

UNDERSTANDING THE IMPACT OF DIET, HOST GENETICS AND EARLY LIFE INTERVENTIONS ON RUMEN MICROBIOME

***Okpara M. O. and Ozuo U. K.**

Department of Animal Nutrition and Forage Science, Michael Okpara University of Agriculture,
Umudike, Nigeria

*Correspondence author's email: morganokpara@gmail.com

ABSTRACT

The rumen microbiome often considered as the ruminant's second genome, facilitates the transformation of low quality feeds into high quality protein food (meat and milk) and other valuable animal products. These microbes alter the ruminal environment and help produce substrates for the host's energy and body requirements. Several key factors influence rumen microbiota and fermentation, including diet, host genetics, and early life interventions. The potential to manipulate the rumen microbiome and meet global livestock challenges through animal breeding and introduction of dietary interventions during early life have recently emerged as promising new technologies. Advances in computational tools, high-throughput sequencing technologies and cultivation-independent "omics" approaches have provided profound insights into the rumen microbiome world, wherein a consortium of archaea, bacteria, protozoa, fungi, and viruses exist and interact. This will ultimately provide the knowledge framework needed to solve current and future ruminant livestock challenges. Understanding the effect of diet, host genetics, and early life interventions on the rumen microbiome is crucial for optimizing ruminant animal health, productivity, and efficiency of feed utilization while minimizing the environmental impact of ruminant production.

Keywords: host, metagenomics, microbes, performance, rumen

INTRODUCTION

The rumen is a complex ecosystem composed of anaerobic bacteria, protozoa, fungi, methanogenic archaea and phages. These microbes interact closely to breakdown plant material that cannot be digested by humans, whilst providing metabolic energy to the host and, in the case of archaea, producing methane (Huws *et al.*, 2018). Feed and husbandry practices, host genetics, early life interventions, age and environment have been identified as factors that affect variation of the ruminant microbiota (Zened *et al.* 2020). Although diet has been considered the main factor to drive the rumen microbiota shift, more and more evidence has highlighted the effect of the host's genetics and the composition and relationship with host phenotypes (Roehe *et al.*, 2016). A more recent study by Li *et al.* (2019) revealed the potential heritability of some rumen bacterial and archaeal taxa, providing further evidence that host genetics, together with dietary and environmental factors, drives the composition of rumen microbiota. The rumen microbiome is central to addressing the grand challenges facing agriculture globally. A better understanding of the factors that affect 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).

The rumen microbiome composition

The rumen microbiome refers to the diverse community of microorganisms, including bacteria, archaea, protozoa, fungi, and viruses, residing in the rumen (McCann *et al.*, 2014). These microorganisms play a vital role in breaking down and fermenting plant material that ruminants consume, aiding in the digestion and extraction of nutrients from cellulose and other fibrous components of their diet (Mizrahi, 2013). Bacteria (such as *Fibrobacter* spp, *Ruminococcus* spp, *Butyrivibrio* spp, *Prevotella* spp, *Bacteroides* spp, *Streptococcus* spp, *Lactobacillus* spp.) are the most abundant microorganisms in the rumen and are primarily responsible for fermenting and breaking down complex carbohydrates into simpler compounds (McSweeney and Mackie, 2012). They produce volatile fatty acids (VFAs), such as acetate, propionate, and butyrate, which serve as essential energy sources for the host animal. Protozoa (such as *Entodinium* spp., *Diplodinium* spp., *Isotricha* spp., *Ostracodinium* spp.) are single-celled organisms that aid in breaking down fibrous plant material by engulfing and digesting solid particles, particularly cellulose and starch. They also contribute to the

fermentation process and help in the degradation of complex carbohydrates (Coleman, 1986). Rumen Fungi such as (*Neocallimastix* spp., *Piromyces* spp., *Orpinomyces* spp.) assist in the breakdown of fibrous material, especially cellulose, through their ability to produce enzymes like cellulases and hemicellulases (Akin *et al.*, 1983). These enzymes break down complex plant cell walls into simpler compounds that can be further fermented by bacteria. Methanogenic archaea (e.g. *Methanobrevibacter* spp.) are responsible for producing methane gas as a byproduct of fermentation (Hook *et al.*, 2010). Viruses, specifically bacteriophages (viruses that infect bacteria), are indeed part of the rumen microbiome. These viruses play a significant role in shaping bacterial populations and influencing microbial dynamics within the rumen ecosystem. Bacteriophages infect and replicate within bacterial cells, leading to the lysis (bursting) of the bacteria, which releases viral progeny and further influences the composition and diversity of bacterial communities (Feiner *et al.*, 2015).

Factors affecting rumen microbiome

Diet

Different diets, including forage-based, grain-based, or mixed diets, have a profound impact on the rumen microbial community (Henderson *et al.*, 2015). Dietary components such as fiber content, carbohydrate sources, and protein levels influence the abundance and diversity of rumen microbes (Zened *et al.*, 2020). For instance, a shift from forage to grain-based diets can alter microbial populations, leading to changes in fermentation patterns and metabolite production within the rumen (Zened *et al.*, 2020). Fernando *et al.* (2010) reported rumen microbial community changes associated with a shift in dietary forage:concentrate from 60:40 to 40:60 (i.e., from higher forage to higher concentrate) and even greater changes when the diet was further shifted to 20:80. The predominantly forage-based diet had greater number of bacteria from the Fibrobacteres phylum and fewer from the Firmicutes and Bacteroidetes phyla. Also associated with this transition from a high forage to a high concentrate diet were increases in *Megasphaera elsdenii*, *Streptococcus bovis*, *S. ruminantium*, and *Prevotella bryantii*; these species have known roles in lactic acid utilization to stabilize ruminal pH and response to increased starch and decreased pH (Owens *et al.*, 1998). Fibrolytic bacteria, including *B. fibrisolvens* and *F. succinogenes*, tend to decrease with rising levels of dietary concentrate, further demonstrating bacterial differences in substrate preference (Cammack *et al.*, 2018). Ultimately, understanding how diet and dietary changes affect the rumen microbiome may lead to manipulation strategies to optimize performance and health during these inevitable transition periods in the ruminant livestock production cycle.

Host Genetics

Recent studies focused on the ruminal microbiota of cattle (Li *et al.*, 2019) and sheep (Rowe *et al.*, 2015) report the existence of genetic control of microbial communities. Hernandez-Sanabria *et al.* (2013) reported sire breed influences on particular microbial phylotypes (both bacterial and methanogenic) in progeny. Variation in rumen microbial communities was associated with breed differences in Holsten versus Jersey dairy cows (Paz *et al.*, 2016). Roehe *et al.* (2016) demonstrated a host genetic influence on rumen microbial activity and more specifically microbial metabolic activity related to methane production. Gonzalez-Recio *et al.* (2017) reported a strong association between the relative abundance of rumen microbes and the host genetic background, including both breed and single nucleotide polymorphism genotypes. Finally, Li *et al.* (2016) reported that the rumen microbiome of progeny of a sika deer × elk cross was different from either parental species, providing additional evidence of a host genetic association with the rumen microbiome. Taken together, these studies infer a host genetic association with microbiome characteristics and a potential for genetic selection based on these characteristics for a desired phenotype.

Early Life Interventions

Factors during early life, including diet during the neonatal phase, exposure to microbes, and management practices, can have long-lasting effects on the rumen microbiome (Arshad *et al.*, 2021). Unlike a developed rumen where a stable and resilient microbial community is established, during the development of the rumen after birth a succession of different microbial groups colonize and start occupying the different ecological niches (Huws *et al.*, 2018). The instability occurring during this period potentially allows for manipulation to assemble a specific community composition that persist later in life for better health and productivity within a given production system (Yáñez-Ruiz *et al.*, 2015). Colonization of the developing rumen begins immediately after birth and progresses through the first few months of life until a stable community establishes (Jami *et al.*, 2013). The rumen and its

microbiota changes throughout the first year of the calf's life as it grows, with various microbial groups beginning to occupy and colonize quickly. As the ruminant is weaned, this decreases *Actinobacteria*, which are essential early colonizers for converting milk components in the neonate's gut. On the other hand, fiber degrading *Bacteroidetes* and *Fibrobacteres* increase along with the replacement of milk with a total mixed ration (TMR), including grass silage (Amin *et al.*, 2021). This period of instability in the gastrointestinal tract during the process of weaning provides an opportunity for manipulation wherein supplements can be added to program the rumen microbiome development (Yáñez-Ruiz *et al.* 2015).

CONCLUSION

Diet, host genetics, and early life interventions all exert significant effects on the composition, diversity, and function of rumen microorganisms. Understanding the interplay between these factors is crucial for optimizing rumen health, nutrient utilization, and animal performance in ruminant livestock production systems. Further research is needed to elucidate the specific mechanisms underlying these effects and to develop targeted strategies for manipulating the rumen microbiota to improve animal productivity and sustainability.

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