

# Does the host animal control the activity and composition of its gut microbiota?

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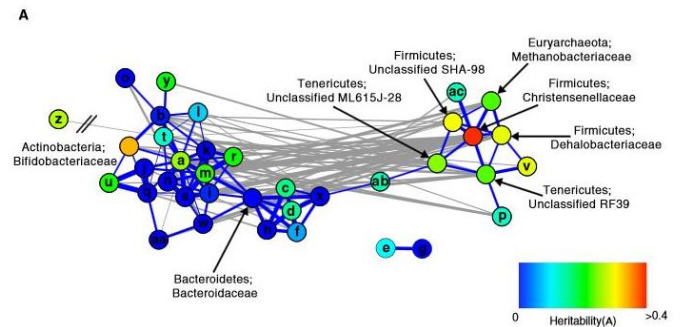
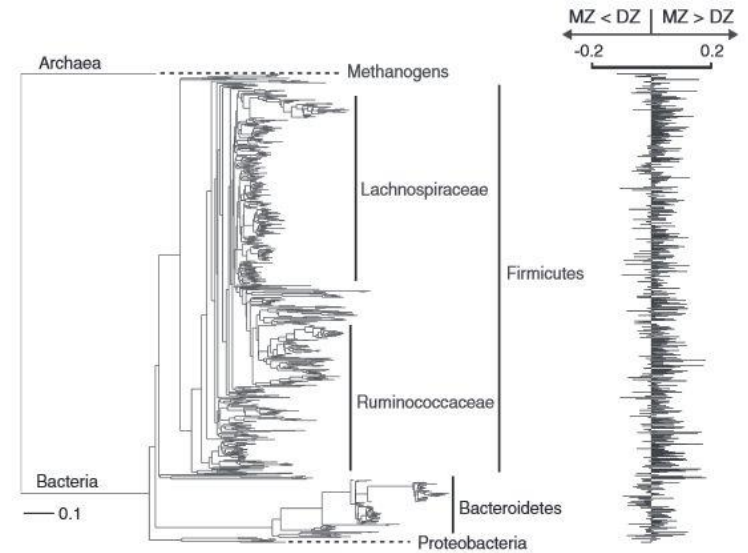
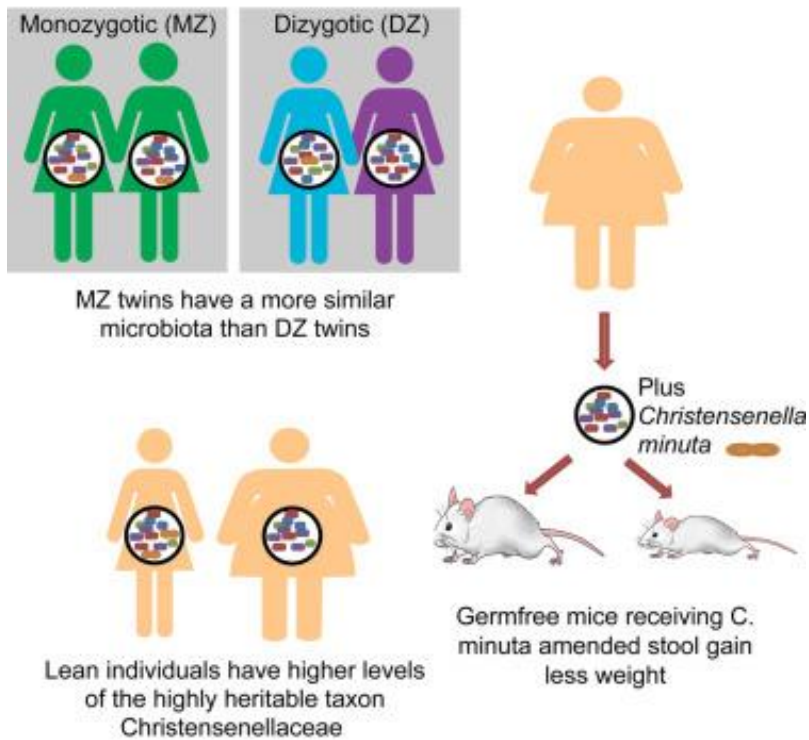
# Content of the presentation

- Introduction
- Experimental design
- Hypotheses
- Data collected
- Preliminary results
- Concluding remarks

# Human Genetics Shape the Gut Microbiome

Julia K. Goodrich,<sup>1,2</sup> Jillian L. Waters,<sup>1,2</sup> Angela C. Poole,<sup>1,2</sup> Jessica L. Sutter,<sup>1,2</sup> Omry Koren,<sup>1,2,7</sup> Ran Blekhman,<sup>1,8</sup> Michelle Beaumont,<sup>3</sup> William Van Treuren,<sup>4</sup> Rob Knight,<sup>4,5,6</sup> Jordana T. Bell,<sup>3</sup> Timothy D. Spector,<sup>3</sup> Andrew G. Clark,<sup>1</sup> and Ruth E. Ley<sup>1,2,\*</sup>

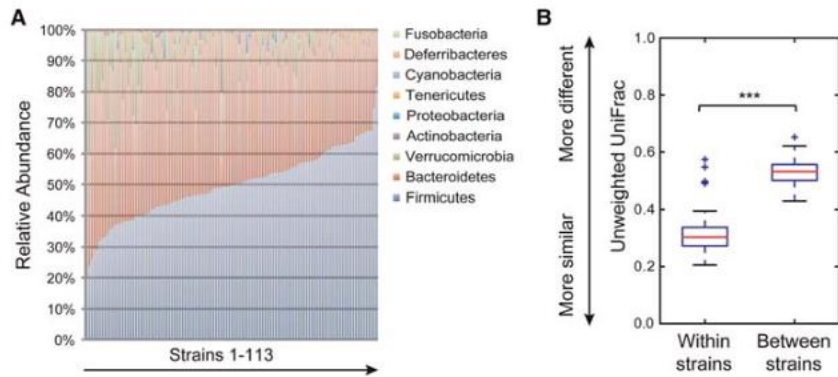
Cell 2014



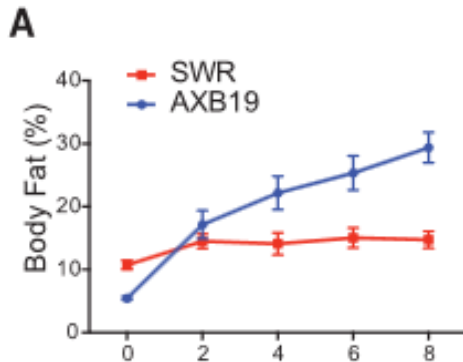
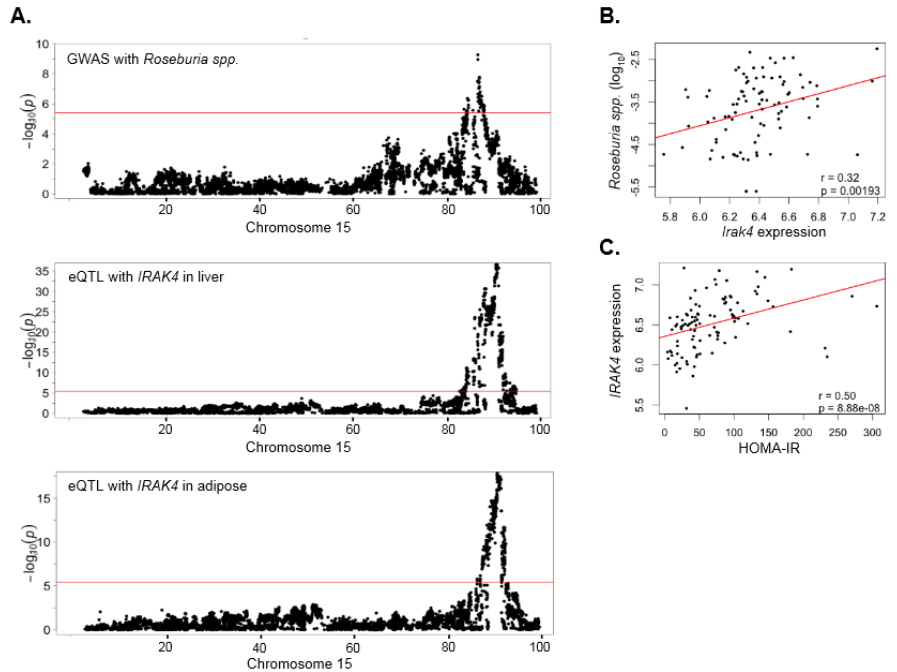
# Genetic and environmental control of host-gut microbiota interactions

Elin Org,<sup>1</sup> Brian W. Parks,<sup>1</sup> Jong Wha J. Joo,<sup>2</sup> Benjamin Emert,<sup>1</sup> William Schwartzman,<sup>1</sup> Eun Yong Kang,<sup>3</sup> Margarete Mehrabian,<sup>1</sup> Calvin Pan,<sup>4</sup> Rob Knight,<sup>5</sup> Robert Gunsalus,<sup>6</sup> Thomas A. Drake,<sup>7</sup> Eleazar Eskin,<sup>3,4</sup> and Aldons J. Lusis<sup>1,4,8</sup>

Genome Res. 2015

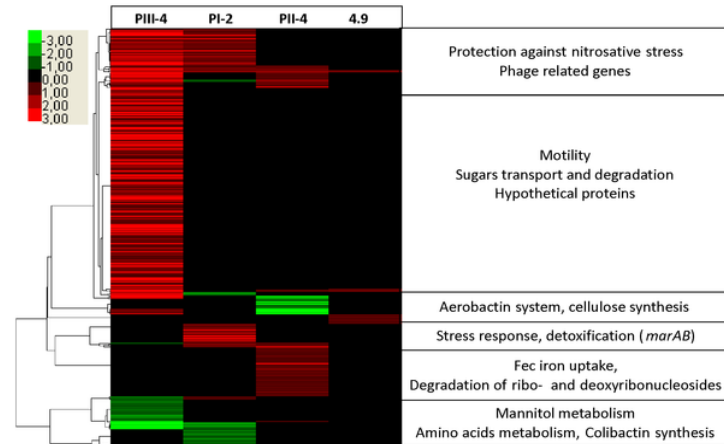
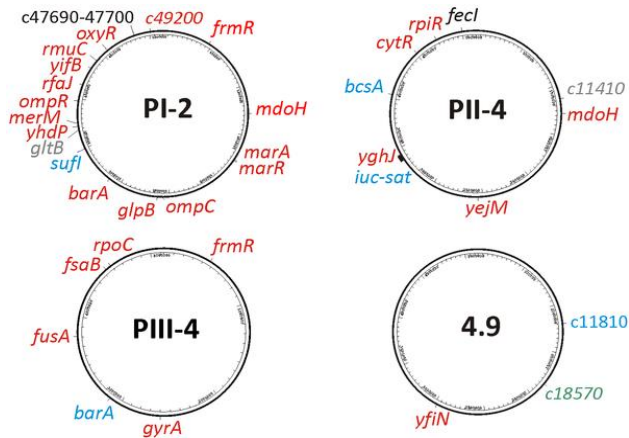
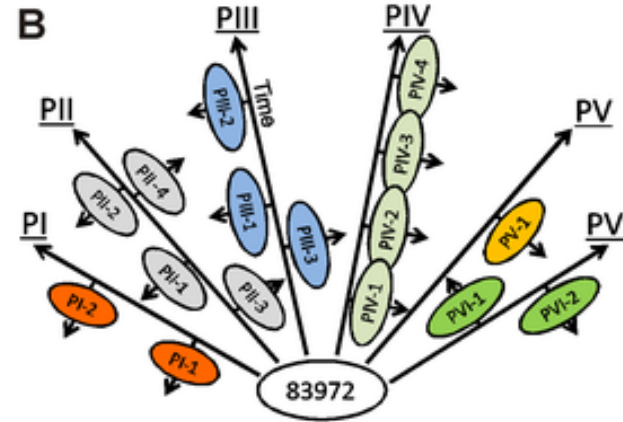
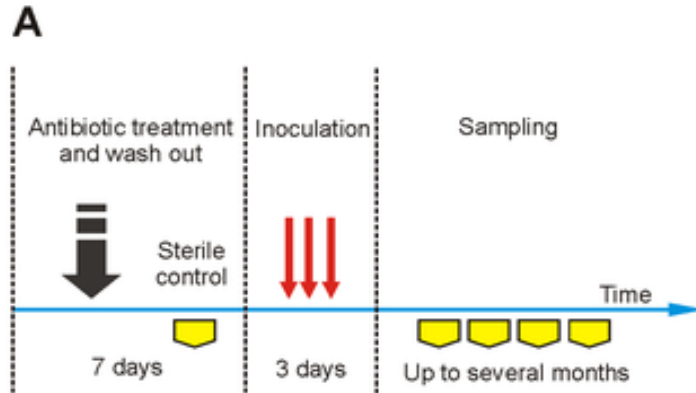


**Figure 1.** Phylum-level variability of gut microbiota composition across 113 inbred strains of mice. (A) Columns represent the relative abundance of microbial phyla in 113 strains (327 male and 297 female). (B) Box plot of  $\beta$  diversity distances between microbial communities obtained when comparing mice within and between strains. The specific distance metric used is indicated on the axes. (\*\*\*)  $P < 0.001$  for Student's  $t$ -test with 1000 Monte Carlo simulations. See also Supplemental Table 2.



# Host Imprints on Bacterial Genomes—Rapid, Divergent Evolution in Individual Patients

Zdziarski J, Brzuszkiewicz E, Wullt B, Liesegang H, Biran D, et al. (2010) PLoS Pathog 6(8): e1001078.

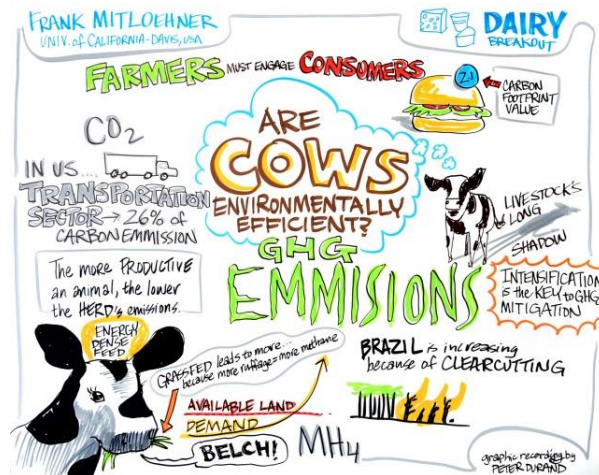


# How about ruminants?



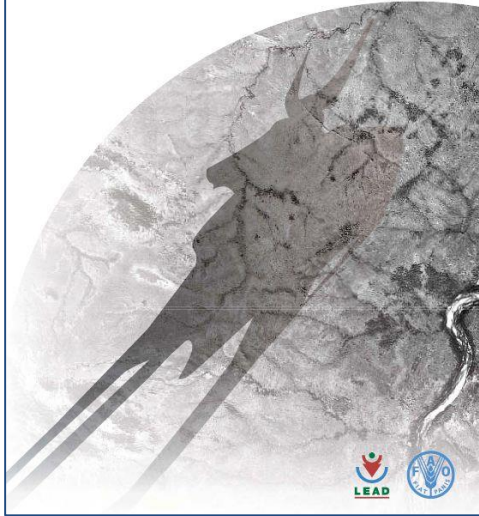
Some ruminants utilize feed more efficient than the others

Some ruminants produce less methane even if they are fed the same diet

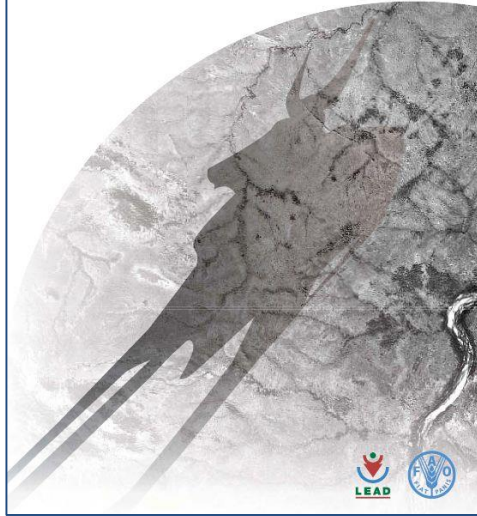


# What are we dealing with?

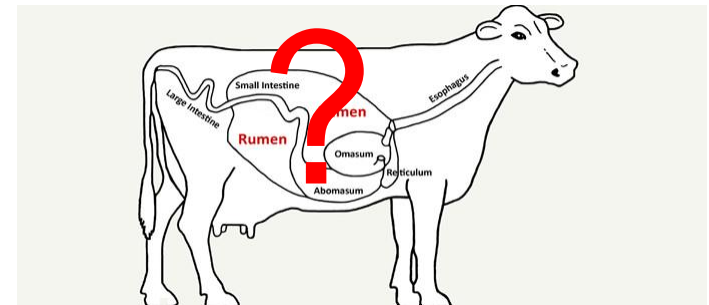
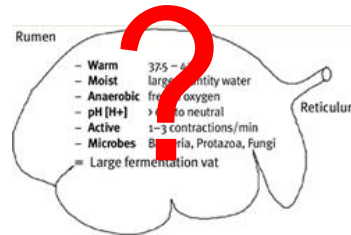
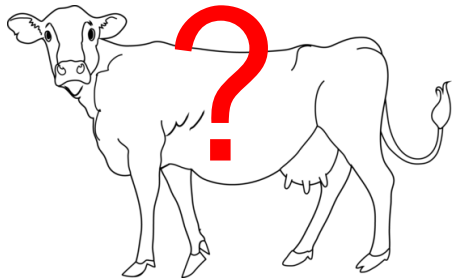
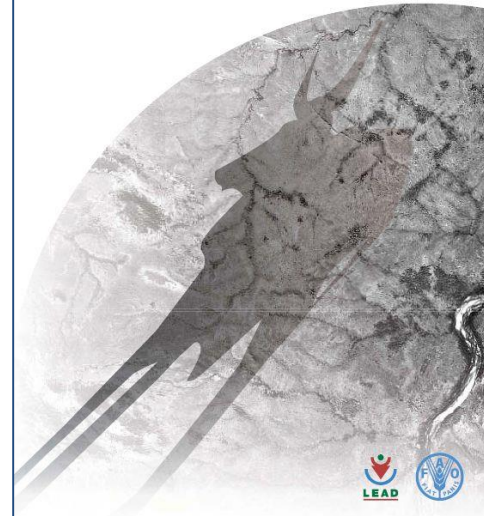
livestock's long shadow  
environmental issues and options



Microbiome long shadow  
environmental issues and options



Pan-genome long shadow  
environmental issues and options





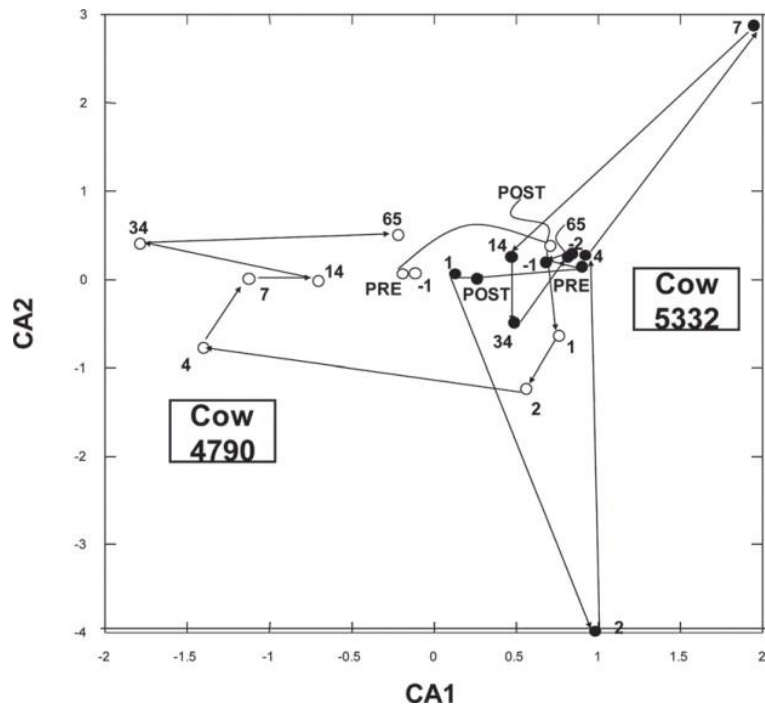
## Host specificity of the ruminal bacterial community in the dairy cow following near-total exchange of ruminal contents<sup>1</sup>

P. J. Weimer,\*<sup>†2</sup> D. M. Stevenson,\* H. C. Mantovani,‡ and S. L. C. Mant†

\*USDA-ARS, US Dairy Forage Research Center, Madison, WI 53706

†Department of Bacteriology, University of Wisconsin–Madison, Madison 53706

‡Departamento de Microbiologia, Universidade Federal de Viçosa, Viçosa-MG, 36571-000, Brazil



Following exchange of ruminal contents, ruminal pH and total VFA concentration **returned** to their pre-exchange values within 24h.

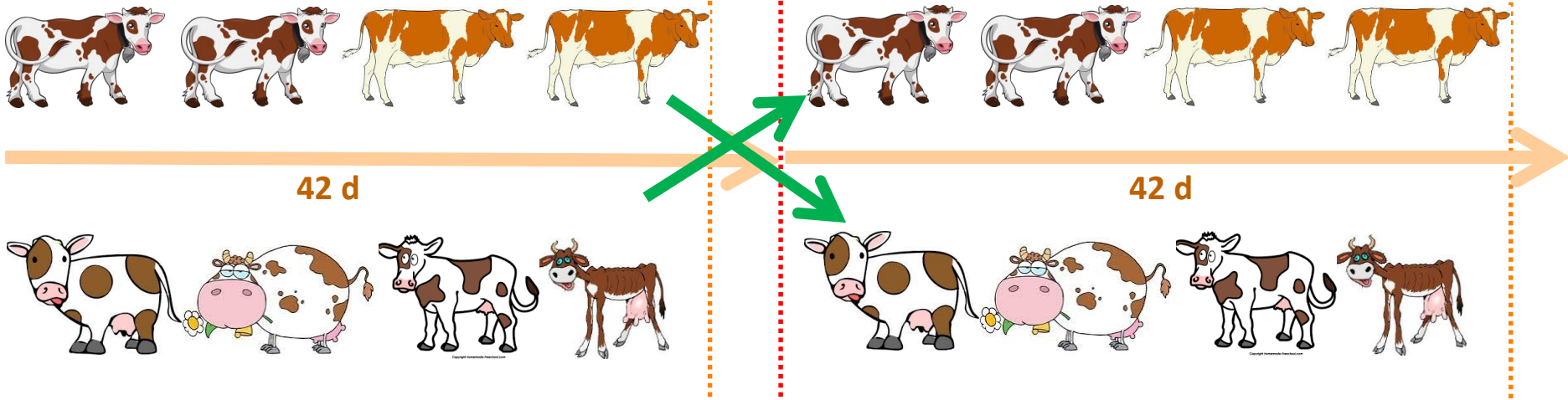
Ruminal bacterial community composition displays substantial host specificity that **can re-establish itself with varying success** when challenged with a microbial community optimally adapted to ruminal conditions of a different host animal.



# Experimental design

Measurements Digesta exchange

Measurements

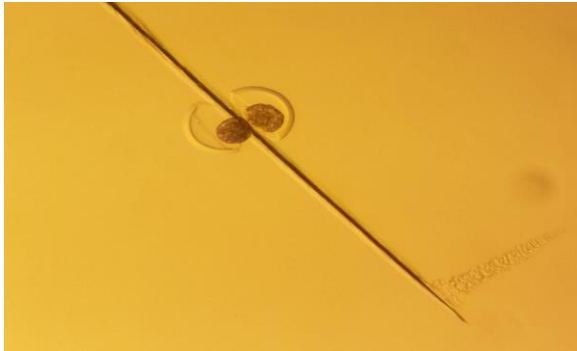


42 d

42 d

Rumen sampling at exchange and in weekly intervals

# Experimental design



Identical twins were created by splitting embryo into 2 parts and implanting them back to their mother



Several pairs of twins were born in Luke barn



Animals were kept in the same barn, fitted with cannulae and recruited to the experiment

# Hypotheses

## H1

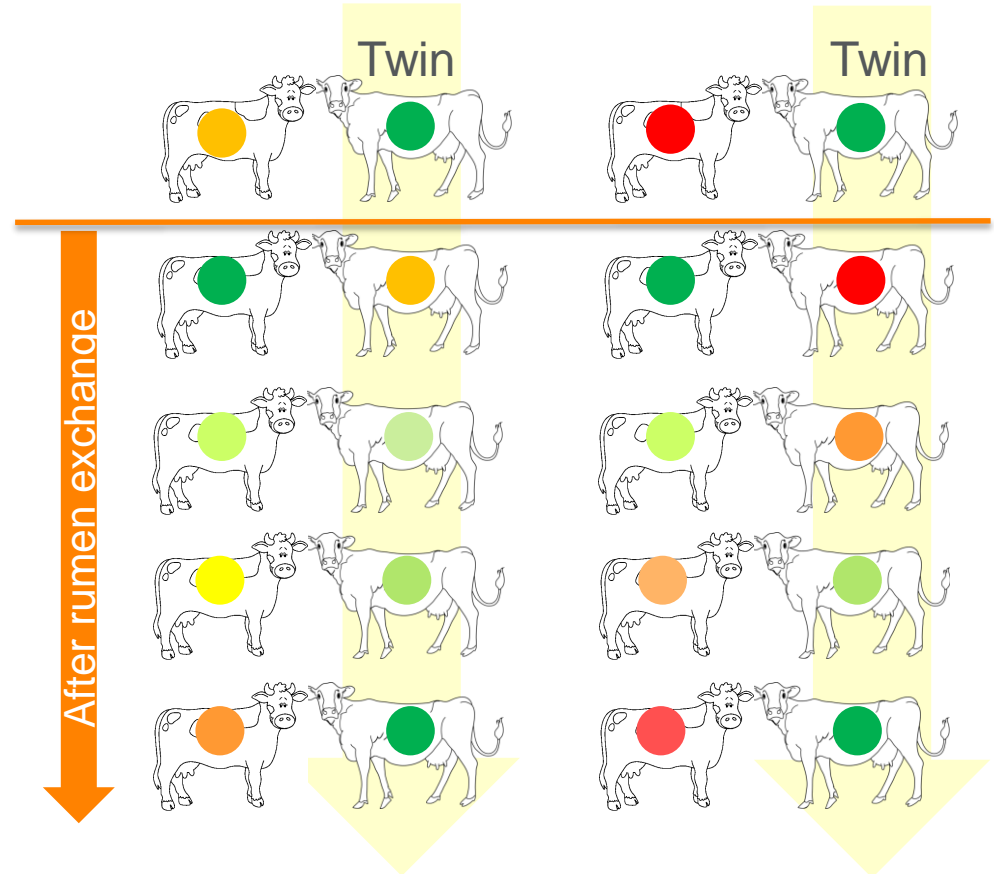
- differences in the rumen microbiome composition are smaller between genetically identical twins compared with genetically non-identical animals

## H2

- the rumen microbiome composition will revert to original composition after complete exchange of rumen contents

## H3

- the host animal has some control over its own rumen microbiome



# Data collected

Intake

Rumen fermentation characteristics

Digestibility by total fecal collection

Urinary output

Enteric methane production using the SF6 tracer technique

Rumen pool sizes

Samples of ruminal digesta collected pre-exchange and at weekly intervals post-exchange

# Rumen sampling design

Rumen sampling

Rumen sample processing

DNA extraction

Amplicon library preparation  
(bacteria, archaea, ciliates, fungi)

Metabarcoding sequencing

Sequencing data analysis

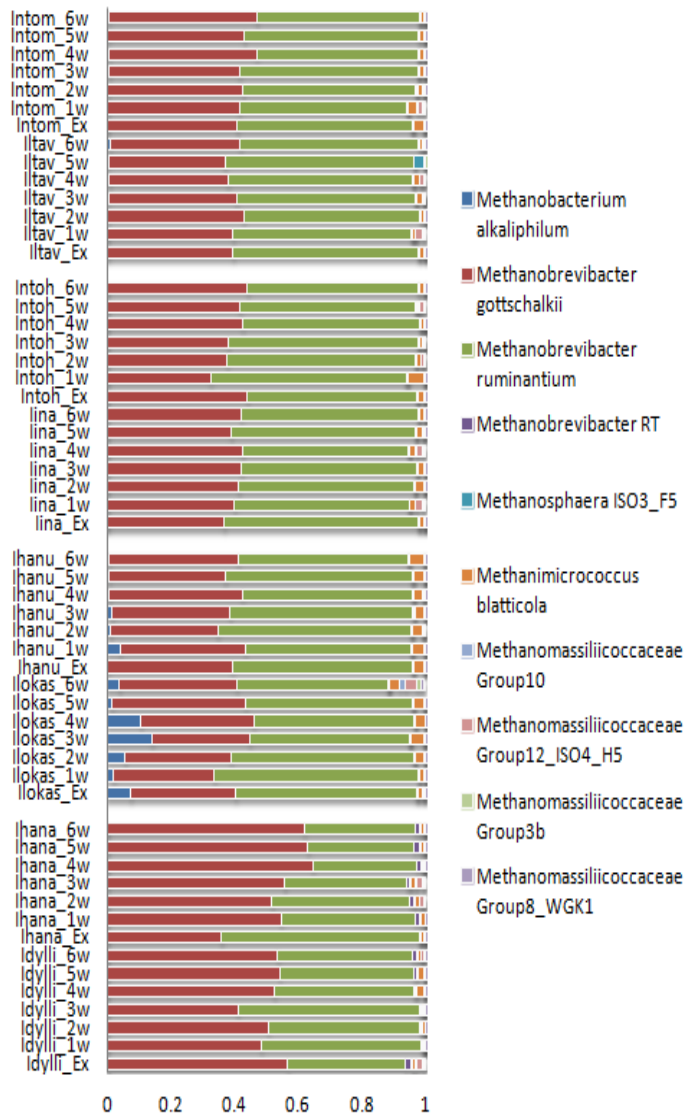


**Milk yield**

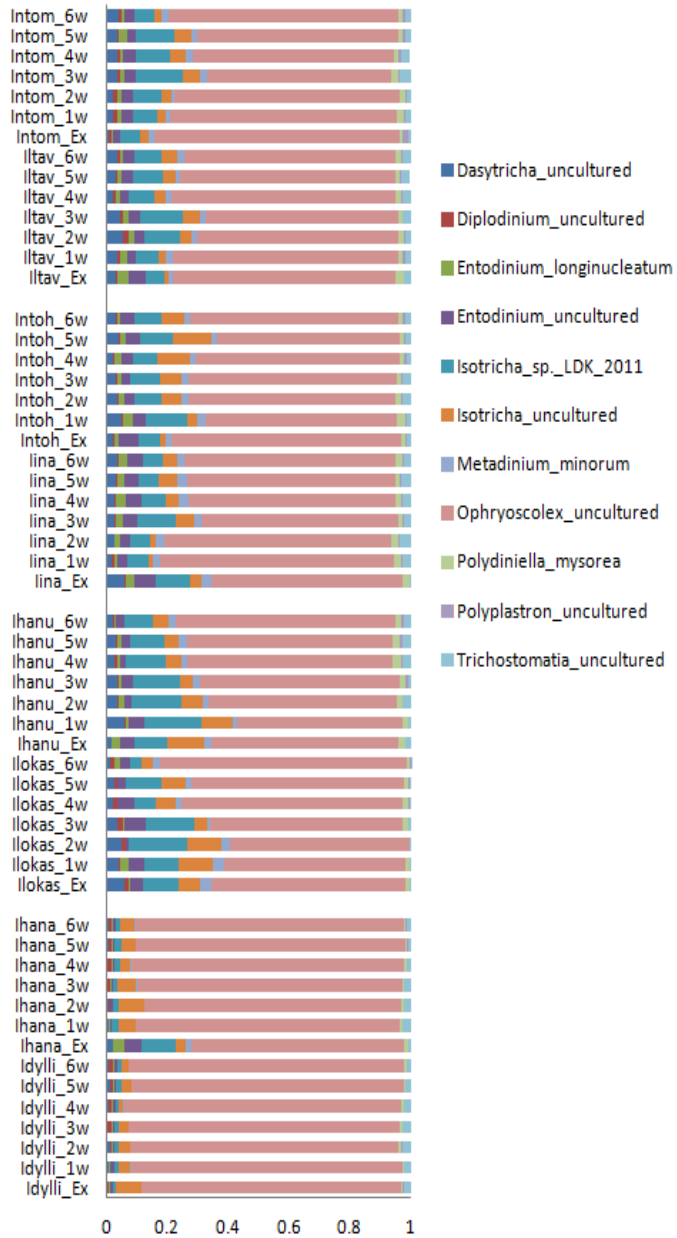
**Digestibility**

**Rumen fermentation**

# Archaea

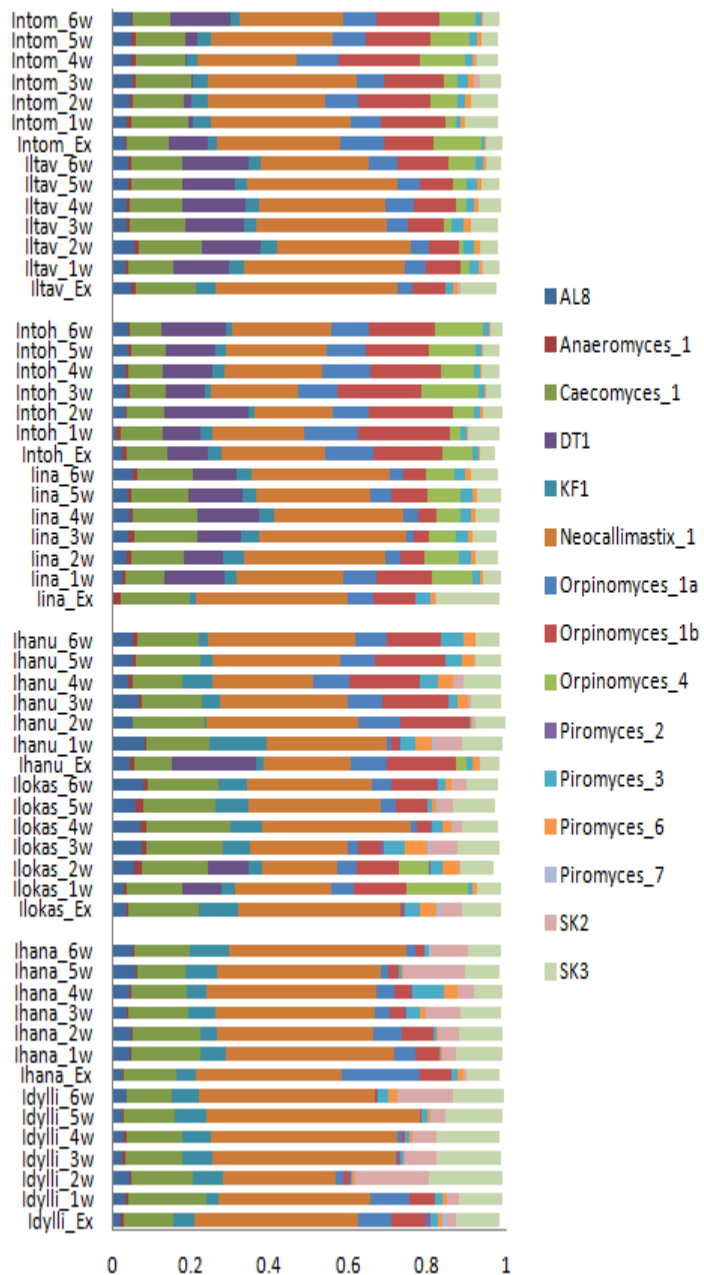


# Ciliate protozoa



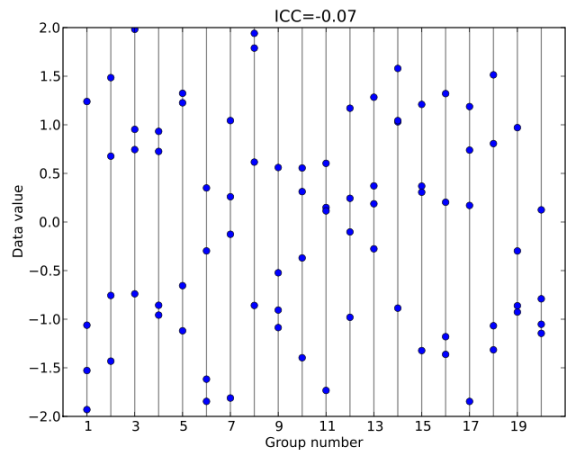
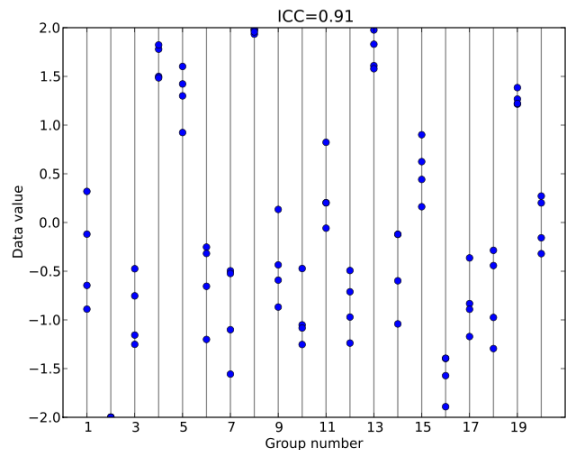


# Anaerobic fungi



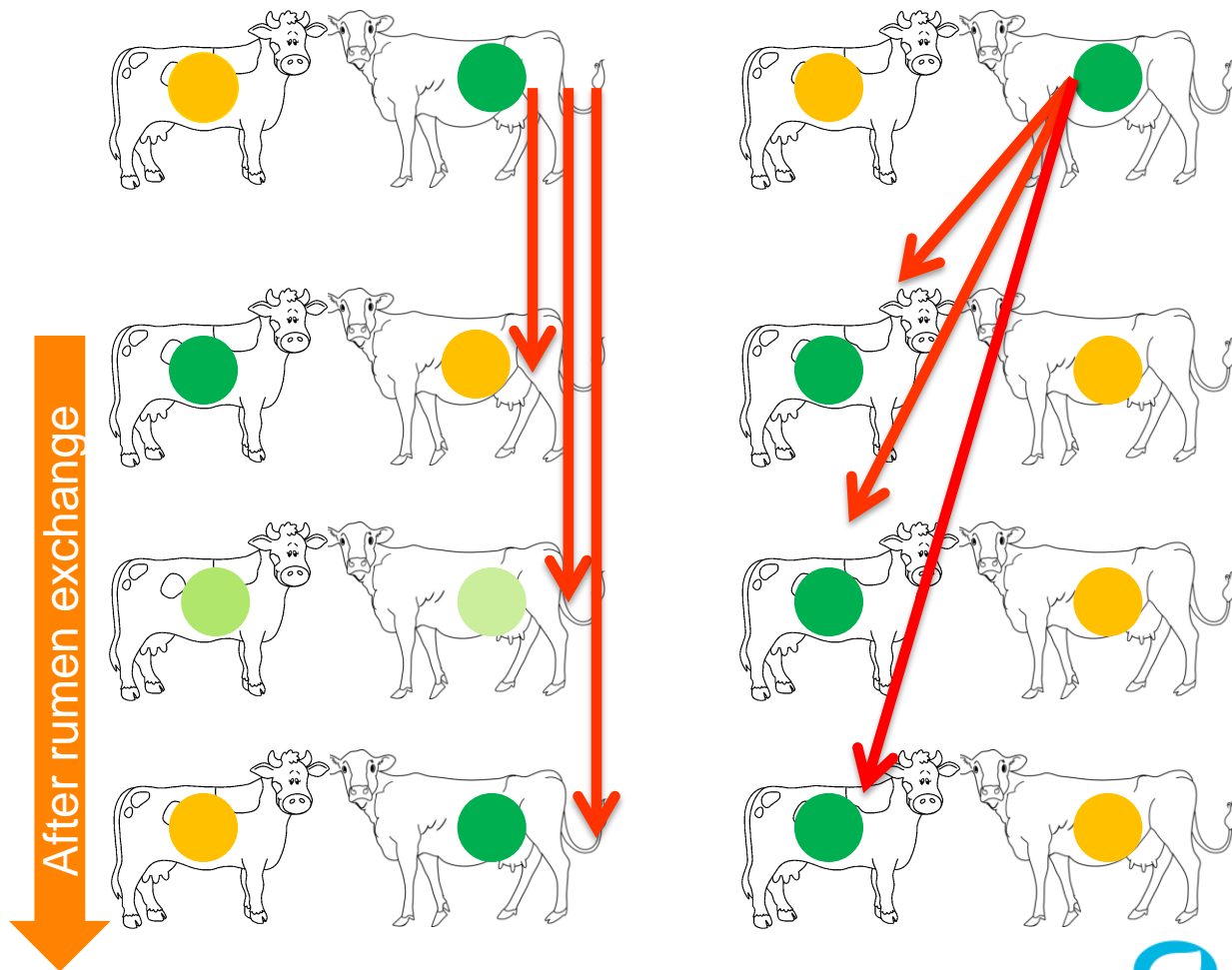


**Intraclass correlation coefficient (ICC)** describes how strongly individuals within a group resemble each other in terms of a particular trait (rumen microbiota)

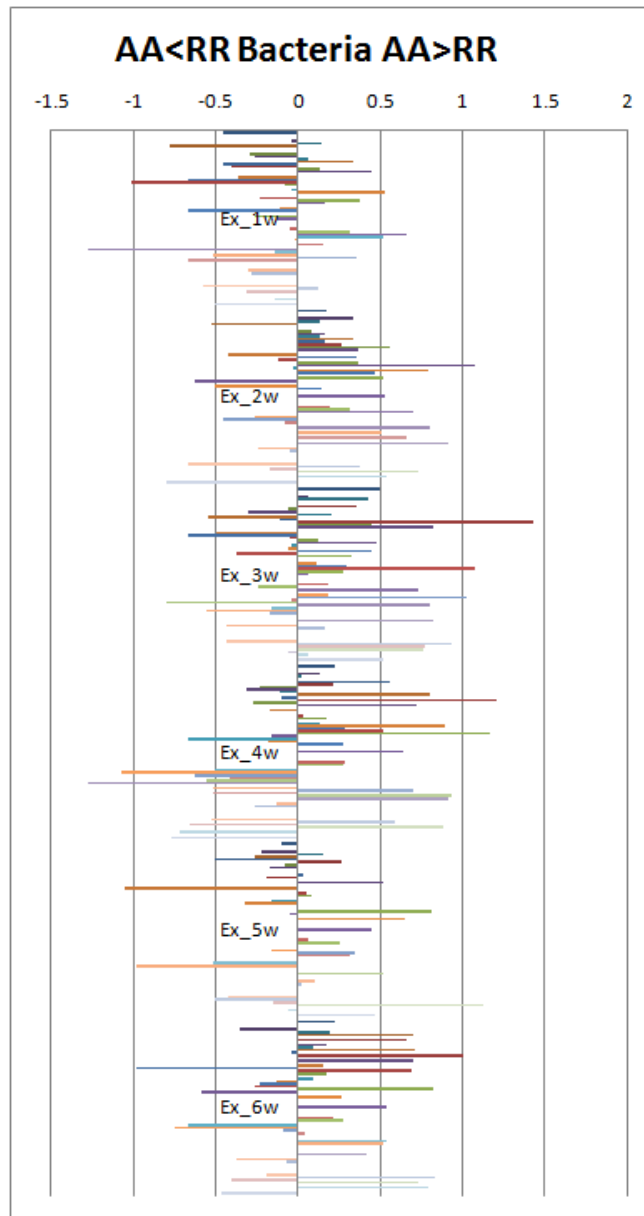


Animal-effect (AA)

Rumen-effect (RR)



<https://commons.wikimedia.org/wiki/File:ICC-example2.svg#/media/File:ICC-example2.svg>



# Concluding remarks

Rumen microbial composition in twins is not identical

High between animal variation as a response to rumen content exchange

There are indications that the host ruminant may exert genetic control on some of the microbiota in the rumen - microbial group specific

An interval of 42 d may be too short to fully evaluate the adaptation of the rumen microbiome to rumen perturbation

Thank you!