

# RuminOmics

Connecting the animal genome,  
the intestinal microbiome and  
nutrition to enhance the  
efficiency of ruminant digestion  
and to mitigate the  
environmental impacts of  
ruminant livestock production



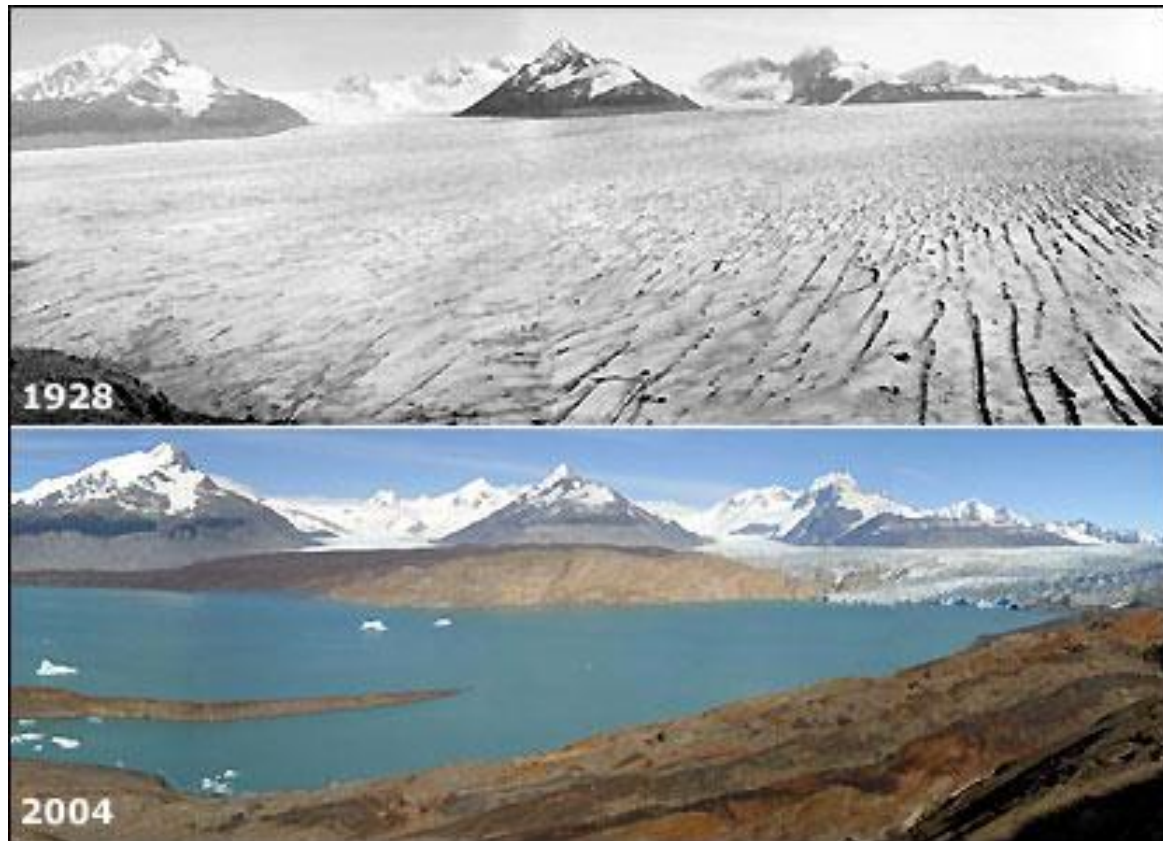
RuminOmics



*John Wallace*

Collaborative project  
Jan. 2012 – Dec. 2015  
[www.ruminomics.eu](http://www.ruminomics.eu)

# Methane, ruminants and the environment



***Positive proof of global warming.***



**18th  
Century**

**1900**

**1950**

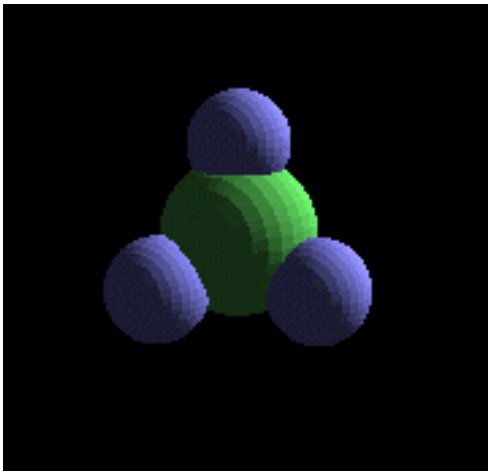
**1970**

**1980**

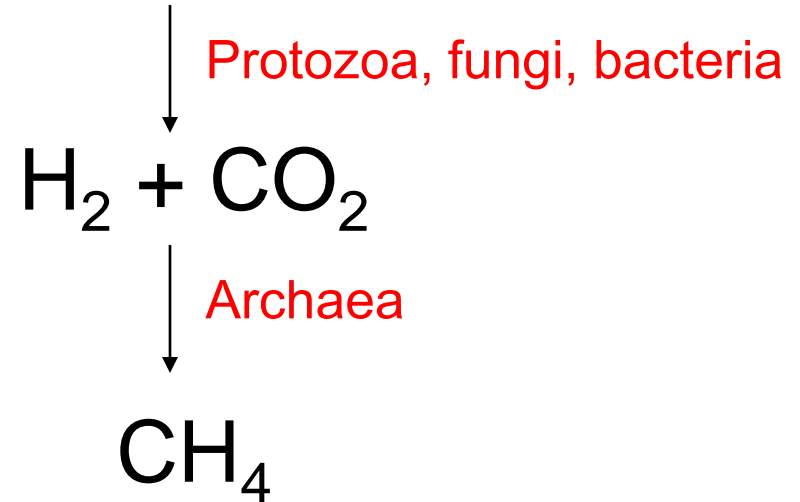
**1990**

**2006**

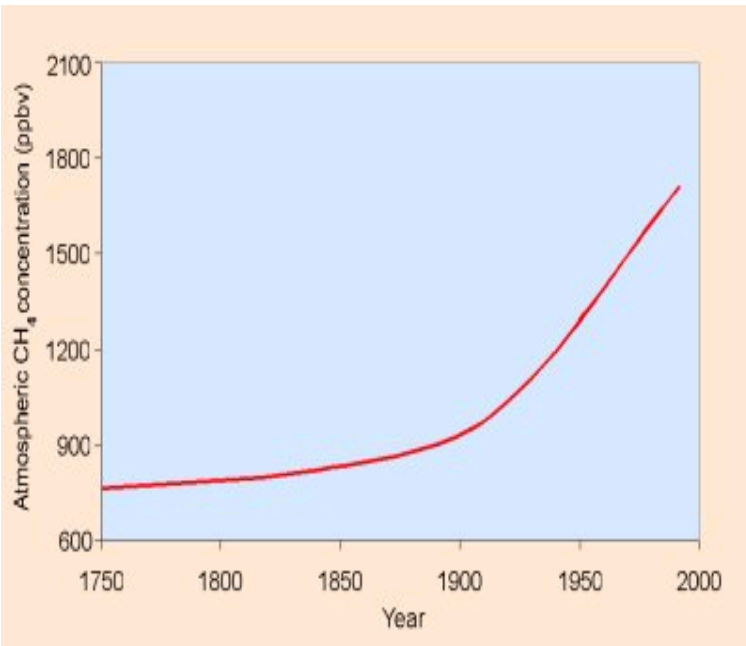
# Methane production in ruminants



Fermentation



# Methane as a greenhouse gas

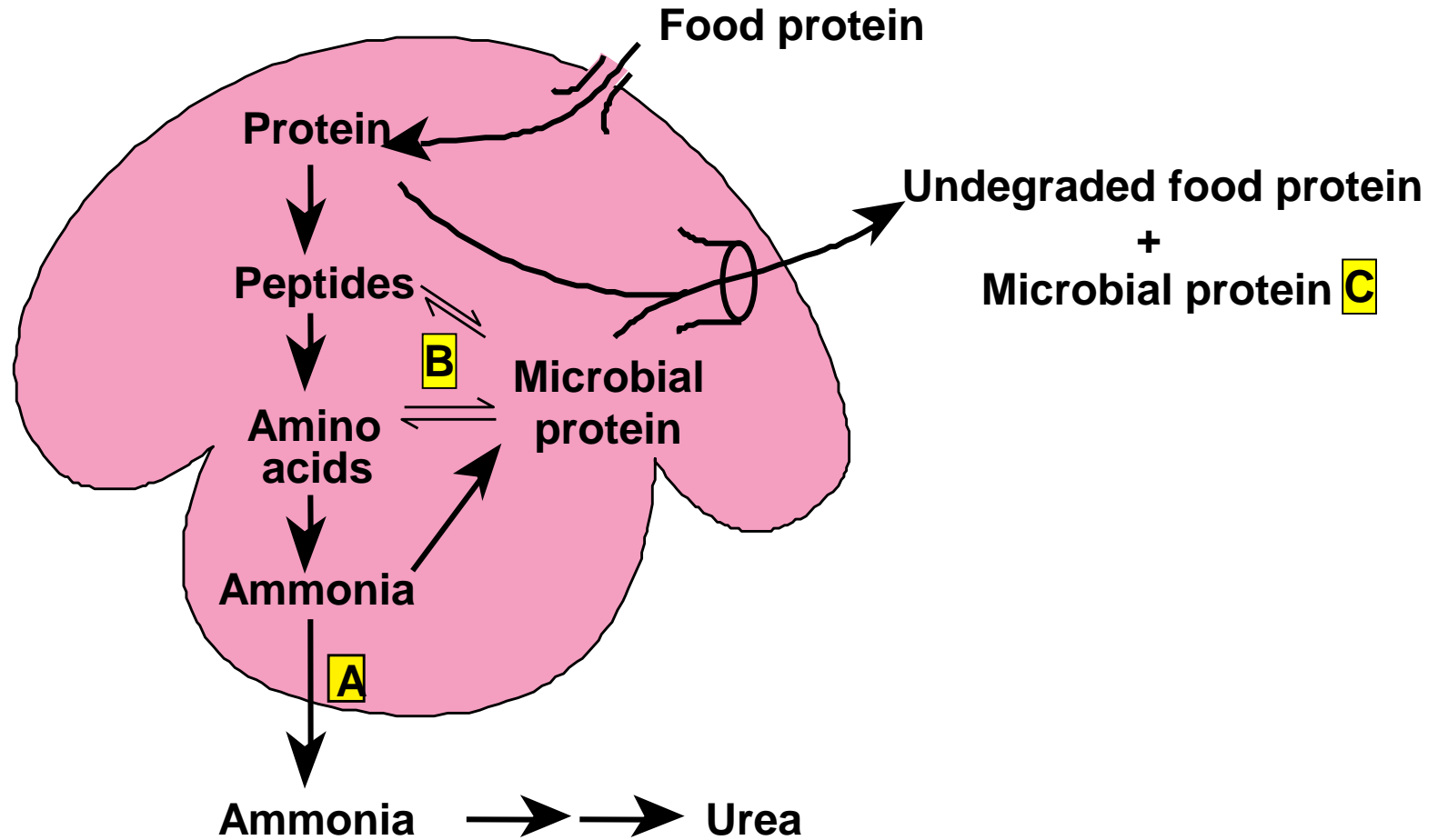


US Environmental Protection Agency, 2000

CH<sub>4</sub> has a global warming potential (“radiative forcing”) 28 times that of CO<sub>2</sub>

Methane contributes approximately 18% to the overall global warming effect

# Protein metabolism





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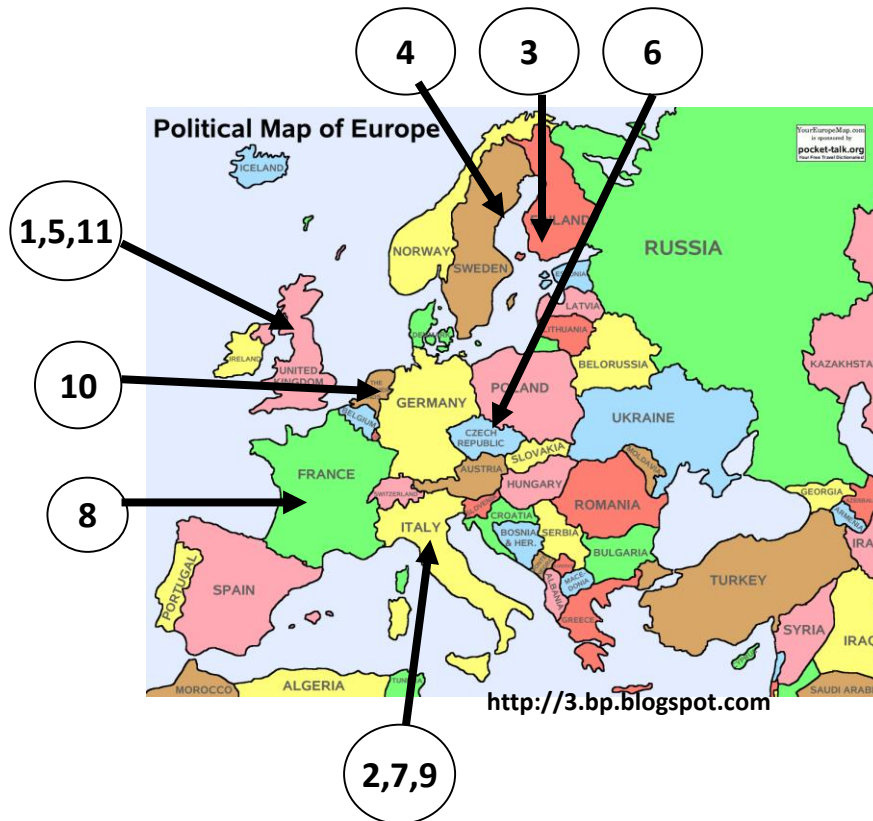
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# RuminOmics - Partners

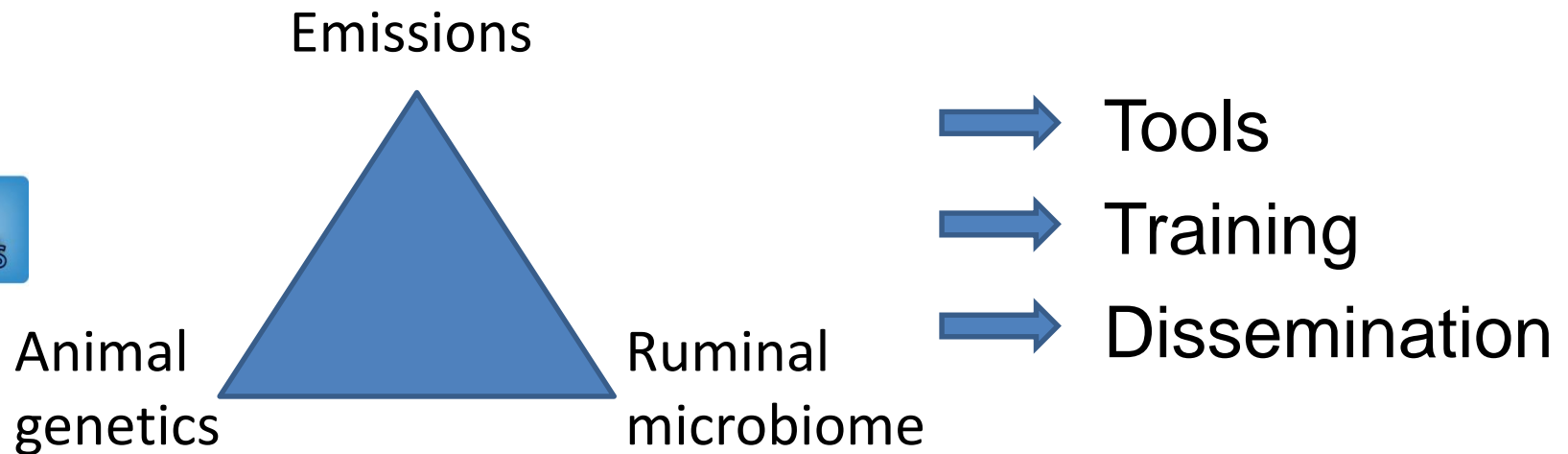


Participant no.	Participant organisation name
1 (Coordinator)	University of Aberdeen
2	Parco Tecnologico Padano
3	Agrifood Research Finland
4	Swedish University of Agricultural Sciences
5	University of Nottingham
6	Institute of Animal Physiology & Genetics
7	Università Cattolica del Sacro Cuore, Piacenza
8	Centre National de la Recherche Scientifique
9	European Association of Animal Production
10	European Forum of Farm Animal Breeders
11	Quality Meat Scotland





# RuminOmics - Aims of project



- Does the animal itself determine its ruminal microbiome?
- If so, is this a heritable trait?
- How does nutrition affect this relationship?

# RuminOmics - Response to technology

## THE CALL:

**KBBE.2011.1.1-03: Efficiency of ruminant digestive systems and reduction of the ecological footprint through a combination of systems biology, 'omics'**



# RuminOmics - Experiments

- **1000 cows in UK, Italy, Sweden, Finland**

Methane

N emissions

FCE

Milk quality



Ruminal  
microbiome



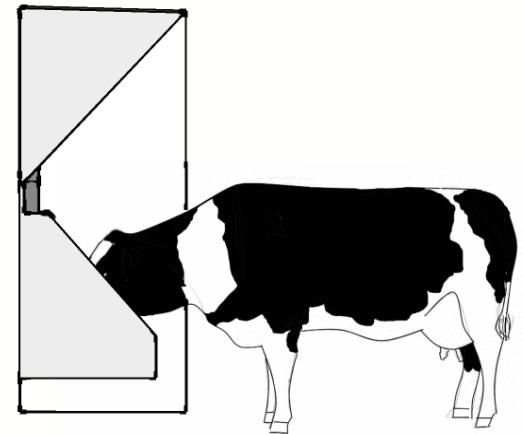
Animal  
genotype

- **20 cows in Sweden, Finland**

Impact of N, CHO, lipid nutrition

- **50 cows in UK, Italy, Sweden, Finland**

Full metagenome analysis



# RuminOmics - Experiments II

## Bovine single-egg twins

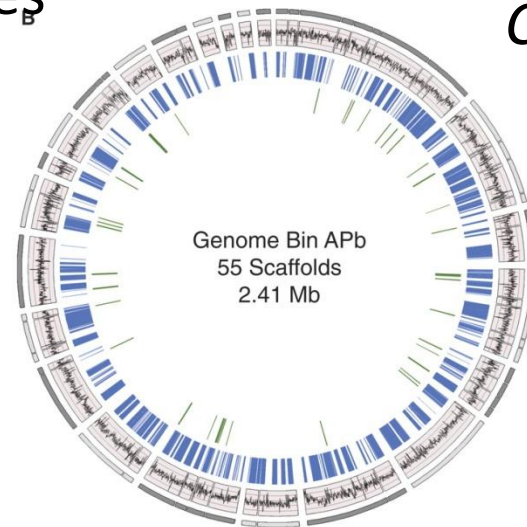


## Interspecies digesta transfer



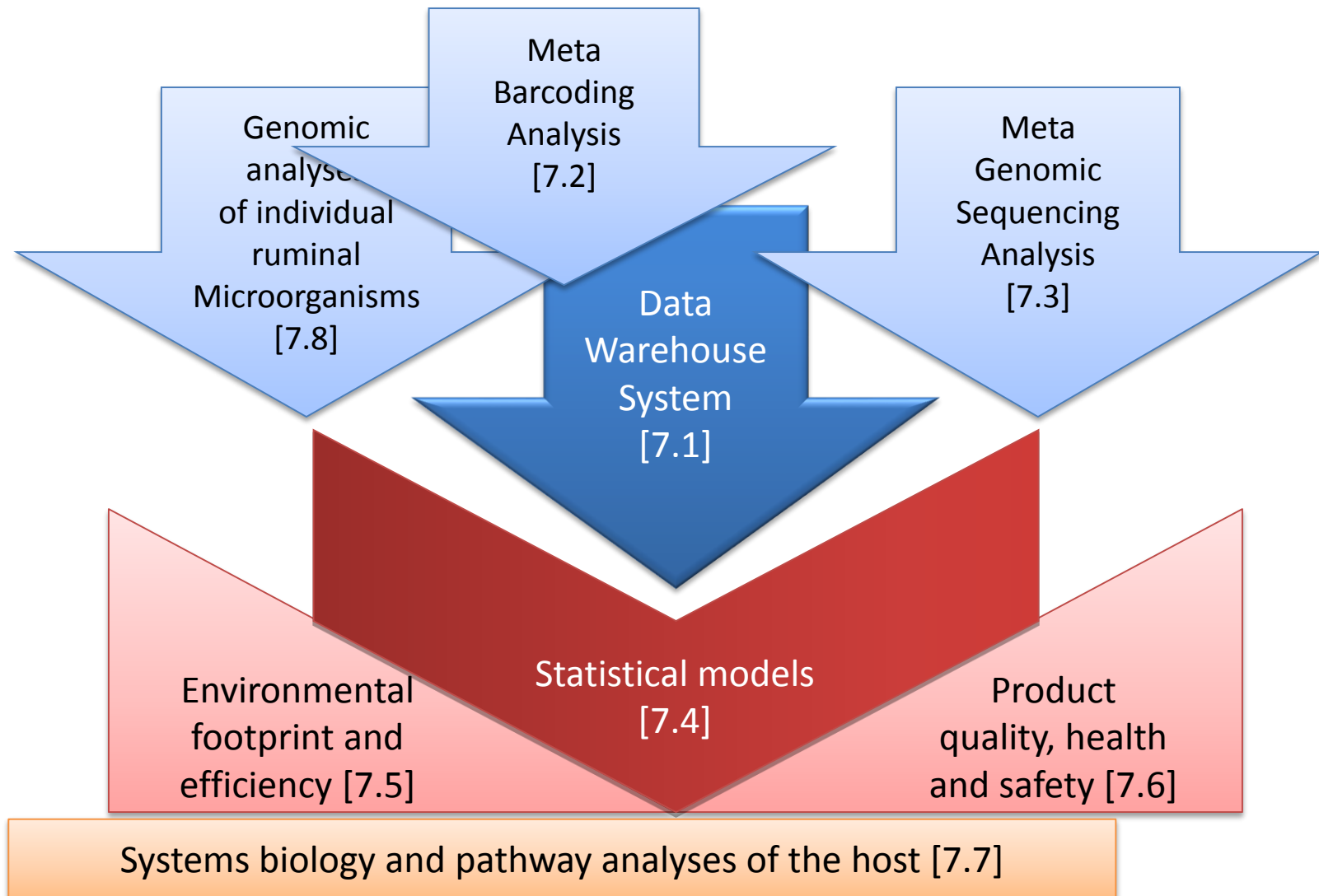
# RuminOmics - Experiments III

- **Bacterial genomes**  
Six *Butyrivibrio* spp.  
Two HAP species
- **Fungal genomes**  
*Anaeromyces* sp.  
*Caecomyces* sp.



# Tools, resources, legacy

## Data warehouse





# Tools, resources, legacy

## Proxies

## Milk fatty acids

Relationship with methane

Positive	Negative
iso C14:0	trans 10+11 C18:1
iso C15:0	C15:0
anteiso C17:0	C17:0+C17:1

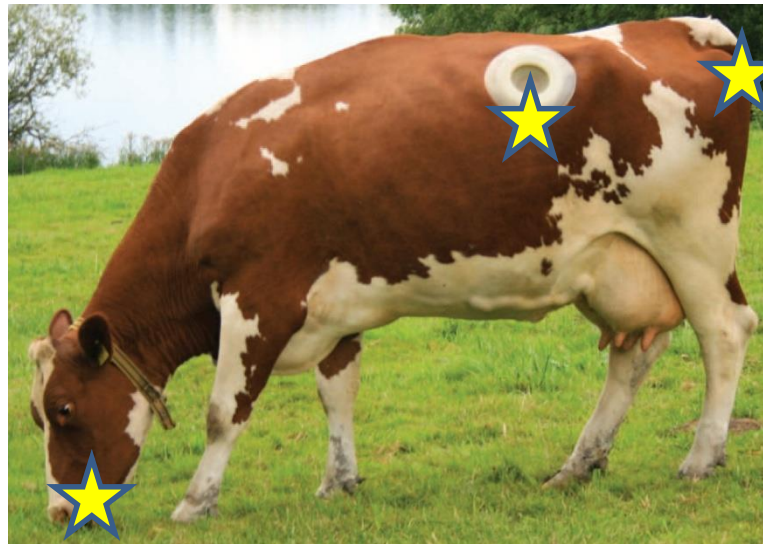
**CH<sub>4</sub> production was positively correlated with a dominance of sequences representing T-RFs related to *Methanobrevibacter thaueri*, *Methanobrevibacter millerae*, and *Methanobrevibacter smithii* relative to *Methanobrevibacter ruminantium* and *Methanobrevibacter olleyae*. Total numbers of methanogens**

**and total numbers of *Methanobacteriales* were significantly higher with the 500/500 diet (*P* < 0.0004 and *P* < 0.002**



# Tools, resources, legacy

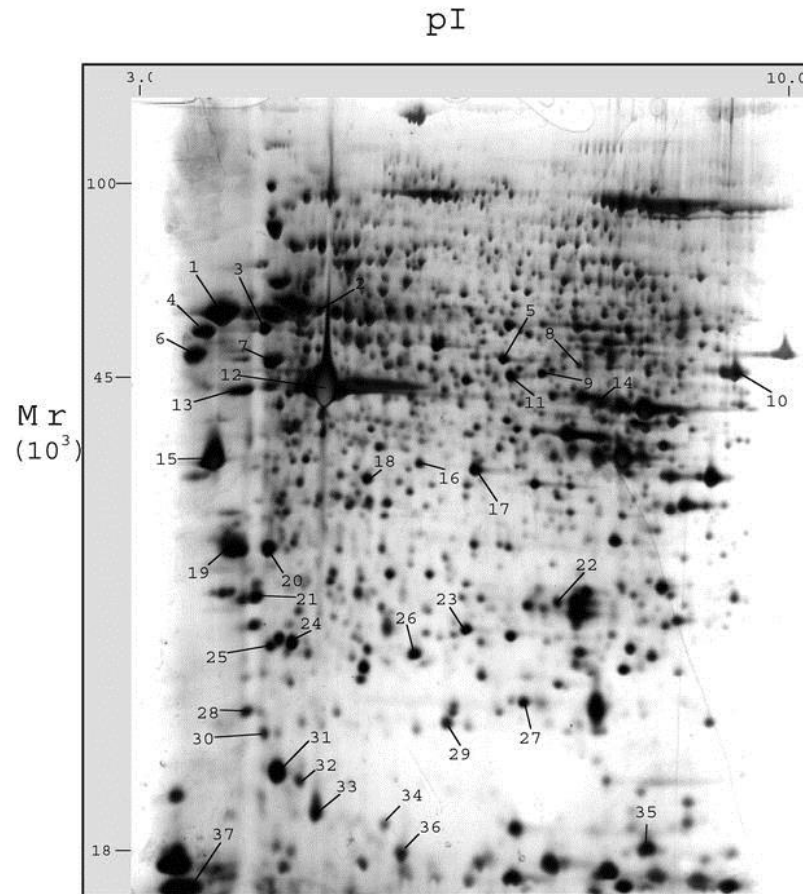
- **Proxies**      Buccal-ruminal-faecal microbiomes



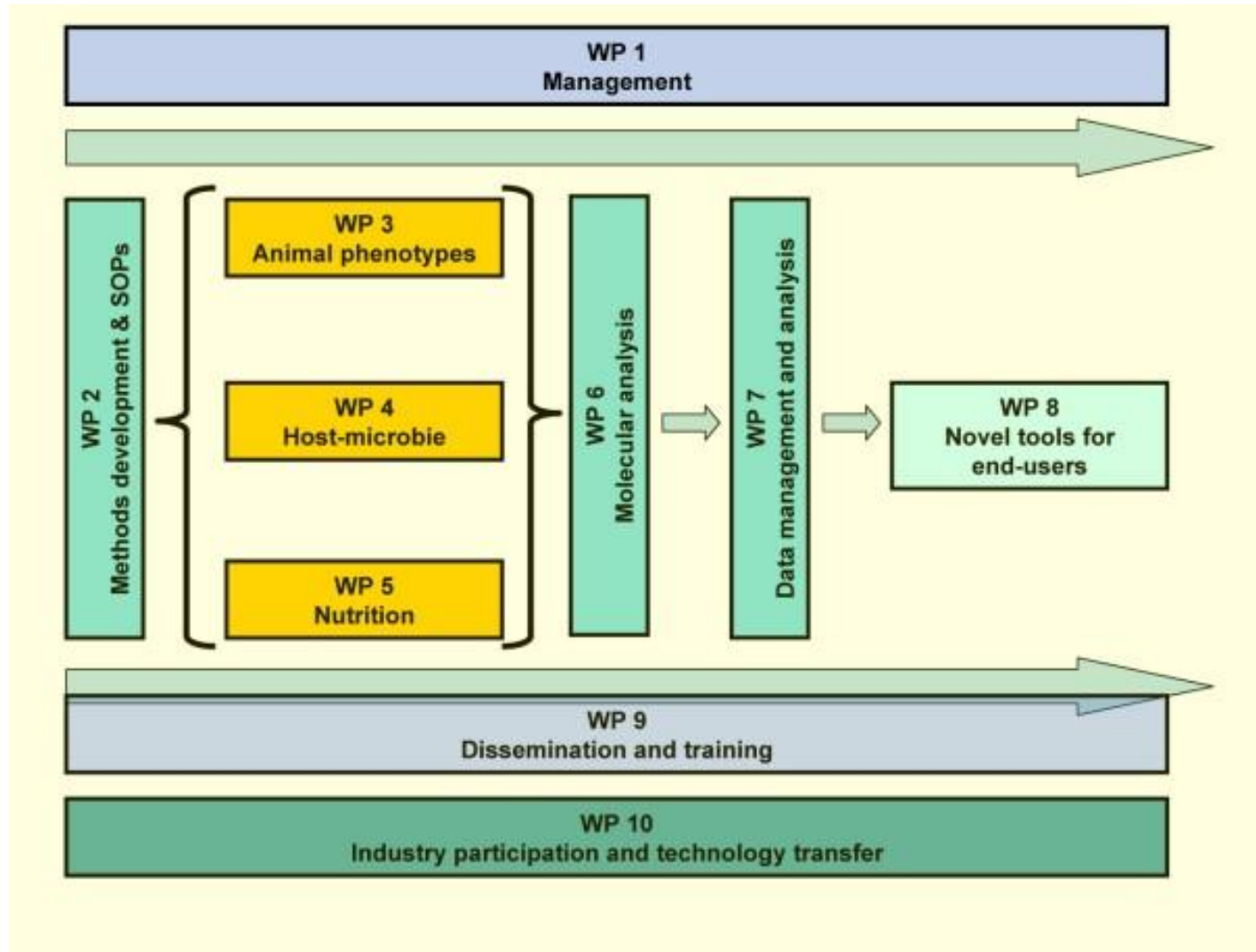
# Tools, resources, legacy

- Tools

## Metaproteomics



# Work Package Structure

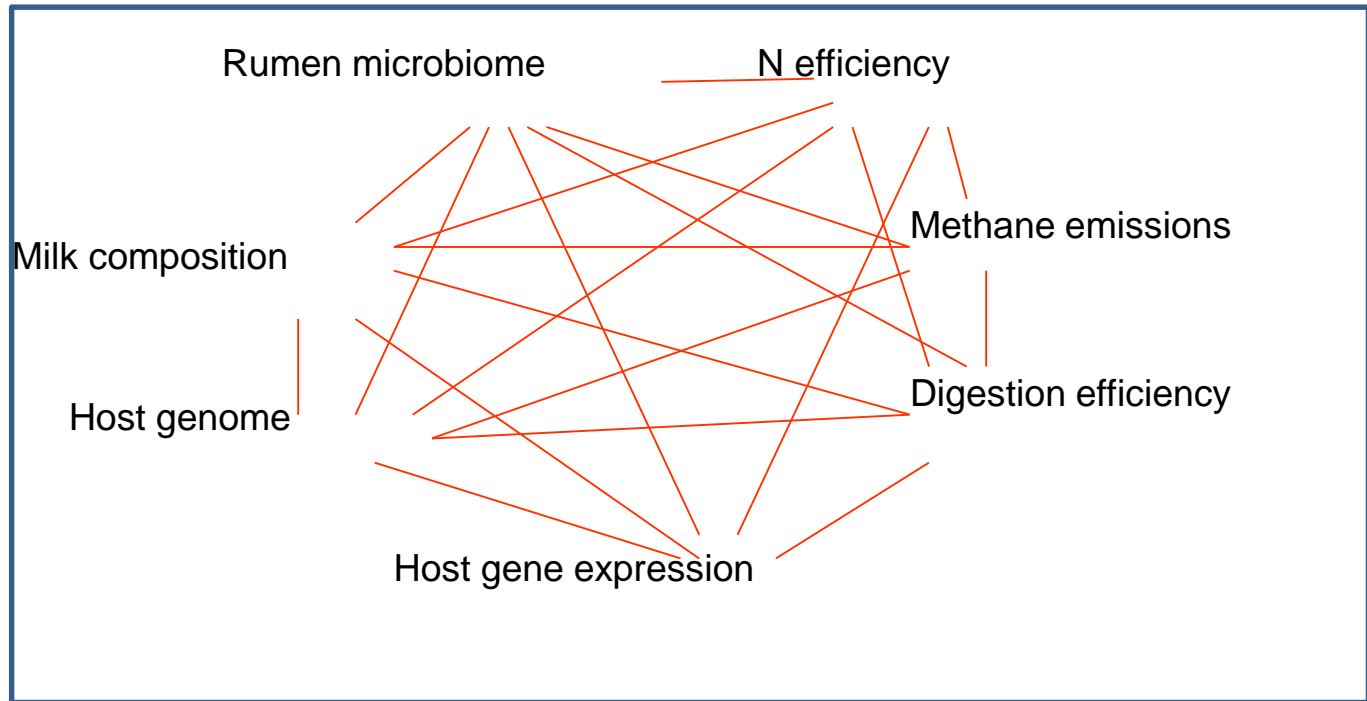


# RuminOmics - Aspirations

- **The answer to the animal-microbe conundrum**
- **Bioinformatics legacy**
- **Trained & more efficient industry**
- **Environment legacy**



# The Bioinformatics challenge





RuminOmics

