

Enteric Fermentation Flagship Project: Profiling Rumen Microbiomes for Methane Emission Prediction in Bovine Species

Timothy P. Bilton¹, Paul Smith^{2,3}, Sinead M. Waters², Holly Flay⁴, Larissa Zetouni¹, John Roche⁵, Melanie K. Hess¹, Patricia L. Johnson¹, Hannah Henry¹, Juliana C. C. Budel^{1,6}, John C. McEwan¹, Gerlane Noronha⁶, Lorna R. McNaughton⁷, Pablo Peraza⁸, Elly A. Navajas⁸ and Suzanne J. Rowe¹

¹Invermay Agricultural Central, AgResearch, Mosgiel, NZ

²Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Dunsany, Ireland

³UCD, School of Agriculture and Food Science, University College Dublin Belfield, Dublin 4, Ireland

⁴DairyNZ Limited, Private Bag 3221, Hamilton, NZ

⁵School of Biological Sciences, University of Auckland, Private Bag 92019, Auckland, New Zealand

⁶Universidade Federal do Pará (UFPA), Graduate Program in Animal Science, Castanhal, Brazil

⁷Livestock Improvement Corporation, Private Bag 3016, Hamilton 3240, New Zealand

⁸Instituto Nacional de Investigación Agropecuaria (INIA), Estación Experimental Las Brujas, Canelones, Uruguay

The Enteric Fermentation Flagship project, funded by the Global Research Alliance, was initiated in 2018 to investigate rumen microbiomes to predict methane emissions in bovine species. A major objective of this project was to implement a low-cost, high-throughput method for profiling the rumen microbiome in bovine species across different production stages and systems used around the globe. The aim was to utilize this method for identifying and selecting low methane emitting animals while retaining or improving productivity. In this project, we implemented a protocol successfully tested and applied in sheep that utilizes freeze-dried rumen samples and restriction enzyme reduced representation sequencing for microbial sequencing to generate rumen microbiome profiles. To date, approximately 1015 rumen samples from Brazil (Buffalo), Ireland (Beef), New Zealand (Dairy/Beef) and Uruguay (Beef) have been collected and sequenced using this protocol. These samples were from animals across a diverse range of environments and production systems. Methane emission and feed intake were measured on 62% and 90% of the animals, respectively. We explored the variation in the rumen microbiome profiles across all samples and found large differences not only between countries but also between different systems within a country. Phenotype prediction was performed using a linear mixed model with a cohort-adjusted microbial relationship matrix as a random effect. We obtained prediction accuracies around 40%-60% for methane and 20%-30% for residual feed intake when predicting across cohorts. This work suggests that there is potential for using rumen microbiomes to predict important livestock traits in diverse production systems used around the world.