

**Rumen microbiome: Exploring the adaptive roles of viruses and bacteria in the rumen**

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Complex and diverse microbial communities mediate the cycling of nutrients within ruminants. The structure of this complex microbial community is shaped by the highly variable physical, chemical and predatory environment. In turn, the microbial community regulates the environment and nutrient cycling including the export of energy to the host in the form of volatile fatty acids. The diversity of the enteric microbial community is both ecologically and biochemically important. In addition to the important role of the rumen microbiome on its host, the anaerobic conversion of complex organic matter to methane in ruminants is an essential link in the global carbon cycle, and has a significant contribution towards global warming and climate change. However, our understanding of the rumen microbial community structure and function is in its infancy and we are just starting to understand microbial community structure within ruminants.

As a first attempt to better understand the influence of viruses on host bacterial populations, we investigated viral and total, microbial community structure and function using metagenomic shotgun sequencing under changing dietary conditions. When a shared read approach and protein clusters were used, the structure of total microbial communities significantly differed based on diet and host, while viral metagenomes differed only by diet. Using community level metabolic networks, we further explored why different diets enrich phage communities for specific metabolic pathways. Enzymes differentially abundant in the total metagenome and virome were more centrally located and a shorter path length compared to non-differential genes in the network. This ongoing work begins to suggest diet, rather than host factors, has a strong influence on the structuring of rumen phage populations and that phages encode for an adaptive repository of central metabolic functions related to selection pressures driven by altering environmental conditions. Current efforts are focused on better understanding what governs, why certain central metabolic genes are enriched and how this is related to the flow of information through metabolic networks.

**Keywords:** Bacteria, Microbiome, Phage, Rumen, Virome