PhD Project Advertisement

Project title: How and why do rumen bacteria talk to each other?
Project No: FBS2024-064-Huws-qa

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Project description:

Background:

Ruminants provide an important source of protein and micronutrients for human consumption and health with demand rising due to increases in World population and an increased demand from the Asian continent. In parallel, ruminants are also a contributor to climate change, with agriculture as a whole contributing to around 18% of agricultural greenhouse gases, mainly in the form of eructated methane coming produced by rumen methanogens. Indeed, ruminants possess a complex specialised four-compartment forestomach. The rumen, the primary fermentative compartment, harbouring a dynamic ecosystem comprising bacteria, protozoa, fungi, archaea (containing the methanogens), and bacteriophage, primarily benefiting the host animal by deriving energy from plant material breakdown.

The microbes which inhabit the rumen, and many other ecosystems in nature, often exist in close communities and they envelop themselves in an extacellular polymeric matrix, such that they exist in what is often termed as the 'biofilm' more of existence. Existence as a biofilm affords many evolutionary advantages to the microbes in terms of their ability to coordinate behaviour and survive in a largely hostile environment. In terms of enabling coordinated behaviour, we know that bacteria within a biofilm are densely packed and can often communicate to each other in order to coordinate behaviour via mechanisms such as quorum sensing. Quorum sensing (QS is a density-dependent signalling mechanism involving the release of autoinducer (AIs) compounds which can affect bacterial function, ecology, biofilm dynamics etc. The AIs used in QS are classified as mainly being N-acyl-homoserine lactones (AHL); commonly used by Gram-negative bacteria) or Autoinducer-2 based systems (AI-2; used by Gram-positive and Gram-negative bacteria); although other less common AI systems exist. Most of our understanding of QS comes from bacterial pathogens, with much being unknown on a commensal bacterial and ecosystem level, especially in the context of the rumen microbiome. A small number of studies have explored QS within the rumen bacteria, revealing a prevalence of AI-2 QS systems. Indeed, the lead supervisor has published 2 papers showing that AI-2 based QS systems are prevalent in the rumen microbiome and that these systems are most abundant in the dominant rumen bacteria Prevotella, Butyrivibrio and Pseudobutyrivibrio (Won et al., 2020). We have also published metatranscriptome data tracking the colonization of perennial ryegrass by rumen microbes over time, with the resultant data suggesting that these chemicals may influence transitions in bacterial diversity during colonization, likely through promoting competitive behaviour (Huws et al., 2020).

Objectives:

This is an exciting project as we now have the baseline data on QS chemical communication in the rumen and our aim is to go beyond describing the existence of AI-2 based QS in the rumen to a more fundamental understanding of how these chemicals are transmitted and the consequences of such mechanisms on microbial function, ecological interactions, ability to form biofilms and ultimately their ability to effectively degrade plant material and provide energy to the host. We will also look at mechanisms of transfer of these chemicals from one organism to the next, especially with respect to forming membrane vesicles, in which the supervisory team have vast expertise. These aims are summarised in these project objectives:

1. Identify AI-2 target genes using genomics, transcriptomics and bioinformatics i.e those affected directly by AI-2

signal molecule binding to the receptor site.
2. Understand the consequences of QS on gene regulation to confirm correlations with suspected target genes outlined in 1, using in vitro incubations with and without the QS inhibitor chemical.
3. To investigate mechanisms of transfer of QS signals via membrane vesicles. We will isolate membrane vesicles using our own standard operating procedures at peak times of AI-2 QS and use proteomic techniques to identify QS molecules in the membrane vesicles.

This project is fundamental in nature with the aim of using this data to ultimately improving the productivity and reducing the environmental impact of ruminant production .

Training opportunities:

Queen's University Belfast offers an array of courses available through the graduate school https://www.qub.ac.uk/graduate-school/ and it is expected that the student completes a minimum of 10 days training each year.

The student will spend time with the supervisor in Aberystwyth to gain training in proteomic techniques. The placement will take place in the latter part of the PhD when all samples are available. The student will also be encouraged to attend relevant courses outside both universities, attend and present at least two national conferences and 1 international conference throughout the PhD. The student will also be able to attend external training events as deemed appropriate.

Student profile:

The student should have a minimum of a 2.1 in animal science, microbiology, biochemistry or computational biology.

Stipend (Salary):

FoodBioSystems DTP students receive an annual tax free stipend (salary) that is paid in instalments throughout the year. For 2023/24 this is £18,622 and it will increase slightly each year at rate set by UKRI.

Equality Diversity and Inclusion:

The FoodBioSystems DTP is committed to equality, diversity and inclusion (EDI), to building a doctoral researcher(DR) and staff body that reflects the diversity of society, and to encourage applications from under-represented and disadvantaged groups. Our actions to promote diversity and inclusion are detailed on the FoodBioSystems DTP website.

In accordance with UKRI guidelines, our studentships are offered on a part time basis in addition to full time registration. The minimum registration is 50% FT and the studentship end date will be extended to reflect the part-time registration.

References:

Won et al. 2020. Microbiome. 8(1):23. doi: 10.1186/s40168-020-00796-y

Huws SA et al. (2021). Microbiome. 9(1):143. doi: 10.1186/s40168-021-01087-w

For up to date information on funding eligibility, studentship rates and part time registration, please visit the FoodBioSystems website.