

Joint RuminOmics/Rumen Microbial Genomics Network Workshop

22 June 2013 08.30 – 18.00

High-level objective: *Harmonization of techniques associated with ruminal microbiome and metagenome analysis*



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



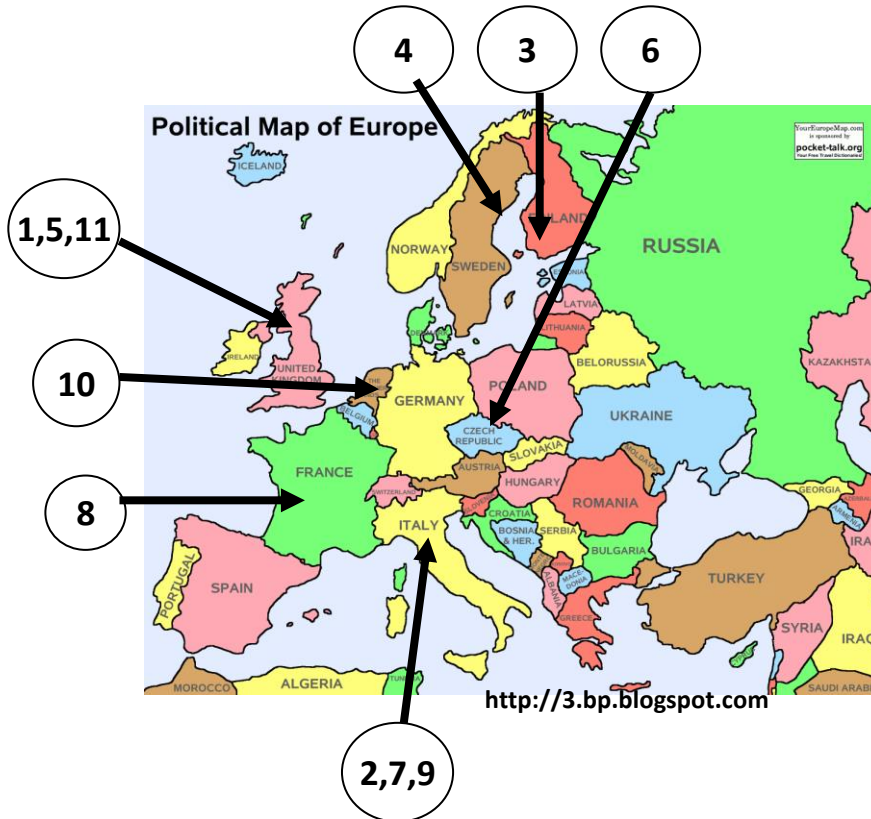
John Wallace

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

RuminOmics - Partners



RuminOmics

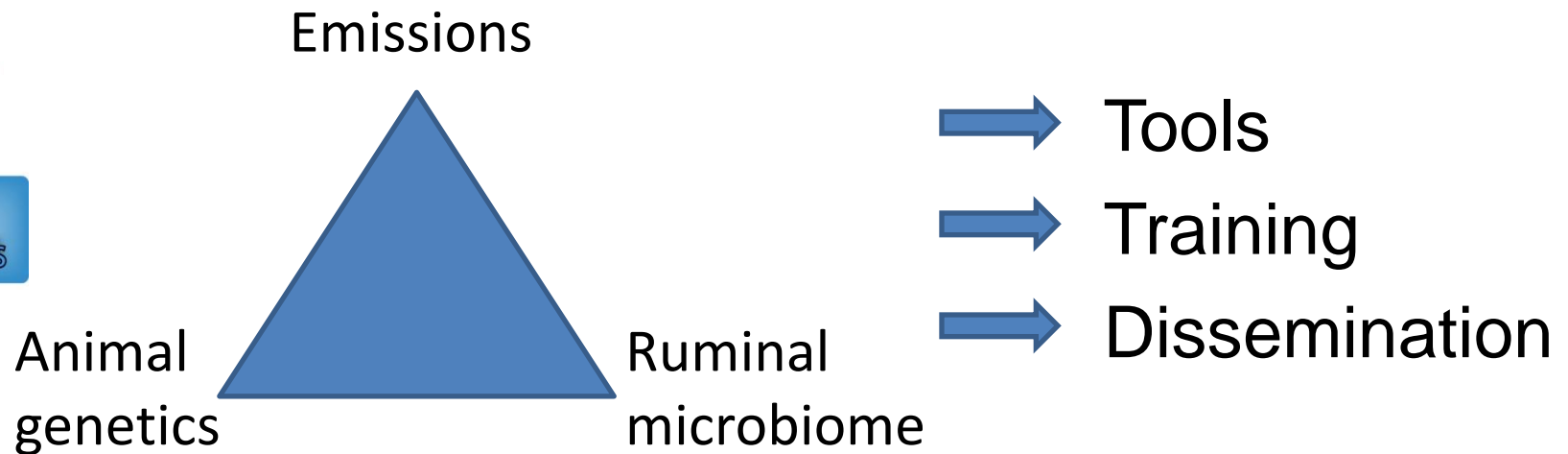


Participant no.	Participant organisation name
1 (Coordinator)	University of Aberdeen
2	Parco Tecnologico Padano
3	Agrifood Research Finland
4	Swedish University of Agricultural Sciences
5	University of Nottingham
6	Institute of Animal Physiology & Genetics
7	Università Cattolica del Sacro Cuore, Piacenza
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



RuminOmics



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

RuminOmics - Experiments



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

Methane

N emissions

FCE

Milk quality



Ruminal
microbiome



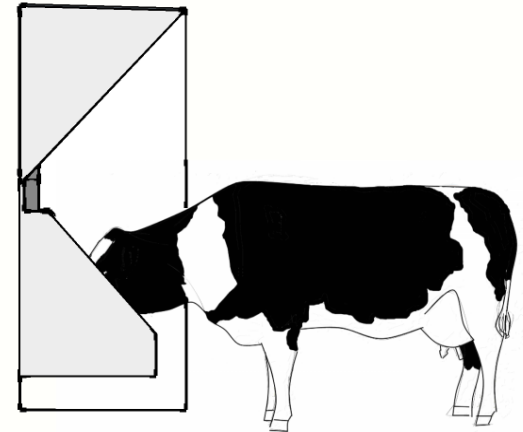
Animal
genotype

- **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

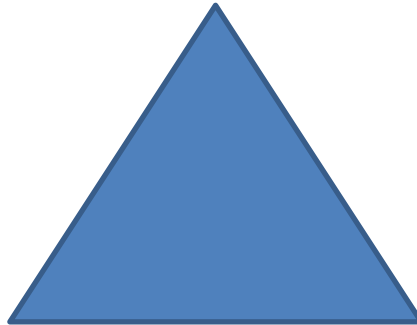


RuminOmics - Aims of project



Emissions

Animal
genetics



Ruminal
microbiome



Tools



Training



Dissemination

9.00 Introduction to Ruminomics

John Wallace, UK

9.10 Sampling and sample storage

Gemma Henderson, NZ
Ilma Tapio, Finland

9.30 Existing and emerging sequencing technologies

Mick Watson, UK

9.50 Microbiome analysis

Leluo Guan, Canada
Sinead Waters, Ireland

10.10 Metagenome analysis, community structure

Stewart Denman, Australia

10.30 Coffee

11.00 Genomics

Sinead Leahy, NZ

11.20 Functional metagenomics

Graeme Attwood, NZ

11.40 Metatranscriptomics

Chris Creevey, Ireland

12.00 Metaproteomics

Tim Snelling, UK

12.20 Bioinformatics for metagenomic sequence analysis

John Williams, Italy

12.40 Discussion

13.00 LUNCH

