Rumen Microbial Genomics Network (RMG)

Professor Sharon Huws

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8th RMG workshop in conjunction with FNN network

Website: http://www.rmgnetwork.org/home.html

Twitter: @RMG_network

Do tweet!





Rumen Microbial Genomics Network (RMG)

16.30-16:50: Update on the RMG (Sharon Huws, Queen's University, Belfast)

16.50-17.10: Update on RumenPredict project (Paul Smith, Teagasc, Ireland)

17.10-17.30: Developments on metabolomics technologies to study the rumen microbome (Rodolpho Prado, Universidade Estadual de Maringa, Brazil)

17.30: Closing remarks (Sharon Huws)







The RMG Network was formed following a workshop held in NZ in February 2011 and is an initiative of the Livestock Research Group of the Global Research Alliance.

Purpose

- Enhanced communication and collaboration between research groups
- Improved ability to attract funding with integrated, international studies
- Streamline future RMG research to prevent duplication
- Training exchange of students, technicians, staff
- Accelerated access to protocols, cultures, primer sets and facilitate sharing of knowledge and technologies
- Generation of reference datasets
- Facilitate research in microbial genomics, ecology and physiology



RMG Network meetings

1st RMG Network meeting

Palmerston North, New Zealand, February 2011

2nd RMG Network meeting

Associated with INRA-RRI meeting, France, June 2012

3rd RMG Network meeting (jointly with RuminOmics)

Associated with GGAA2013, Dublin, Ireland, June 2013

4th RMG Network meeting (jointly with RuminOmics/ECO-FEC)

Associated with INRA-RRI meeting, Scotland, June 2014

5th RMG Network meeting (GRC/Hungate 100 workshop)

Associated with the 2015 Congress on Gastrointestinal Function Chicago.

6th RMG Network meeting Associated with INRA-RRI meeting. Clarmont Forra

Associated with INRA-RRI meeting, Clermont Ferrand, June 2016 (80 attendees)

7th RMG Network meeting Associated with INRA-RRI meeting, Aberdeen, June 2018 (80 attendees) 8th RMG Network meeting (with FNN) Linked to GGAA conference, Fos de Iguasu, Brazil



Collaborative projects

- Global Rumen Census <u>www.globalrumencensus.org.nz</u>
 - Culture-independent study based on sequencing ribosomal RNA genes to identify the extent of diversity of the rumen microbes.
- Hungate1000 <u>www.hungate1000.org.nz</u>
 - Aimed to produce a reference set of rumen microbial genome sequences from cultivated rumen microbes including bacteria, methanogens, phage, anaerobic fungi and ciliate protozoa.
- Several Network-based collaborative projects since been funded e.g :
 - EU ERA-NET Gas Cofund RumenPredict

http://www.eragas.eu/research-projects/rumenpredict

• EU Horizon 2020 MASTER

https://cordis.europa.eu/project/rcn/218782/factsheet/en





Front Microbiol. 2018 Sep 25;9:2161. doi: 10.3389/fmicb.2018.02161. eCollection 2018.

Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future.

Huws SA¹, Creevey CJ¹, Oyama LB¹, Mizrahi I², Denman SE³, Popova M⁴, Muñoz-Tamayo R⁵, Forano E⁶, Waters SM⁷, Hess M⁸, Tapio I⁹, Smidt H¹⁰, Krizsan SJ¹¹, Yáñez-Ruiz DR¹², Belanche A¹², Guan L¹³, Gruninger RJ¹⁴, McAllister TA¹⁴, Newbold CJ¹⁵, Roehe R¹⁵, Dewhurst RJ¹⁵, Snelling TJ¹⁶, Watson M¹⁷, Suen G¹⁸, Hart EH¹⁹, Kingston-Smith AH¹⁹, Scollan ND¹, do Prado RM²⁰, Pilau EJ²⁰, Mantovani HC²¹, Attwood GT²², Edwards JE²³, McEwan NR²⁴, Morrisson S²⁵, Mayorga OL²⁶, Elliott C¹, Morgavi DP⁴.

Author information

Abstract

The rumen is a complex ecosystem composed of anaerobic bacteria, protozoa, fungi, methanogenic archaea and phages. These microbes interact closely to breakdown plant material that cannot be digested by humans, whilst providing metabolic energy to the host and, in the case of archaea, producing methane. Consequently, ruminants produce meat and milk, which are rich in high-quality protein, vitamins and minerals, and therefore contribute to food security. As the world population is predicted to reach approximately 9.7 billion by 2050, an increase in ruminant production to satisfy global protein demand is necessary, despite limited land availability, and whilst ensuring environmental impact is minimized. Although challenging, these goals can be met, but depend on our understanding of the rumen microbiome. Attempts to manipulate the rumen microbiome to benefit global agricultural challenges have been ongoing for decades with limited success, mostly due to the lack of a detailed understanding of this microbiome and our limited ability to culture most of these microbes outside the rumen. The potential to manipulate the rumen microbiome and meet global livestock challenges through animal breeding and introduction of dietary interventions during early life have recently emerged as promising new technologies. Our inability to phenotype ruminants in a high-throughput manner has also hampered progress, although the recent increase in "omic" data may allow further development of mathematical models and rumen microbial gene biomarkers as proxies. Advances in computational tools, high-throughput sequencing technologies and cultivation-independent "omics" approaches continue to revolutionize our understanding of the rumen microbiome. This will ultimately provide the knowledge framework needed to solve current and future ruminant livestock challenges.

KEYWORDS: diet; host; methane; microbiome; omics; production; rumen



Long term aspirations

• Currently:

- >200 scientists registered as members of the network.
- The workshops are well attended.
- Social media drastically improved due to contribution of Dr Tamsin Lyons, University College Dublin, Ireland.

• Future Vision:

- Encourage more active involvement from postgraduate students and early-stage postdocs.
- Develop global flagship projects.



Flagship activities to date



Court of the I

Enteric Fermentation Flagship Project

RUMEN MICROBIOME TO PREDICT METHANE EMISSIONS FROM CATTLE

HOW?

- Methodology developed by Hess et al. (2018)* with sheep rumen samples has been validated with dairy cattle rumen samples from New Zealand
- High quality DNA produced that can be used to generate rumen microbial community profiles
- Genotyping by Sequencing (GBS) to optimise processing time and cost





THE PROJECT

- Develop microbial and genomic predictors for differences in CH4 production among different large ruminant species (Bos taurus, Bos indicus, buffaloes, ...)
- Open to different production systems (grazing, confinement, dairy, beef, ...)
- 1,000 samples fully funded by Global Research Alliance (GRA)
- Allowance for sequencing costs for developing countries

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*Hess MK, Rowe SJ, Van Stijn TC, Brauning R, Hess AS, Kirk MR, Attwood GT, Janssen PH, McEwan JC (2018) High-throughput rumen microbial profiling using genotyping-by-sequencing. Paper presented at the World Congress for Genetics Applied to Livestock Production, Auckland, New Zealand



Flagship activities: Culturomics

Hungate Collection: Excellent resource for furthering our understanding of the rumen microbiome in order to increase our ability to develop solutions for enhanced production and reducing environmental impact Seshadri et al. (2018) Nat Biotechnol. 2018 Apr; 36(4): 359–367.



But: Missing key microbial genomes as not in culture



Flagship activities: Culturomics

- Major advances in culturomic technologies suggest that culturing underrepresented microbes is now less challenging
- Examples of advances:

Khelaifia et al. (2016) Culture of previously uncultured members of the human gut microbiota by culturomics. Nature Micro 1: 16203.

Mizrahi et al. (2018) Insights Into Culturomics of the Rumen Microbiome. Front Microbiol. 29;9:1999.

Vaidya et al. (2019). *Propionibacterium ruminifibrarum* sp. nov., isolated from cow rumen fibrous content. Int J Syst Evol Microbiol. doi: 10.1099/ijsem.0.003544.



Need to develop flagship activities to culture missing rumen microbes

Why?

1. Improved understanding of rumen function

- Generate novel strategies to improve production and reduce GHG emissions
- Understand mechanism of action of technologies that reduce GHG emissions
- Improve likelihood of strategies being commercialised

2. Biotechnological resource

- Sourcing novel bioactive compounds e.g Glycosyl hydrolases
- Enhancing bioprocessing

An enhanced culture collection will improve the likely impact of our science



Need to develop flagship activities to culture missing rumen microbes

How?

For those interested please could we meet at the end of the workshop to discuss potential mechanisms to build this global culture strategy



Animal Microbiome – launched 2019

- Editor-in-Chief: Sharon Huws (Queen's University Belfast)
 - Animal Microbiome is a community focused open access journal welcoming all animal microbiome studies either from a regional or global point of view.
 - Animal Microbiome is a sister journal to Microbiome
- Reasons to publish with us:
 - A single place for animal microbiome studies (domestic or non-domestic)
 - Supporting authors in communicating their research to a wider audience
 - Introductory APC (25% discount) for first three years