

PROJECT PARTNERS

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- Parco Tecnologico Padano S.R.L. (Italy)
- Maa Ja Elintarviketalouden Tutkimuskeskus (Finland)
- Sveriges Lantbruksuniversitet (Sweden)
- Ustav Zivocisne Fyziologie A Genetiky AV CR, V.V.I. (Czech Republic)
- Universita Cattolica Del Sacro Cuore (Italy)
- University Of Nottingham (UK)
- Centre National De La Recherche Scientifique (France)
- European Association for Animal Production (Italy)
- European Forum Of Farm Animal Breeders (Netherlands)
- Quality Meat Scotland (UK)

For more detail see www.ruminomics.eu
Contact us though info@ruminomics.eu



RUMINOMICS

Connecting the animal genome, gastrointestinal microbiomes and nutrition

Ruminomics aims to improve digestion efficiency and reduce the environmental impacts of ruminant livestock production



Ruminomics is a project supported by the EU - FP 7 (FP7/ 2007-2013)



Background

Ruminant livestock make a significant contribution to greenhouse gas (GHG) emissions. Enteric emissions in the form of methane together with losses from manures and those associated with land use changes comprise the majority of livestock related GHG.

Technologies that increase rumen efficiency and lower methane emissions form a vital mitigation strategy to reduce global warming impacts.

Objective

Ruminomics will integrate expertise and technologies to increase rumen efficiency and decrease the environmental footprint of ruminant production, significantly advancing current knowledge in this sector.

Methods

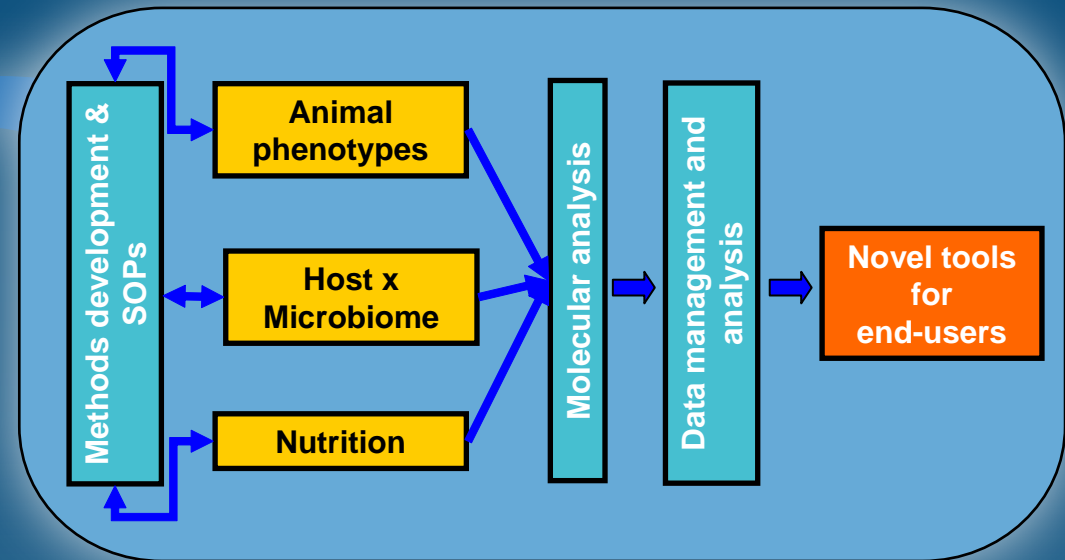
Ruminomics will exploit state-of-the-art omics technologies to understand how ruminant gastrointestinal microbial ecosystems, or microbiomes, are controlled by the host animal and by the diet consumed, and how this impacts on greenhouse gas emissions, efficiency and product quality.



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TAATTGCCGCTATTAAGAA  
TTATTGGGCCCAAATAATGCGCC  
GGCTAATGCGCGTAATTGCGC  
TATAGCCGCCTTCCAAATTAA  
GCGCGTAATTGTTGGG
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Project structure

Ruminomics is organized into 7 interlinked Work Packages



Outputs

Ruminomics will:

- Relate the animal genome to microbiome, feed efficiency, and methane emissions
- Determine host-microbe interactions in genetically identical and genetically diverse animals
- Relate changes in the nutrient supply to the ruminant with the composition and function of the ruminal microbiome, as assessed by methane and N emissions.
- Provide tools and bioinformatics for rapid analysis of phenotypes, microbiomes
- Create a public metagenomics database
- Effectively disseminate project technologies and results.