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

John Wallace

Rowett Institute of Nutrition and Health
University of Aberdeen

Collaborative project
Jan. 2012 – Dec. 2015
www.ruminomics.eu

SEVENTH FRAMEWORK PROGRAMME

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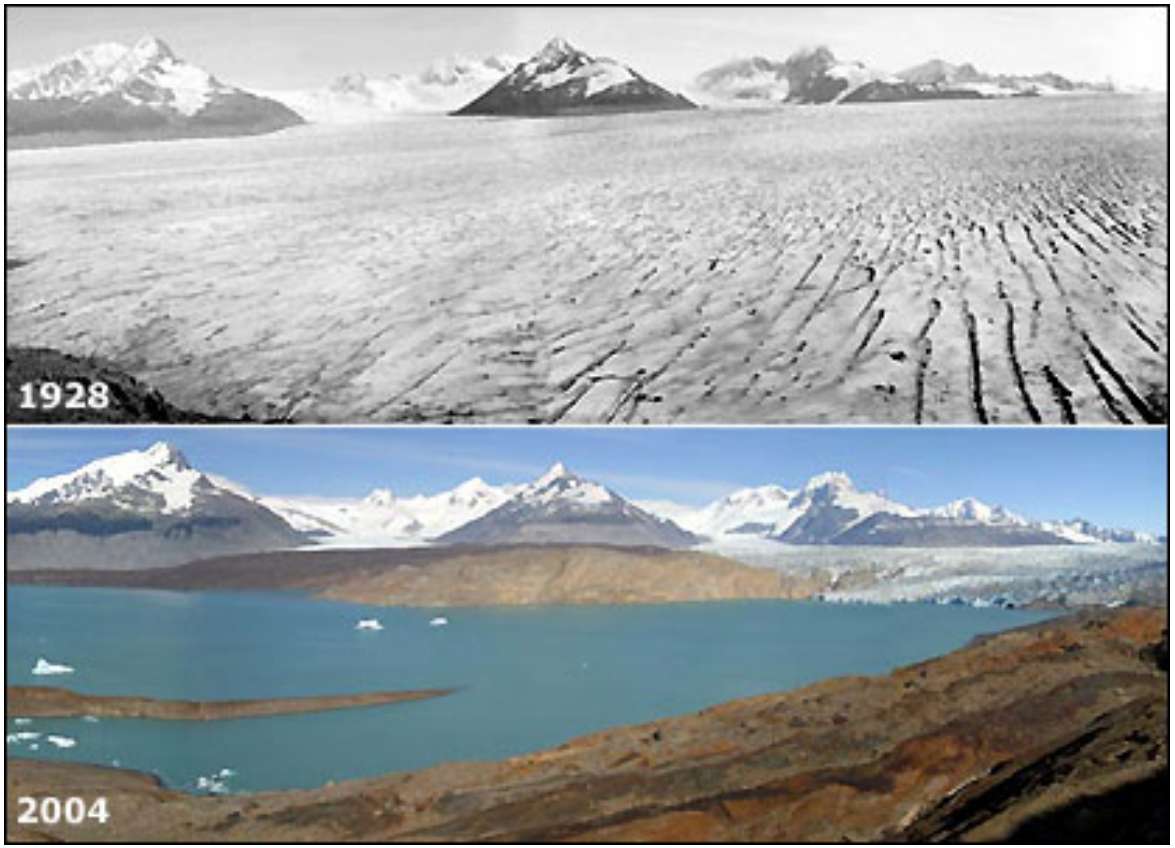
Methane, ruminants and the environment



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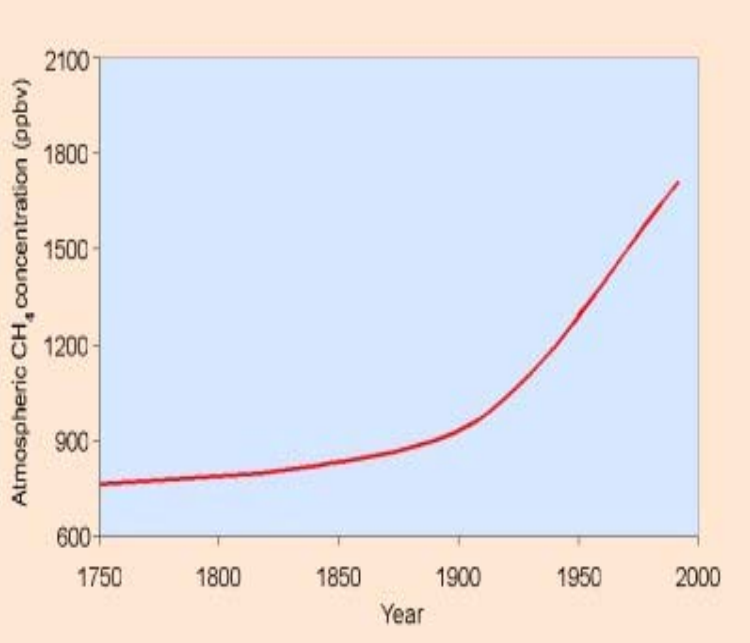
Positive proof of global warming.
18th Century
1900
1950
1970
1980
1990
2006

Methane as a greenhouse gas

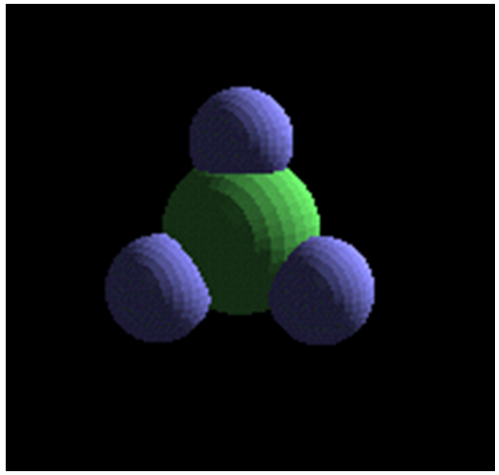


US Environmental Protection Agency, 2000

CH_4 has a global warming potential ("radiative forcing") 28 times that of CO_2

Methane contributes approximately 18% to the overall global warming effect

Methane production in ruminants



Fermentation

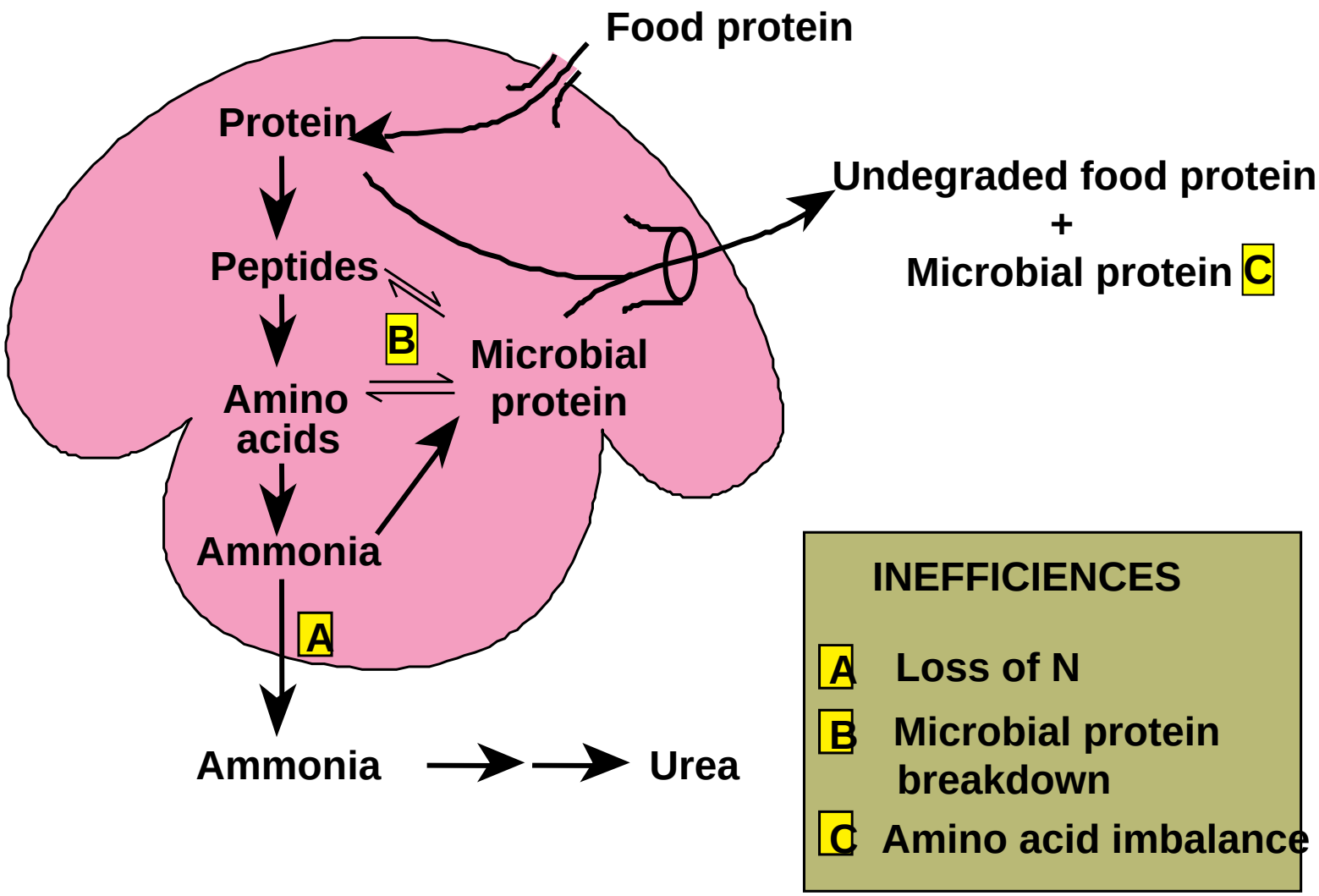
↓ Protozoa, fungi, bacteria

$H_2 + CO_2$

↓ Archaea

CH_4

Protein metabolism



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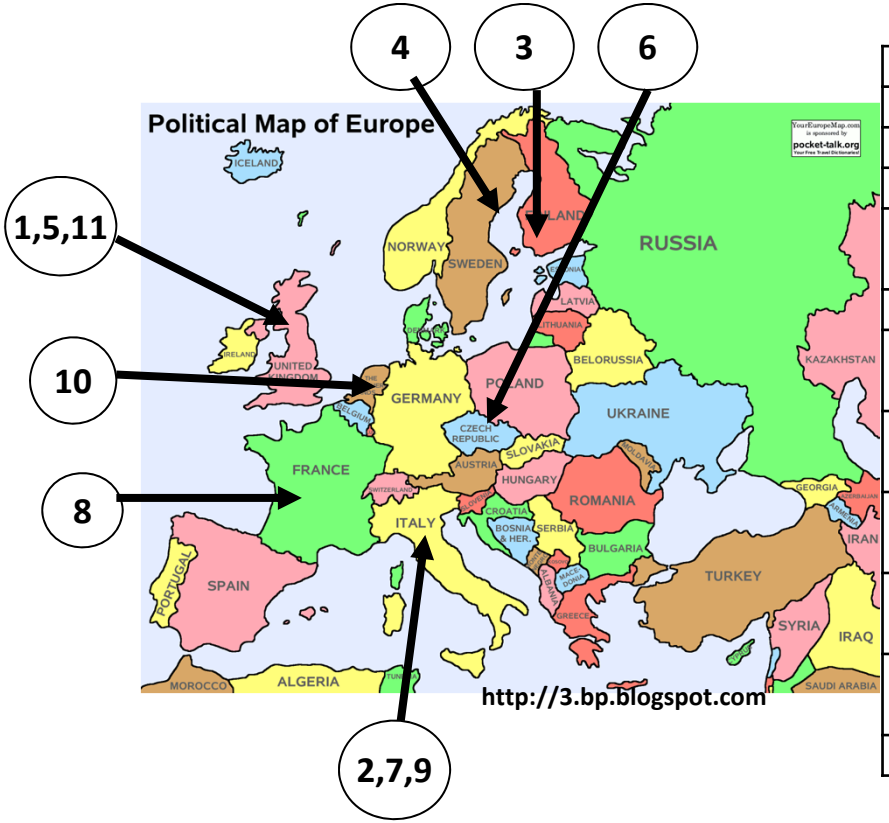
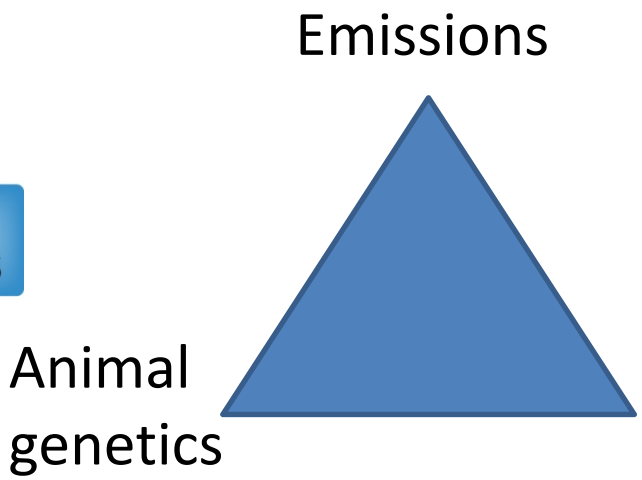
RuminOmics - Partners



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



- Tools
- Training
- Dissemination

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

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RuminOmics - Response to technology

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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

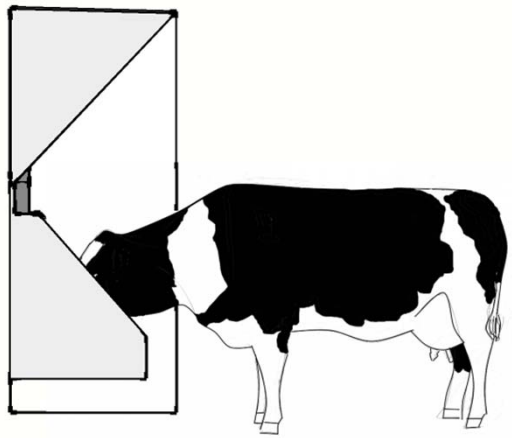
  ✖ Ruminal microbiome ✖ Animal genotype

- **20 cows in Sweden, Finland**

  Impact of N, CHO, lipid nutrition

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

  Full metagenome analysis



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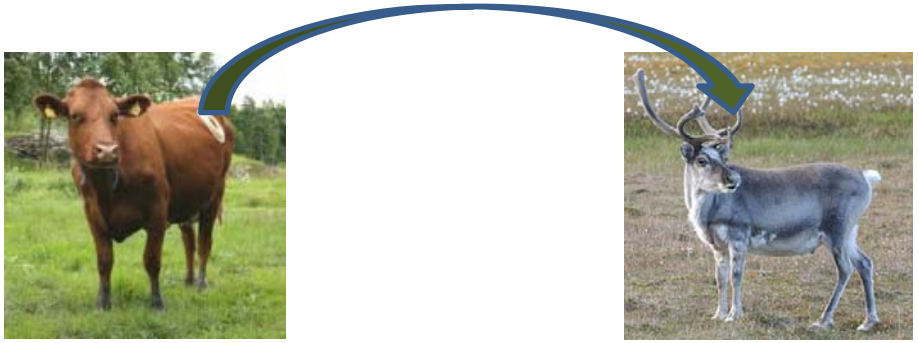
RuminOmics - Experiments II

Bovine single-egg twins

Interspecies digesta transfer



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RuminOmics - Experiments III

- **Bacterial genomes**

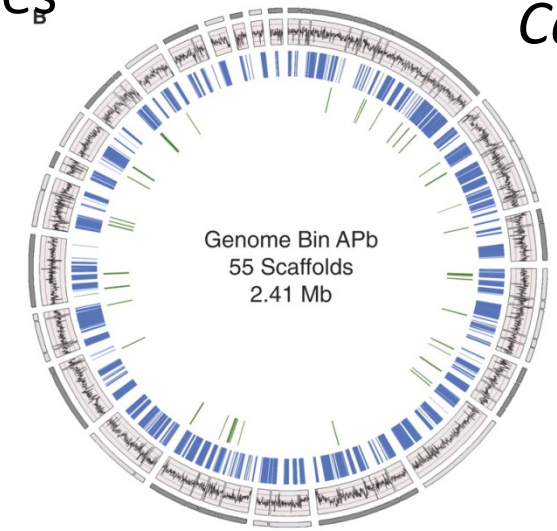
  Six *Butyrivibrio* spp.

  Two HAP species

- **Fungal genomes**

  Anaeromyces sp.

  Caecomyces sp.



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Tools, resources, legacy

Proxies Milk fatty acids

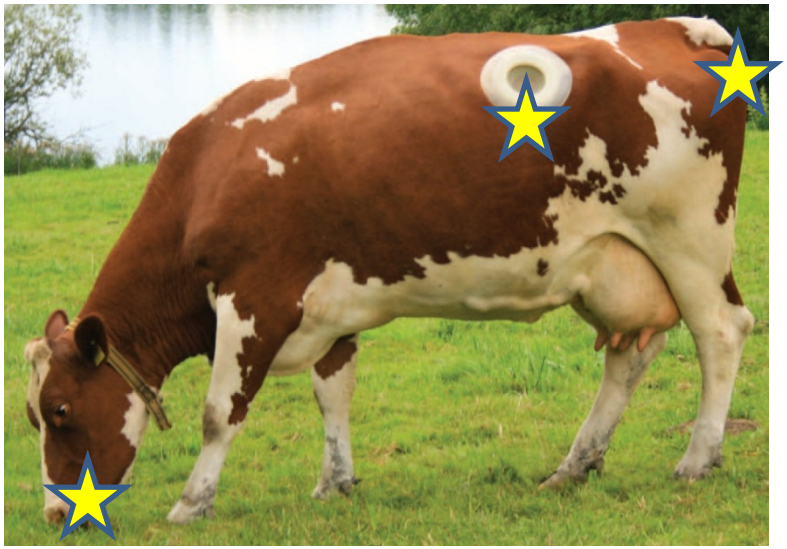
Relationship with methane

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

CH4 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

Tools, resources, legacy

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



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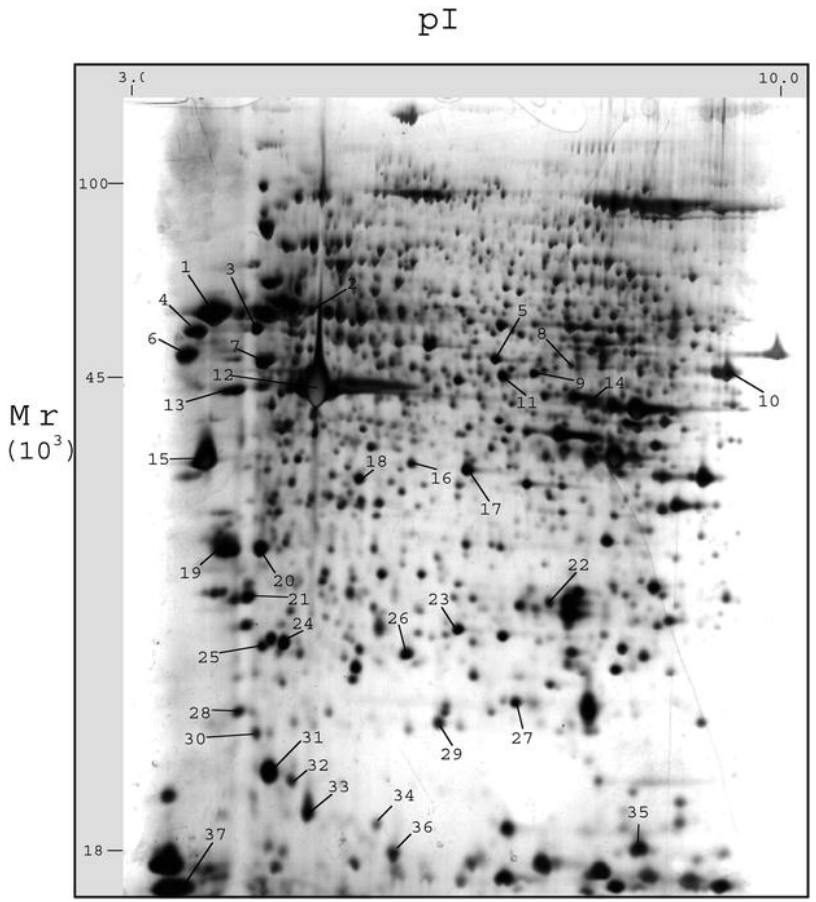
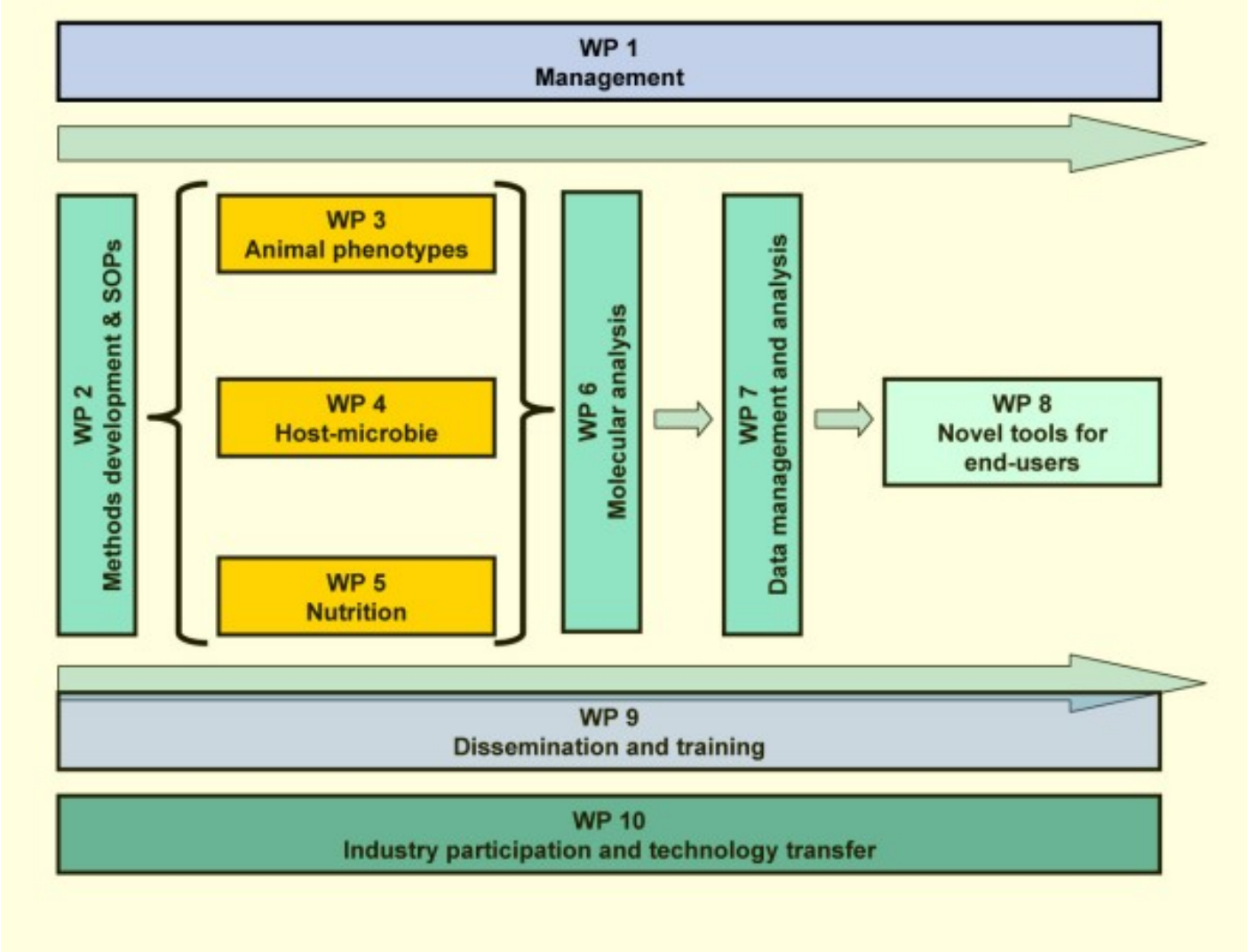
Tools, resources, legacy

- **Tools**

Metaproteomics



Work Package Structure



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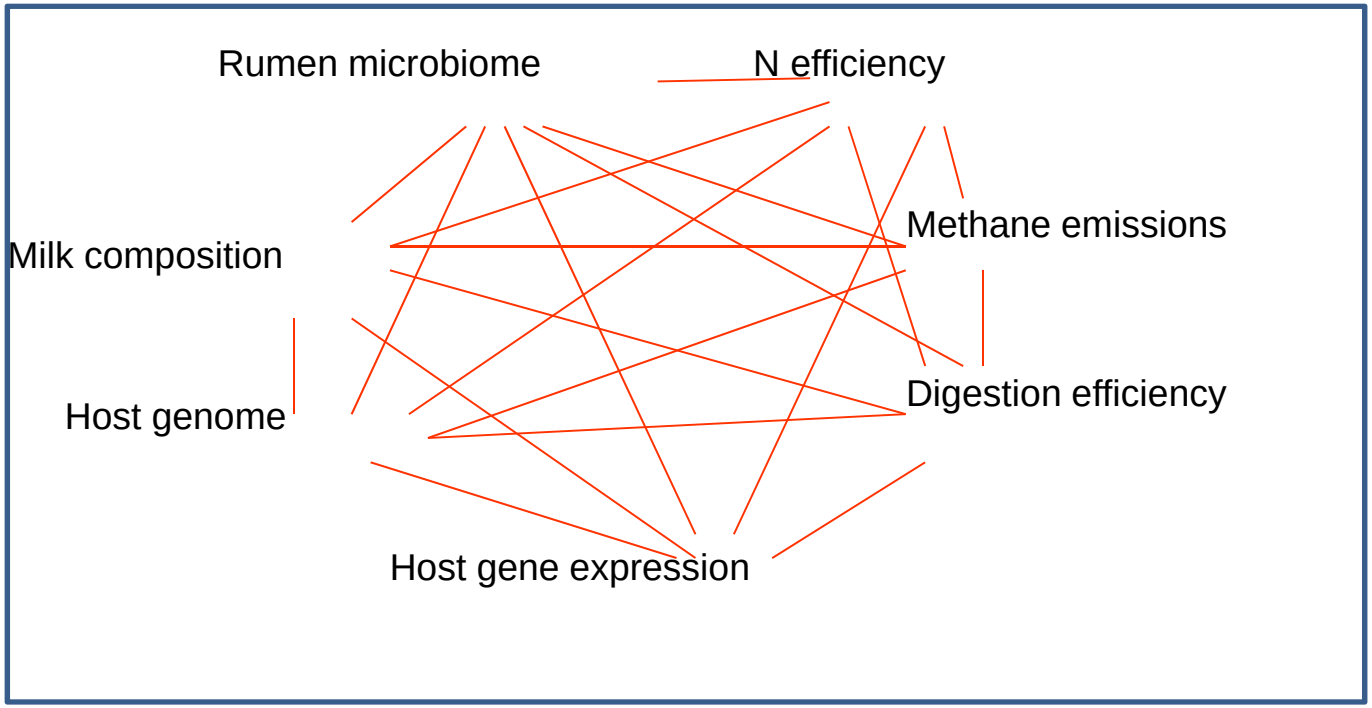
RuminOmics - Aspirations

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

The Bioinformatics challenge



SEVENTH FRAMEWORK PROGRAMME

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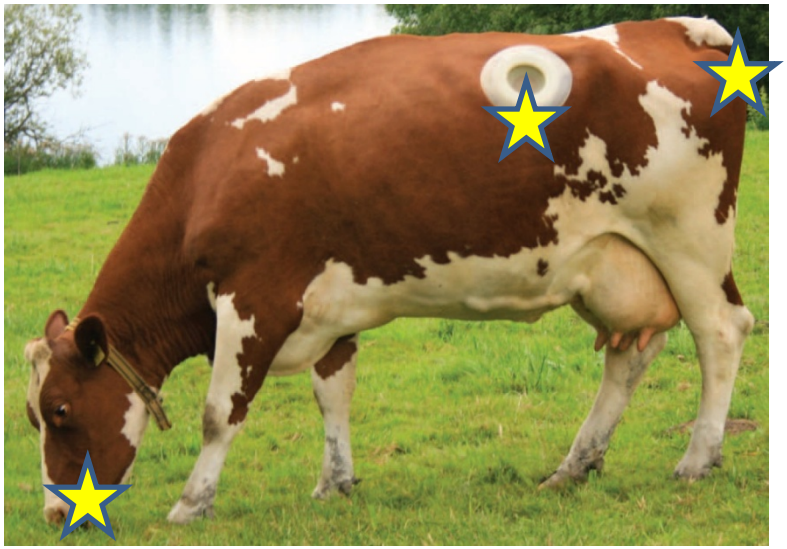
Tools, resources, legacy

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



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The rumen

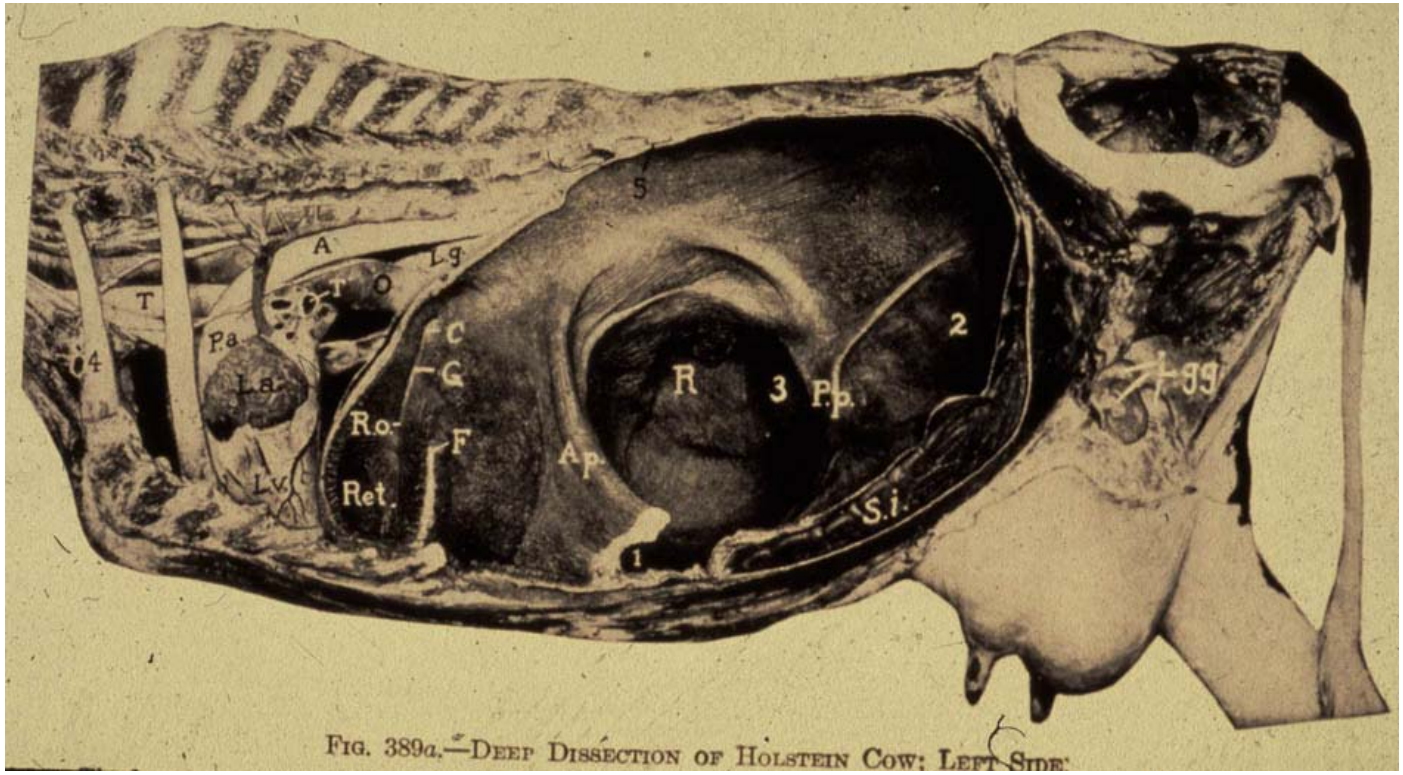
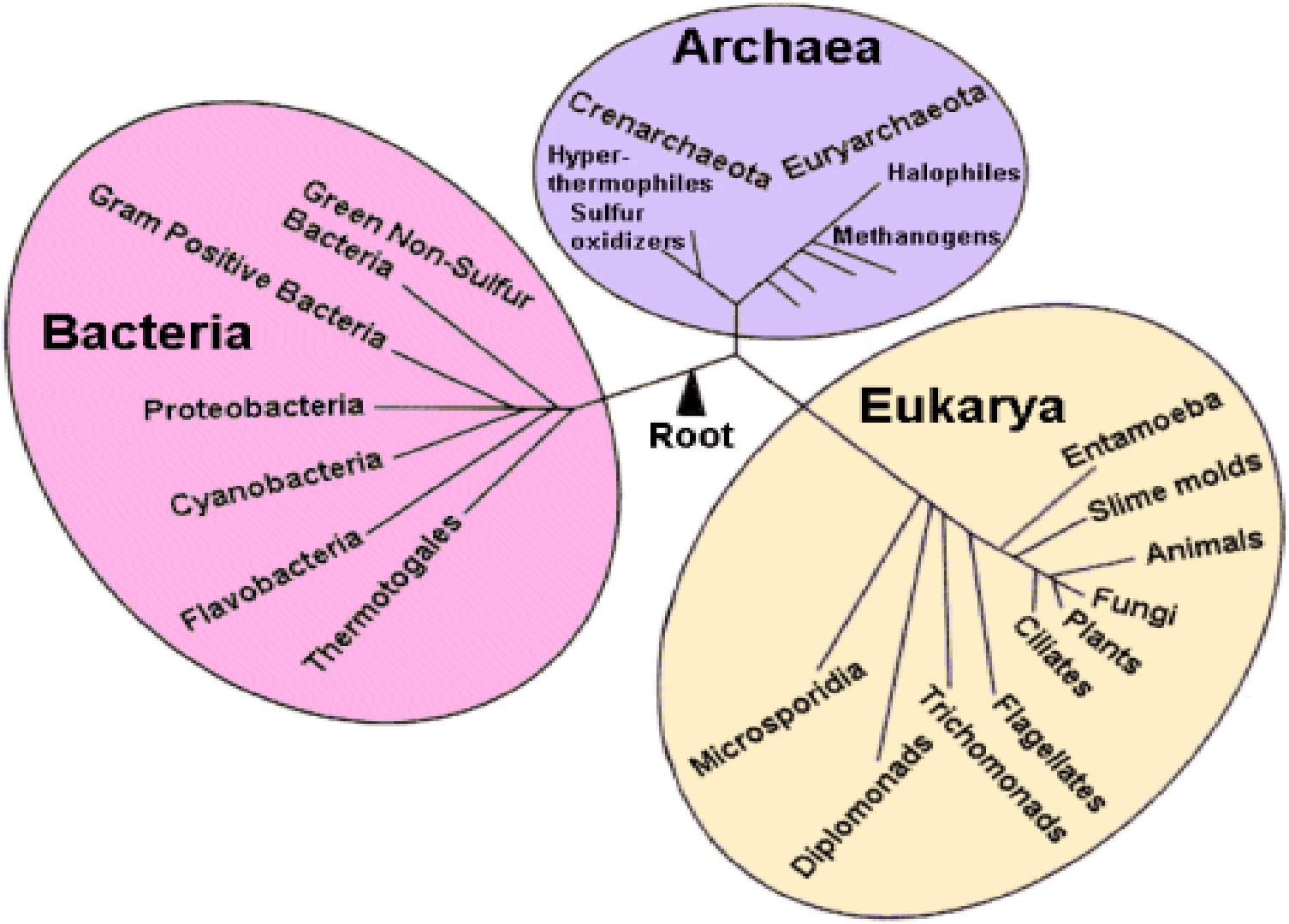
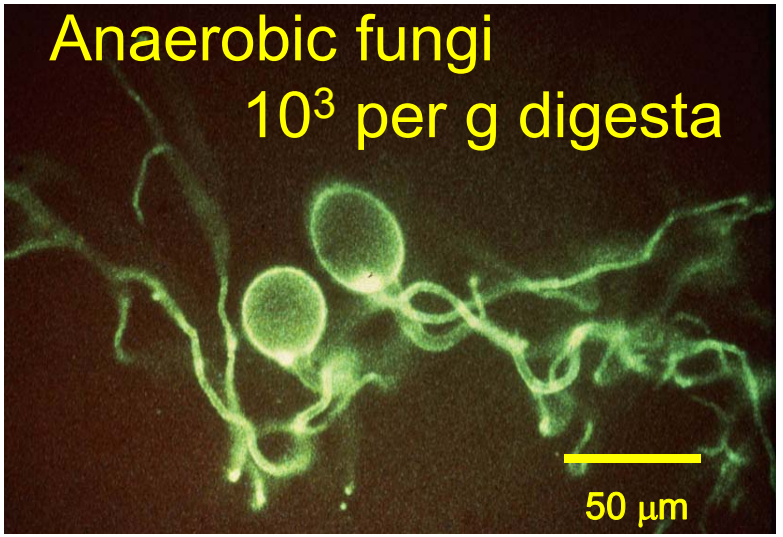


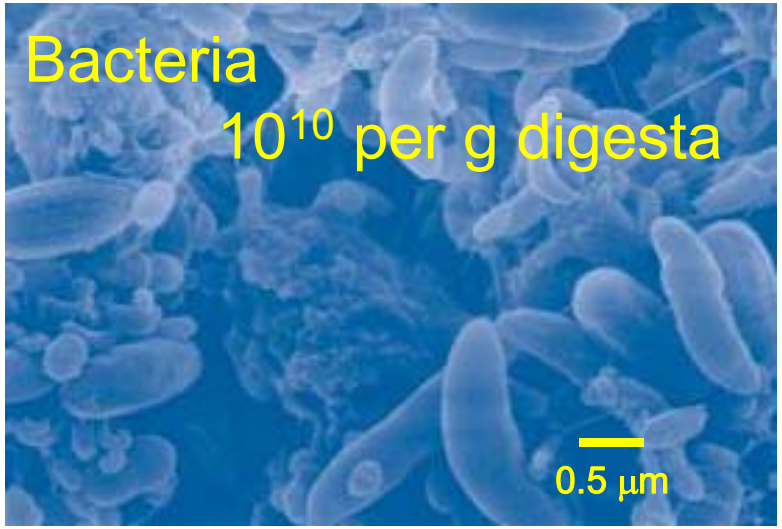
FIG. 389a.—DEEP DISSECTION OF HOLSTEIN COW: LEFT SIDE.

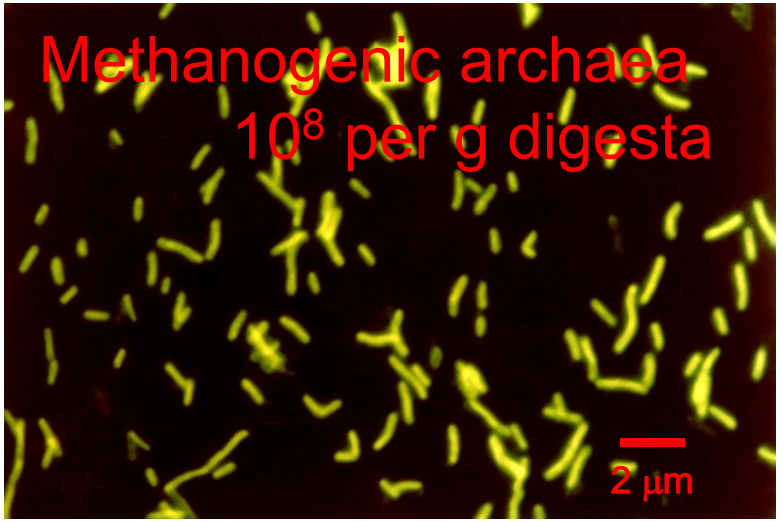
The three domains of life



Ruminal microorganisms







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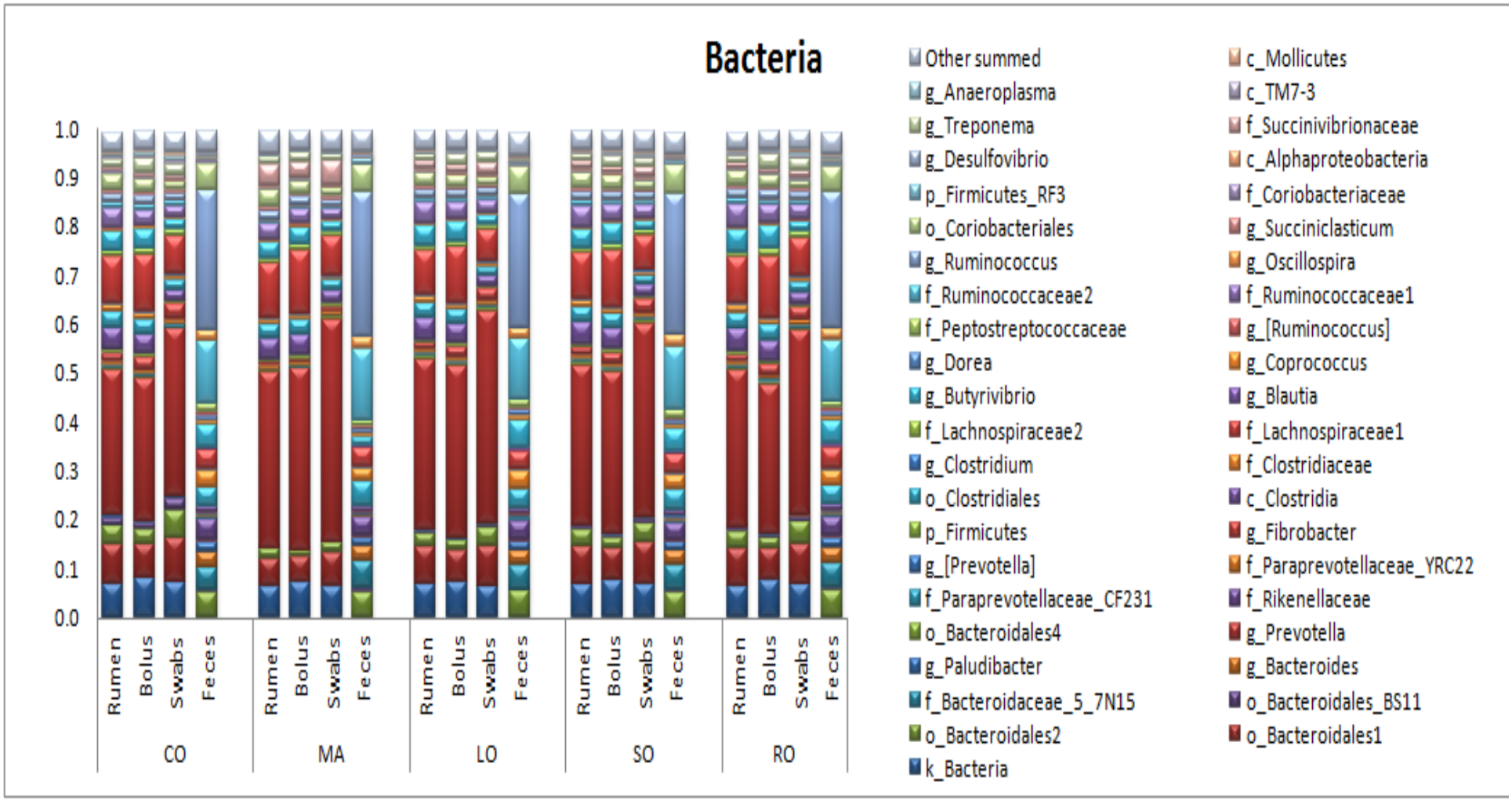
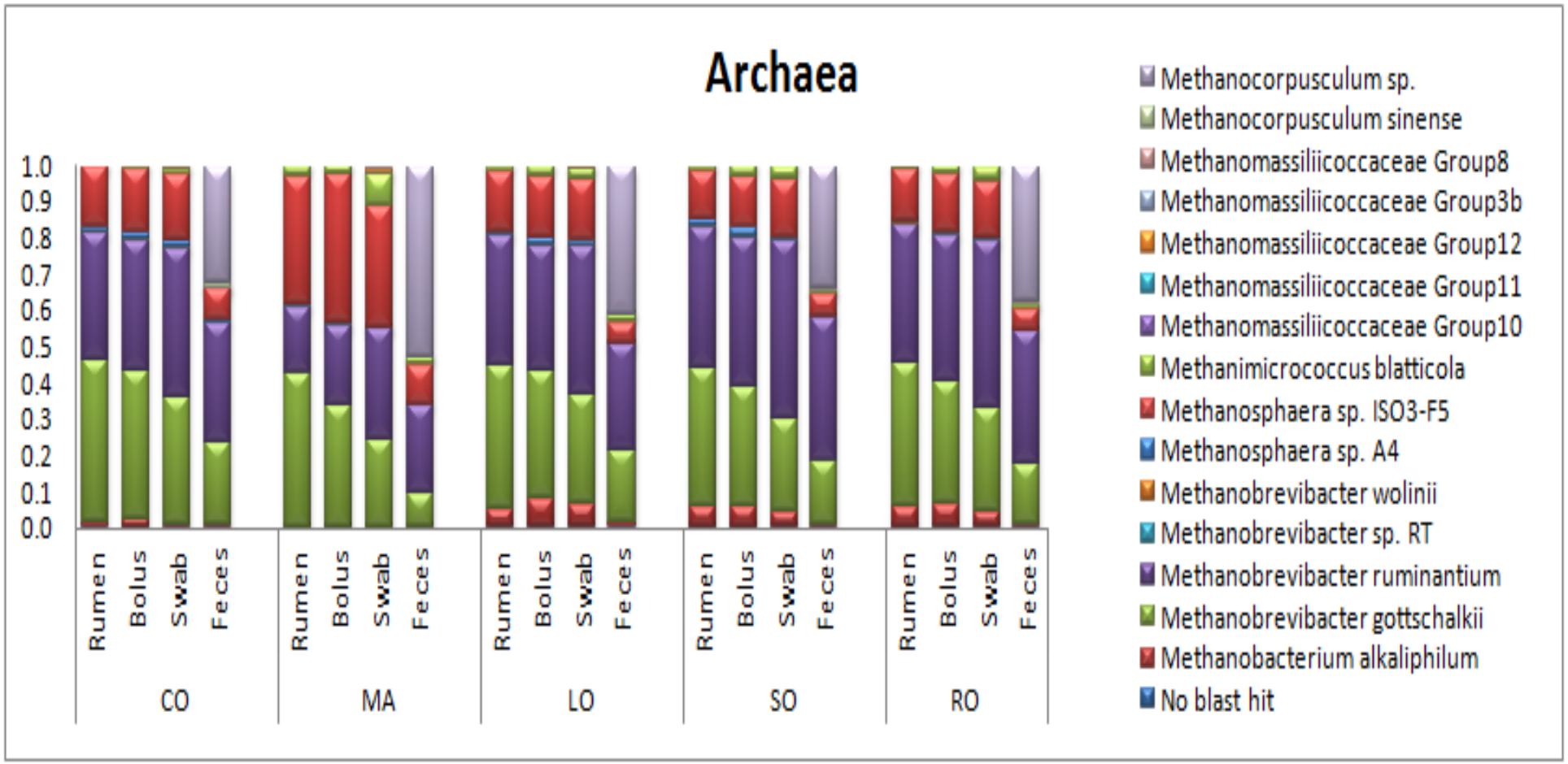
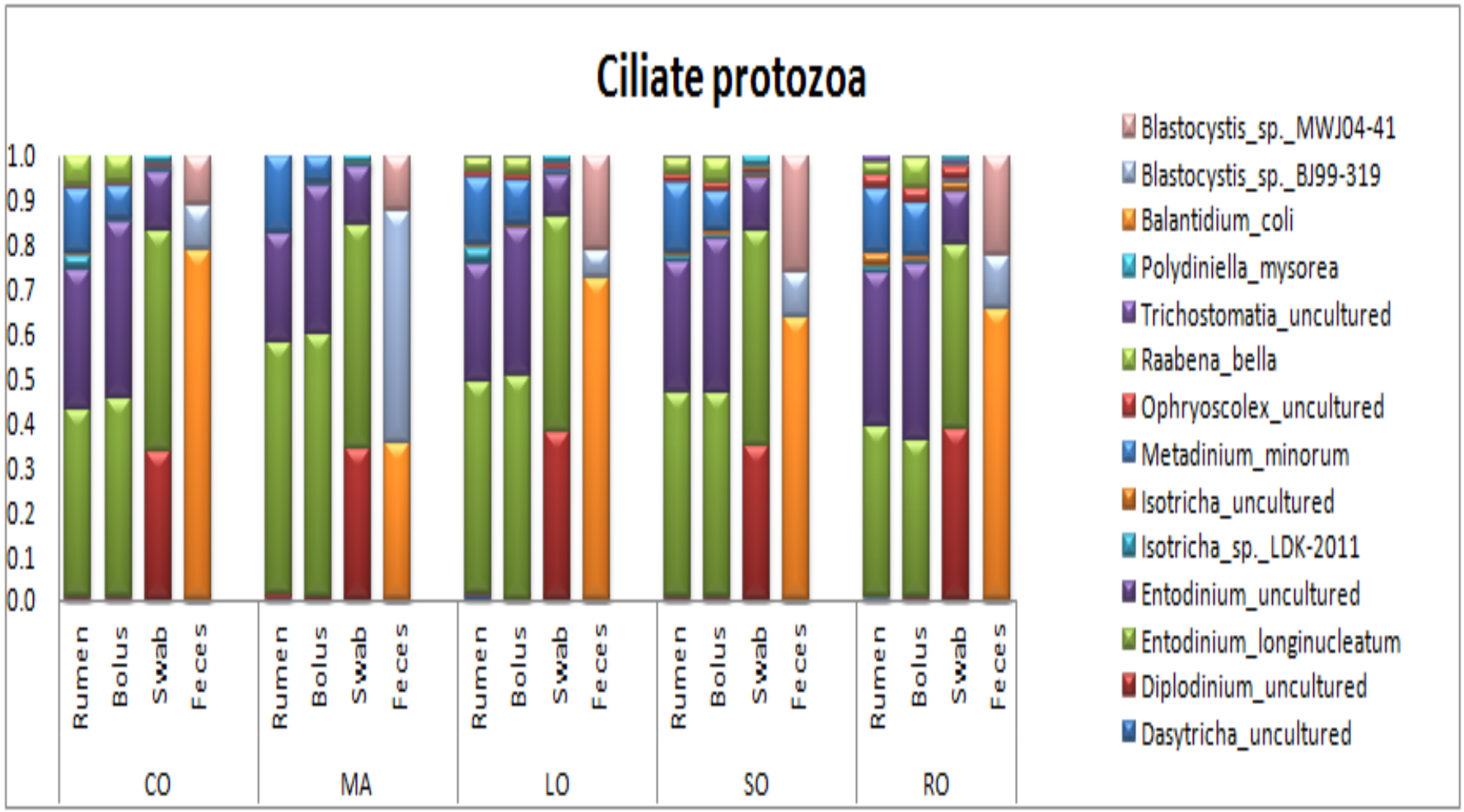
Proxies for rumen sampling – mouth (swab and bolus) and faeces: bacteria



Proxies for rumen sampling – mouth (swab and bolus) and faeces: archaea



Proxies for rumen sampling – mouth (swab and bolus) and faeces: protozoa



Conclusions on rumen digesta proxies

- Oral samples useful for bacteria and archaea
- Bolus samples needed for protozoa
- Faecal samples of no predictive value (BUT archaeol, etc.)
- Oral sampling will facilitate sampling of large cohorts without surgical intervention: breeding, inventory

Acknowledgements

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