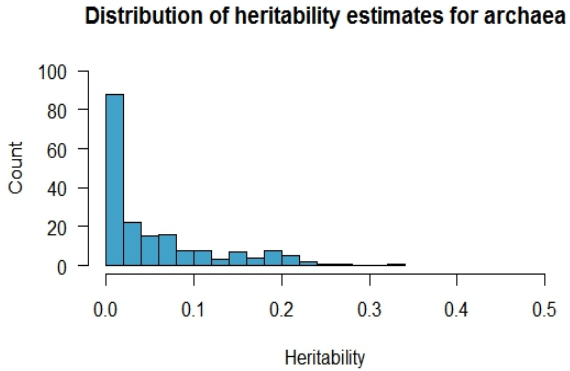
- Rumen Bacterial (4030) & Archaeal (203) OTU's
- Pedigree ~16000

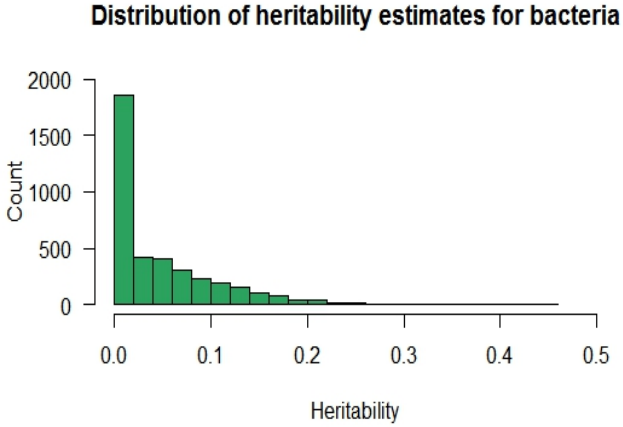
Are rumen microbes heritable?

$$\boldsymbol{Y} = \boldsymbol{Xb} + \boldsymbol{Za} + \boldsymbol{e}$$

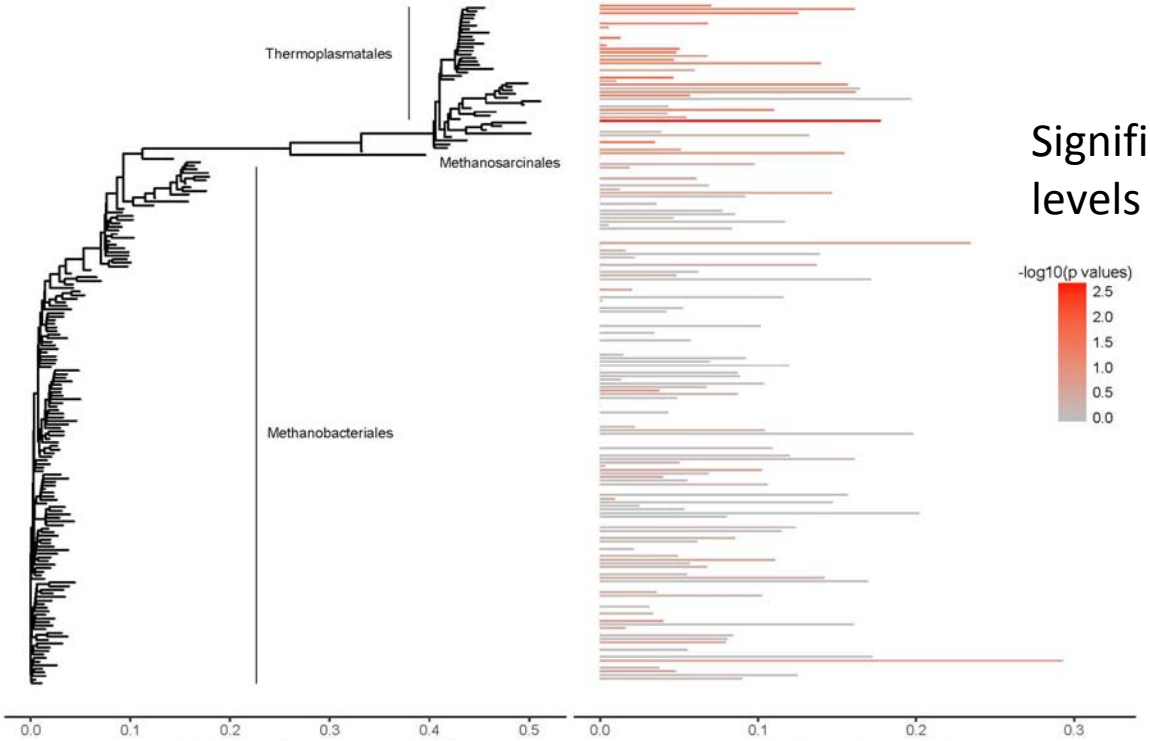
Results (1): heritability

- Archaea
  - 12% h^2
  - h^2 ranging from 0 – 0.35
- Bacteria
  - 6% h^2
  - h^2 ranging from 0 – 0.45





Results (1) h^2 of microbes



Significance levels

#Sub per site

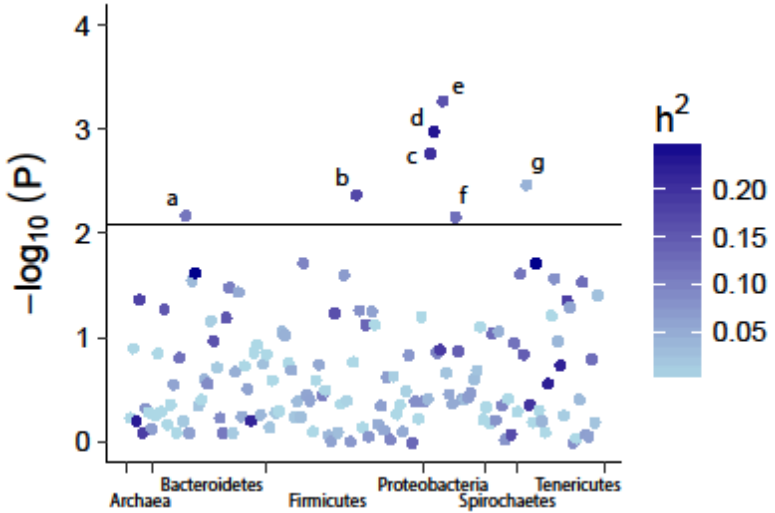
h^2 0 – 0.35

Is the relative abundance of rumen microbes associated with CH4?

$$CH4 = Xb + Za + e$$

Results (2) microbes and CH4

- ***MWAS***



- *Sporobacter*
- *Sphaerochaeta*
- *Unclassified* BS11
- *Unclassified Victivallaceae*

Is variation in the rumen microbiome explaining variation in CH4 emission?

$$Y = Xb + Za + Wm + e$$

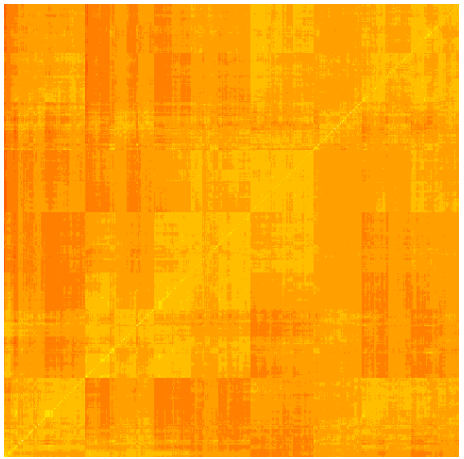
Analysis

- Variance components estimation DMU

$$Y = Xb + Za + Wm + e$$

- Microbial relationship matrix

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

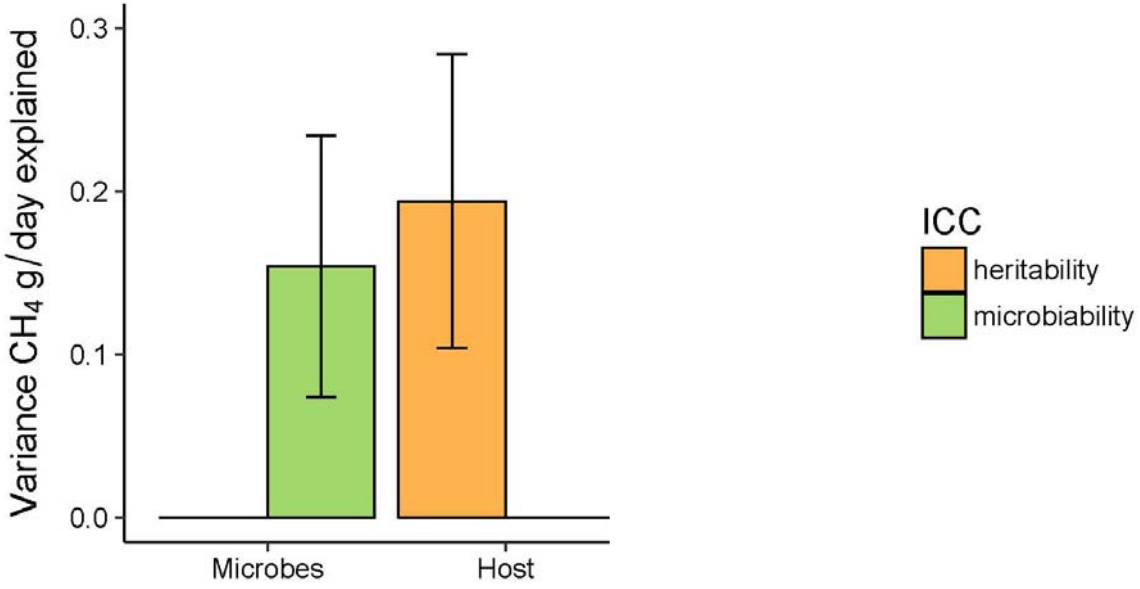


16S rRNA bacterial & archaeal abundance intra-class correlation coefficient

Microbiability (m^2)

Results 3 - Microbiability

- $\boldsymbol{Y = Xb + Za + Wm + e}$



*See Camarinha-Silva et al 2017 similar findings in pigs

Conclusions

- *Some* rumen microbes – h^2
- Associations between rumen microbes & CH4
- Are our cows holobionts? – Yes!
- h^2 of CH4 is (almost) independent of m^2
- m^2 - a tool for identifying and quantify M contributions to complex phenotypes (holobiont)

WCGALP – Application?

- Rumen transfaunation – probiotics?
- Possible indicator traits?
- Selection for holobiont (EBV + MV) over EBV?
- Many questions remain…

Thanks for your time

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