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

Project coordinator:
John Wallace

Collaborative project
www.ruminomics.eu
RuminOmics - Partners

<table>
<thead>
<tr>
<th>Participant no.</th>
<th>Participant organisation name</th>
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<tbody>
<tr>
<td>1 (Coordinator)</td>
<td>University of Aberdeen</td>
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<td>Parco Tecnologico Padano</td>
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<td>Agrifood Research Finland</td>
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<td>4</td>
<td>Swedish University of Agricultural Sciences</td>
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<td>5</td>
<td>University of Nottingham</td>
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<td>6</td>
<td>Institute of Animal Physiology &amp; Genetics</td>
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<td>7</td>
<td>Università Cattolica del Sacro Cuore, Piacenza</td>
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<td>8</td>
<td>Centre National de la Recherche Scientifique</td>
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<td>9</td>
<td>European Association of Animal Production</td>
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<td>European Forum of Farm Animal Breeders</td>
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<td>Quality Meat Scotland</td>
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http://3.bp.blogspot.com
Does the animal itself determine its ruminal microbiome?
If so, is this a heritable trait?
How does nutrition affect this relationship?
Work Package Structure
RuminOmics – Experiments #1

- 1000 cows in UK, Italy, Sweden and Finland
  - Methane
  - N emissions
  - FCE
  - Milk quality

- 20 cows in Sweden and Finland
  - Impact of dietary N, CHO and lipid

- 50 cows in UK, Italy, Sweden and Finland
  - Full metagenome analysis

- Animal genotype

- Ruminal microbiome

1000 cows in UK, Italy, Sweden and Finland

20 cows in Sweden and Finland

50 cows in UK, Italy, Sweden and Finland

SEVENTH FRAMEWORK PROGRAMME

RuminOmics
RuminOmics - Experiments #2

Bovine identical twins

Interspecies digesta transfer
RuminOmics - Experiments #3

- **Bacterial genomes**
  Six *Butyrivibrio* spp.
  Two HAP species

- **Fungal genomes**
  *Anaeromyces* sp.
  *Caecomyces* sp.
Tools, resources and legacy

Data warehouse

Genomic analyses of individual ruminal Microorganisms [7.8]

Meta Barcoding Analysis [7.2]

Data Warehouse System [7.1]

Meta Genomic Sequencing Analysis [7.3]

Environmental footprint and efficiency [7.5]

Statistical models [7.4]

Product quality, health and safety [7.6]

Systems biology and pathway analyses of the host [7.7]
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<tr>
<th>Proxies</th>
<th>Buccal-ruminal-faecal microbiomes</th>
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<tr>
<td>Proxies</td>
<td>Milk fatty acids</td>
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<td>Tools</td>
<td>Metaproteomics</td>
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Challenges

• **Animal Phenotyping**
  - Performed in different locations
  - Harmonisation of techniques

• **Microbiome and Metagenome**
  - Bioinformatics
  - Fungal genomes

• **Statistical modelling**
  - Large datasets
  - Interpretation of complex biological responses
RuminOmics - Aspirations

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