FoodBioSystems DTP - PhD Project Advertisement

Project title:

FBS2021-74-Huws: Manipulation of the ruminant gastrointestinal tract microbiomes for reduced environmental impact of nitrogen excretion from dairy cows.

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Project description:
Nitrogen use efficiency in ruminants is low, typically 25-30%, with the remaining nitrogen being excreted in urine, and some in the faeces (Huws et al., 2018; Foskolos and Moorby.,2018; Hristov et al., 2019). When faeces and urine mix, N is lost as ammonia which causes terrestrial eutrophication. Furthermore, during slurry storage and following soil application a portion of the N can be converted by bacteria into nitrous oxide, a GHG with a 298-fold greater global warming potential than carbon dioxide (Hristov et al., 2013). Nitrogen loss in waterways via leaching can also cause aquatic eutrophication and biodiversity loss. In addition to the environmental impact of nitrogen losses, nitrogen (protein) feeds are increasingly costly and the low efficiency of nitrogen use represents an economic loss for farmers. However, despite these environmental and economic challenges, dairy cows are in general offered diets containing excess nitrogen, a reflection of the fact that historically protein sources, such as soya, were relatively cheap to buy, a relentless focus on higher milk yields, and uncertainties about the actual protein requirements of dairy cows. However, current environmental and economic challenges mean that over-feeding nitrogen to ruminants is no longer viable.

Ruminants are composed of a complex gastrointestinal tract, composed of the reticulum, rumen, abomasum, omasum and lower gastrointestinal tract (small intestine, caecum and large intestine), which house bacteria, fungi, protozoa and phage (Figure 1). The rumen, in particular, is rich is microbes as this is the main fermentative energy-harvesting organ possessed by ruminants. Indeed, without these rumen microbes the host would be unable to survive. Consequently, the rumen microbiome is central to addressing the grand challenges facing agriculture globally, including improving nitrogen use efficiency, due to its role in proteolysis and catabolism of amino acids, resulting in microbial N, which contributes 60–90% of protein absorbed at the duodenum (Huws et al., 2018). A better

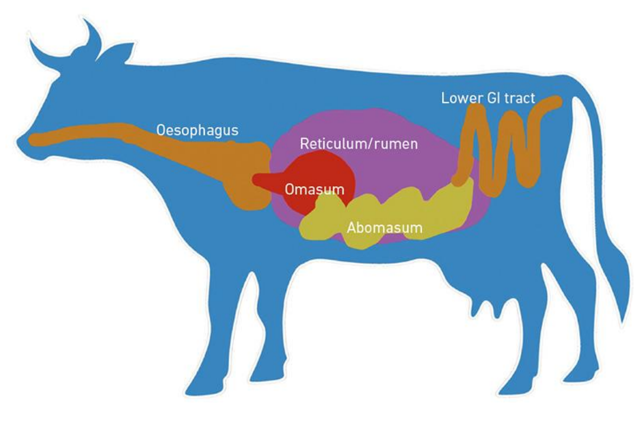

Fig. 1. Ruminant gastrointestinal tract. Most of the microbes (bacteria, archaea, fungi, protozoa and phage) inhabit the large fermentative rumen, resulting in effective digestion of dietary material.

understanding of the roles played by the constituent microbes is central to the development of advanced methods to manipulate the rumen microbiome in a manner that improves ruminant production whilst reducing environmental impact (Yáñez-Ruiz et al., 2015). Furthermore, recent studies have shown that cows which are more efficient at using nitrogen also have better residual feed intake (RFI), i.e require less feed to produce a given milk yield. Rumen microbiome data from animals with enhanced feed efficiency (i.e low RFI) also indicate that the rumen microbiome is focused in amino acid metabolism and has less diverse functionalities, suggesting that these animals focus on nitrogen utilisation, which may be the underlying reason for the improved feed efficiency (Huws et al., 2018).

The hypothesis of this project is that, through an improved understanding the role of the rumen microbiome, and the linkages to RFI, dairy cows can be offered diets containing lower protein levels with minimal loss in milk production and with significant environmental benefits. The project aims to:

1. Use *in vitro* rumen-simulating techniques (RUSTITEC and Ankom systems) to assess the effects of varying dietary protein level on gas production, volatile fatty acids, methane production and the rumen microbes.

2. Assess the effects of varying protein feeding levels in a lactating dairy cow experiment on milk yield, milk composition (including fatty acid profiles), body condition, cow health, ration digestibility, and the rumen, buccal and faecal microbiome.

3. Investigate the use of metabolome proxies for nitrogen use efficiency and other production parameters, for example FTIR of dairy cow digesta, milk fatty acids etc. This experiment will be run over a full lactation enabling an assessment of long term effects of dietary protein inclusion on host parameters and the GI tract microbiome.

Consequently, this project encompasses animal science, microbiology and computational biology, skills which are desirable for a range of careers in the agricultural area.

Training opportunities:
Queen's University Belfast offers an array of courses available through the graduate school https://www.qub.ac.uk/graduate-school/. More specifically the student will spend time with the supervisor in Aberystwyth to gain training in in vitro technologies as well as metabolomics techniques. In addition, to facilitate sample collection at AFBI Hillsborough, the student will encouraged to undergo a course to obtain a personal license from the home office, such that they can handle and sample from the cows. These courses are run at least twice a year in AFBI. Prof Huws and Creevey will also provide training in sample preparation for metataxonomiy and metagenomic and subsequent analysis analysis. The student will also attend relevant courses outside both universities and present at least two national conferences and 1 international conference throughout the PhD and as outlined in the budget plan.

Student profile:
This project would be suitable for students with a degree in biology animal science, microbiology, computational biology or a closely related subject.

Funding Note
This project is part of the FoodBioSystems BBSRC Doctoral Training Partnership (DTP), it will be funded subject to a competition to identify the strongest applicants.
The studentship is open to UK and international students (including EU countries) however due to funding rules, no more than 30% of the projects can be allocated to international students.
The funding will include a tax free stipend (minimum £15, 285 per year), support for tuition fees at the standard UK rate (currently £4,407 per year) and a contribution towards research costs. **Please note** that the host

universities have not yet confirmed the level of fees charged to international students funded by the DTP. Fee levels may vary across the institutions. This information will be shared on the FoodBioSystems DTP website as soon as it becomes available.

To apply

Please go to FoodBioSystems DTP website for information on how to apply for this studentship. The closing date for applications will be 8 February 2021.

Key references

- Hristov et al. J Anim Sci. 2013 Nov;91(11):5045-69. doi: 10.2527/jas.2013-6583.
- Hristov et al. J Dairy Sci. 2019 Jul;102(7):5811-5852. doi: 10.3168/jds.2018-15829.
- Huws et al. Front Microbiol. 2018 Sep 25;9:2161. doi: 10.3389/fmicb.2018.02161.
- Foskolos and Moorby. 2018 Aug 2;13(8):e0201638. doi: 10.1371/journal.pone.0201638.
- Yáñez-Ruiz et al. Front Microbiol. 2015 Oct 14;6:1133. doi: 10.3389/fmicb.2015.01133.