



RuminOmics E-Newsletter

Connecting the animal genome, gastrointestinal microbiomes and nutrition to improve digestion efficiency and the environmental impacts of ruminant livestock production

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In This Issue

- “Animal phenotypes and metagenomic analysis” on page 1
- “RuminOmics/RMGN/ECO-FCE workshop” on page 1
- “Between cow variability in RAN and MUN” on page 2
- “RUP decrease the efficiency of microbial N synthesis” on page 2
- “Better understanding of cows through reindeer” on page 2
- “Rumen anaerobic fungi” on page 3
- “Nottingham technical visit” on page 3

3

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Welcome

Welcome to the second issue of the RuminOmics e-newsletter. In this issue we provide some updates on activities undertaken through the RuminOmics project. You can always keep abreast of the latest news through the website: www.ruminomics.eu. RuminOmics also has a presence on Twitter, so follow us and join in the conversation! <https://twitter.com/RuminOmics>

Animal phenotypes and metagenomic analysis

The project is collecting measurements and samples from animals on a large international scale with the aim to carry out an association study to identify genetic loci controlling the quantitative and qualitative variation in micro-organisms in the rumen through a metagenomic analysis. RuminOmics is also providing data to test the association of the microbiome with efficiency of feed utilisation, methane production and product quality.

So far 540 of 1000 cows have been sampled from commercial and experimental farms using novel techniques to determine intake, milk production, diet digestibility, rumen microbial biomass, methane and feed efficiency, with the aim of providing a large dataset to examine relationships between cow genome, rumen microbiome, digestion and production efficiency under practical conditions.

RuminOmics/RMGN/ECO-FCE workshop

Over 80 scientists from all over the world converged at the Aberdeen Exhibition & Conference Centre in Scotland on June 16th 2014 for a satellite workshop on the theme of How does the gut microbiota influence feed efficiency? Researchers presented on methodologies and data from current and ongoing work from three projects: [RuminOmics](#), [Rumen Microbial Genomics Network \(RMGN\)](#) and [ECO-FCE](#).



This was the second workshop organised by RuminOmics as satellite meetings to major international conferences. Whereas the focus in the first workshop had been technical, this time there was input from two other projects, ECO-FCE, an EU FP7 supported project and the RMGN, describing their results on linking feed efficiency and/or emissions with the gut microbiome. ECO-FCE demonstrated that pigs and poultry respond to the gut microbiota in a way analogous to ruminants, while RMGN described the current status of the [Hungate 1000](#) project and in 'culturing the not-yet-cultivated'. Great interest was shown by participants when Ilma Tapio of RuminOmics described the cow-reindeer digesta transplant experiments.

Although the number of participants was too high to foster a genuine workshop type of discussion, what emerged was a hybrid workshop/focussed symposium that held the attention of all and promoted all three consortia, both individually and collectively, to an international audience. Closing the workshop Professor John Wallace, the coordinator of RuminOmics, said he found it encouraging to see that large datasets were beginning to be managed successfully to understand the role of the gut microbiota in feed efficiency.

Some of the presentations are available for viewing here on the [RuminOmics workshop](#) webpage.

Between cow variability in RAN and MUN

There is considerable between cow variation in both rumen ammonia N (RAN) and milk urea N (MUN) concentration in cows fed the same diet. Coefficient of variation in RAN was 13% in a dataset from rumen fermentation studies (n = 450 cow/period observation). RAN concentration was positively associated with diet digestibility, but neither microbial N flow nor efficiency of microbial N synthesis were influenced by RAN. Between-cow CV in MUN was 13% in a dataset from milk production trials (n = 1772). MUN was negatively associated with milk nitrogen (N) efficiency (Milk N / N intake) and estimated urinary N output. However, per unit of change in MUN responses both in milk N efficiency and urinary N output were smaller than when MUN was influenced by variation in dietary CP concentration. It could be possible to use MUN as a proxy to rank the cows for milk N efficiency.

RUP decrease the efficiency of microbial N synthesis

Crimped barley was gradually replaced at four levels with heat-treated rapeseed meal (RSM) to increased dietary CP concentration in cows fed grass silage-based diets. The flow of nutrients from the rumen was determined using omasal sampling technique. Digesta flow was determined by triple-

marker method and 15N was used as microbial marker. The flow of non-ammonia N (NAN) and feed N increased significantly with increased dietary CP concentration. However, the increase in NAN was only 60% of the increase feed N flow due to decreased microbial N flow. Reduced efficiency of microbial N synthesis can at least partly explain why milk protein yield responses to feeding protein supplements treated to reduce ruminal protein degradability have been smaller than expected from calculated increase supply in metabolisable protein.

Better understanding of cows through reindeer

Semi-domesticated reindeer are intermediate mixed feeders adapted to live under Arctic conditions. Their growth, survival and reproduction capability are greatly affected by wide temperature fluctuations and seasonal changes in food availability and composition. Reindeer have a strong seasonal variation in appetite. During summer, animals eat a wide variety of vascular plants and store energy in body fat deposits. Their appetite declines in the autumn and remains low throughout the winter. Although accumulated fat can cover up to 10-30% of daily energy requirements, the low food intake of reindeer during winter leads to a substantial loss in body mass.



Lichens, eaten by reindeer in winter, are rich in carbohydrates but poor in protein. In addition they synthesize a wide variety of phenolic secondary compounds, e.g. usnic acid, as a defence against damage by UV-light. In contrast to other domesticated ruminants, reindeer can digest up to 90 % of the organic matter in lichens and respond to large variations in the dietary nitrogen content by increasing the recycling of urea into rumen. Our results show that reindeer are more efficient in the recycling of urea into the digestive tract compared with cows as indicated by a lower proportion of N excreted in urine and a higher proportion of N lost in faeces. When offered the same diet at the same level of intake per unit body weight, total tract nutrient digestibility did not differ between cows and reindeer.



The rumen of reindeer represents a unique microbial ecosystem developed through a long evolution of exposure to Arctic flora and contains bacterial lineages not observed in other ruminants. The volatile fatty acids produced by microbial fermentation in the rumen, are the principal sources of dietary energy for the ruminant animal. When fed the same diet, the microbial composition and fermentation pattern in the rumen was found to differ between cows and reindeer. At the same time, reindeer produced less methane than non-lactating cows per kg of feed eaten but slightly more per unit of liveweight. The numbers of rumen methanogens have been reported to be lower in Svalbard reindeer compared to other domestic ruminants. This may represent a survival mechanism to lower energy losses during fermentation in the rumen and thereby increase the amount of energy from the diet to support maintenance and growth in these species.



Fig.2. Bulbous mycelium of *Caecomyces communis*. Light microscopy of native preparation (x 400)

Rumen anaerobic fungi

One of the goals of the RuminOmics project is focused on genome sequencing of less studied genera of rumen fungi, *Anaeromyces* (Fig. 1) and *Caecomyces* (Fig. 2). with the aim to elucidate their polysaccharide hydrolytic system and to understand their role in the rumen ecosystem. Rumen anaerobic fungi produce a broad range of excellent hydrolases, including cellulases, xylanases, mannanases, esterases, glucosidases, and glucanases, which can be organized in cellulosomes, carrying the most active (hemi) cellulases.

Rumen fungi are the only representatives of kingdom Fungi demanding anaerobiosis, and possessing hydrogenosomes instead of mitochondria. Another unique feature of these unusual microorganisms is the extremely low Guanine+Cytosine content (17%) and the duplication of important hydrolytic genes, which is a trait not common among eukaryotes.

The full article can be found on: <http://www.ruminomics.eu/index.php/news/>

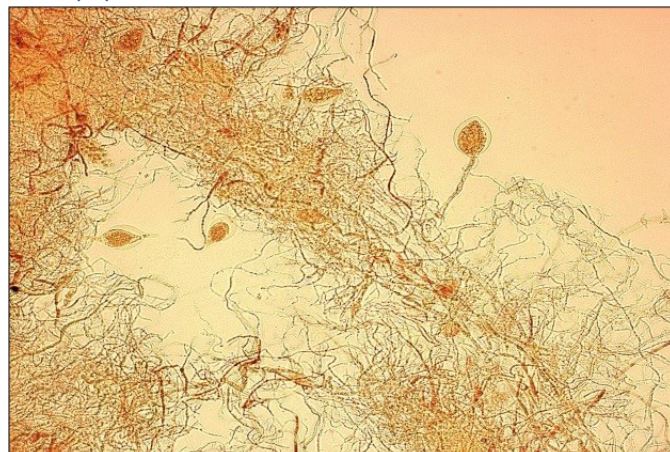
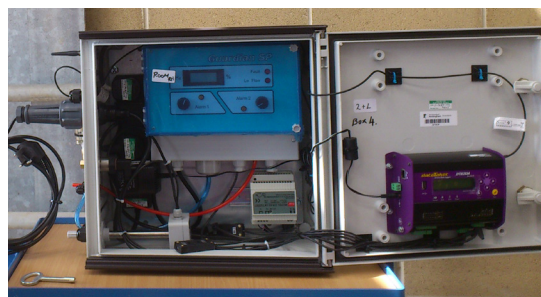


Fig. 1. Rhizomycelium of *Anaeromyces mucronatus* with apical sporangia. Light microscopy of lugol stained preparation (x 400)

Nottingham technical visit

On the 25th of June 2014, RuminOmics' partner, [European Forum For Animal Breeders \(EFFAB\)](#), with support of the [University of Nottingham](#) organised the technical visit on the Sutton Bonington campus of the University.

The aim of the RuminOmics project is to integrate expertise and technologies to increase rumen efficiency and decrease the environmental footprint of ruminant production. The main objective of the Technical Visit was to introduce and provide projects updates on the outcomes and to receive feedback from various stakeholders regarding the relevancy of the tools and technologies being developed under the project.



Methane analyzer used in RuminOmics

Thirty participants including feeding industries, universities, young scientists and representatives from different government institutes attended the technical visit. An introduction to the project including the presentation of intermediate result; feed efficiency and changing diet with respect to lowering methane emissions; research conducted on methane emissions in dairy cows; and pathways through the rumen were presented during the visit. In addition, participants were able to visit the experimental farm on the Sutton Bonington campus where trials on methane emissions are being conducted.

The visit was closed by a lively discussion where organisers collected the needs from the different stakeholders as well as recommendations to further fine tune the developments of the project.

