

# HoloRuminant – Understanding the rumen microbial colonisation of calves and its impact on performance

Michelle Stafford<sup>1,2</sup>, Paul Smith<sup>1</sup>, Sabine Scully<sup>1,3</sup>, Frank Buckley<sup>2</sup>, Sinead Waters<sup>1</sup> and David Kenny<sup>1</sup>

<sup>1</sup>Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath;

<sup>2</sup>School of Biological, Earth & Environmental sciences, Distillery Fields, North Mall, University College Cork, Cork; <sup>3</sup>UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4

## Summary

- The microbiome refers to any organisms such as viruses, bacteria and fungi that live within or on a living host. Examples of microbiome habitats include the skin, body cavities, and mucosal surfaces of respiratory, gastrointestinal, and urogenital tracts.
- Microbes within the rumen play a key role in the conversion of ingested feed into a source of energy and protein for ruminants. However, enteric methane is produced as a by-product of the microbial fermentation in the rumen.
- Understanding the temporal development and colonisation of the rumen of young calves, poses a potential avenue for the development of targeted probiotic and additive treatments aimed at increasing the productivity and sustainability of livestock production.

## HoloRuminant

HoloRuminant, an EU Horizons 2020-funded project, is a consortium of 25 organisations from 17 countries. As part of the project, Teagasc is working to uncover the development of microbiomes across various body sites of dairy cattle and apply that information towards more sustainable dairy production. Research is focused on the development of the microbiomes from early life through to first lactation. This aims to highlight the complexities and factors influencing colonization and maintenance of microbiomes, with relation to animal health, welfare and performance. Thus far, a comprehensive set of samples has been collected from spring-born Holstein-Friesian (HO) and Jersey (JE) 2022 and 2023 heifer calves at the Moorepark research farm. The samples collected will be analysed by meta-Taxonomics, exploring the bacteria, protozoa, fungi, and viruses present, to identify potential variation of microbiomes. This information can then be applied to enhance animal breeding and probiotic-based strategies, aimed at supporting the development of a healthier, more effective microbiome.

## Benchmark database of ruminant-associated microbes

Commensal microbes (these supply the host with essential nutrients and defend the host against opportunistic pathogens) have a positive contribution to the health and performance of cattle. In contrast, when microbial dysbiosis (disruption to the microbiome, causing an imbalance to the microbial community) occurs, pathogenic microbes can colonise the ruminant, and have adverse effects on animal health and contribute to the development of various diseases. An in-depth understanding of the temporal microbial establishment of the bovine neonatal gastro intestinal tract (GIT) is lacking. Overcoming this data void, and establishing the timing of the microbial colonisation of the calf, and sources where key microbes originate from, is crucial in the development of early life preventative measures. These measures aim to decrease the prevalence of pathogenic microbes and promote the establishment of a fully functional commensal microbiome.

## Enhancing dairy calf sustainability via early life manipulation of the rumen microbiome

The digestion of plant matter consumed by ruminant livestock is facilitated by members of a microbial ecosystem residing in the rumen (forestomach). The rumen, which is a specialised fermentation chamber, contains anaerobic bacteria, fungi and ciliate protozoa, all of which contribute to the efficient conversion of lignocellulolytic plant matter, into a source of energy and protein for the host (cow), which is subsequently utilised to produce high quality sources of dairy protein for human consumption. However, an additional group of rumen microbes, known as methanogens, are solely responsible for the production of enteric methane as a by-product of microbial fermentation. Indeed, enteric methane, which is recognised by the UN's International Panel on Climate Change (IPCC) as being 28-times more damaging to the environment than carbon dioxide, is responsible for 63.1% of Irish agricultural GHG emissions (EPA report, 2023). Due to its environmental potency, reducing the volume of methane produced by ruminant livestock is key to achieving a 25% reduction in agricultural GHG emissions, by 2030, in line with the national Climate Action Plan 2030.

Ruminal methanogenesis (methane producing process) is primarily influenced by host genetics and the diet, with previous work by Teagasc having identified the key rumen microbes associated with a high and low methane emissions phenotype. As part of previous work conducted by the EU funded projects Rumen-Predict and MASTER, low methane-emitting beef cattle were shown to have an increased abundance of bacteria associated with the production of lactic acid, and its subsequent conversion into the volatile fatty acid, propionate. More recently, early life manipulation of the rumen microbiome has been promoted as a promising strategy to reduce the abundance of microbes associated with a high methane emissions output. Further work conducted by researchers at Teagasc has identified that ruminant bacterial and archaeal communities stabilise by the third week of life. This research suggests this period is a good time to intervene and manipulate the microbiome. HoloRuminant aims to identify the sources where microbes originate from. This will allow for the identification of methods that could alter farm practices to reduce the prevalence and sources of pathogenic microbes, as well as those associated methane production and reduced animal productivity, on the farm and in the environment. This will allow for a preventative course of action, such as the administration of additives/probiotics to young calves, to be adopted in farm management to reduce potential disease incidence and promote more sustainable ruminant production.

### Conclusion

HoloRuminant aims to identify measures that could be applied to farm management practices in order to reduce the prevalence of pathogenic microbes on the farm. Through the administration of probiotics at identified time points a preventative approach could be adopted in order to reduce disease incidence and methanogenesis.

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