

INFLUENCE OF GASTROINTESTINAL MICROBIOME ON RUMINANT PHENOTYPES: A REVIEW

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ABSTRACT

The microbiome, encompassing the diverse microbial communities in the gastrointestinal tract, plays a critical role in shaping the phenotypic characteristics of ruminants, influencing growth, metabolism, immunity, and overall health. Ruminants rely heavily on their microbiota for the efficient digestion of complex plant materials, and this symbiotic relationship has profound effects on traits such as feed conversion efficiency, milk production, and disease resistance. Recent research has highlighted the complex interactions between host genetics, microbial composition, and environmental factors in shaping ruminant phenotypes. Advances in metagenomics and microbiome profiling techniques have provided insights into the microbial taxa involved in key physiological processes. This review explores the mechanisms by which the gut microbiota influences animal performance, including its impact on digestive efficiency, metabolism, methane emission and immune function and disease susceptibility. Despite the promising advances in microbiome research, challenges remain in understanding the causal relationships between microbial communities and phenotypic outcomes. Future studies on integrating microbiome data with host genetics will provide actionable insights for enhancing ruminant health and productivity.

Keywords: Host microbe interactions, Microbial metagenomics, Microbiomes, Ruminants, Symbiosis.

INTRODUCTION

The gastrointestinal (GI) microbiome plays a fundamental role in shaping the health, productivity, and overall phenotype of ruminants (Schären *et al.*, 2018). Ruminants, such as cattle, sheep, and goats, have evolved a highly specialized digestive system that relies on complex microbial communities to process fibrous plant materials. These microorganisms, primarily residing in the rumen and intestines, are essential for efficient fermentation, nutrient absorption, and metabolic regulation (Cammack *et al.*, 2018). As ruminants rely on their microbiome for energy production, protein synthesis, and detoxification, disruptions in microbial composition or function can lead to significant changes in their phenotypic traits, including growth rate, feed efficiency, milk production, immune responses, and disease susceptibility (Cammack *et al.*, 2018). Recent advancements in metagenomic technologies and microbial profiling have deepened our understanding of the intricate relationship between the host and its microbial communities. Although it is increasingly recognized that the host ruminant-microbiome association, the holobiont, is the biological unit influencing the development, growth, health and environmental footprint of ruminants, there are a lack of high-resolution longitudinal studies investigating the links between GI microbiome establishment and phenotypes in ruminants. This review seeks to elucidate the role of GI microbiome in production efficiency, health and sustainability.

Rumen microbiome composition

The rumen is a complex, dynamic ecosystem composed of mainly anaerobic bacteria, protozoa, anaerobic fungi, methanogenic archaea and phages (Huws *et al.*, 2018). This microbial cohort contains cellulolytic, hemicellulolytic, amylolytic, proteolytic, and biohydrogenating (lipolytic) species, is capable of effectively degrading host-indigestible plant fiber (Firkins and Yu, 2015). Rumen bacteria is the most abundant, diverse, and metabolically active group (Deusch *et al.*, 2017) among other rumen microbes, accounting for approximately 50–70% of the rumen microbial population with 10¹⁰–10¹¹ bacterial cells per gram of rumen content (Newbold and Ramos-Morales, 2020). It is estimated that there are over 7000 species of bacteria representing over 19 diverse phyla in the rumen (Chaucheyras-Durand and Ossa, 2014). In the studies reported to date, *Firmicutes* and *Bacteroidetes* are consistently the most predominant phyla, followed by *Proteobacteria* in the ruminants (Hennessy *et al.*, 2020). Several groups of bacteria belonging to phyla, such as *Actinobacteria*, *Acidobacteria*, *Tenericutes*, *Spirochaetes*, and *Verrucomicrobia*, have been found in the rumen in lower populations. Several species from genera, such as *Ruminococcus*, *Butyrivibrio*, *Prevotella*, *Fibrobacter*, *Coprococcus*, *Porphyromonas*, and *Butyrivibrio*, constitute the core rumen microbiome. They have also been found across different gastrointestinal (GIT) segments (abomasum, duodenum, and rectum) (Khalil *et al.*, 2022).

Rumen archaea is composed largely of methanogenic archaea from the phylum Euryarchaeota and they are responsible for methane production in the rumen, which is then eructed and released to the environment. Methane is produced primarily via the hydrogenotrophic pathway (*Methanobrevibacter*) as a result of the

reduction of CO₂, and less so through the utilization of methyl groups, methylotrophic pathway (*Methanosarcinales*, *Methanospaera*, and *Methanomassiliicoccaceae*), or even less commonly from acetate via the acetoclastic pathway (*Methanosarcinales*) (Tapio *et al.*, 2017). Ruminants commonly harbor distinct protozoal populations from birth, with only minor changes in diversity throughout life, although the abundances of species fluctuate with changes in diet (Williams and Coleman, 1997). In an attempt to get consensus on the diversity of anaerobic fungi inhabiting the guts of herbivores, Paul *et al.* (2018) concluded that among the cultured genera, *Piromyces* was the most represented with *Buwchfawromyces* being the least represented in sequence data obtained from the Genbank database. Paul *et al.* (2018) also suggested that possibly another 25 new genera exist in the guts of herbivores, which remain uncharacterized. Bacteriophages, or phages, are viruses that infect bacteria in the rumen. Complete genome sequences for lytic phages, belonging to the order *Caudovirales*, capable of infecting *Bacteroides*, *Ruminococcus*, and *Streptococcus* have recently been obtained (Gilbert *et al.* 2017). While it's well established that phages significantly impact the ecology and evolution of microbial communities across various environments (Koskella and Brockhurst, 2014), the specific effects of phages on the rumen microbiome are still not fully understood and require further research to fully elucidate their role in this complex ecosystem.

Microbiome of lower gastrointestinal tract

In contrast to that of the rumen, the lower gut, also defined as the post-gastric intestinal tract, consists of both the small intestine and hindgut regions. The microbiome of the lower gut also play an important role, particularly in early life, feed efficiency and gut health. (Meale *et al.*, 2017). The post-ruminal microbial community is composed predominantly of bacteria, but methanogenic archaea and anaerobic fungi have been implicated (Davies *et al.*, 1993). There are significant differences in the microbial community assemblage depending on the region of the GI tract (i.e., rumen vs. post rumen; Zeng *et al.*, 2017), and the post rumen microbiota differ further between the small (duodenum, jejunum, and ileum) and the large (cecum, colon, and rectum) intestine (Yeoman *et al.*, 2018).

Influence of gastrointestinal microbiome on ruminant phenotype

The rumen microbiome play crucial role in the growth and feed efficiency of ruminant animals by converting low-quality, fibrous plant material into usable energy through microbial fermentation, primarily by producing volatile fatty acids (VFAs) which are absorbed by the animal as a primary energy source (Firkins and Yu, 2015). This leads to the production of volatile fatty acids (VFAs), such as acetate, propionate, and butyrate, major products of rumen microbial fermentation, which serve as the primary energy source for ruminants (Bergman, 1990). This symbiotic relationship allows ruminants to efficiently utilize forage-based diets, significantly impacting their overall growth and feed conversion efficiency. The GI microbiome has been shown to influence important traits such as weight gain, milk yield, fat deposition, and reproductive success (Dieterich *et al.*, 2018). The gastrointestinal microbiome plays a key role in modulating the immune system of ruminants. A balanced microbiome supports the development of mucosal immunity in the gut, offering protection against pathogens. Dysbiosis (microbial imbalance) can lead to increased susceptibility to diseases such as bloat, acidosis, and other gastrointestinal disorders (Wang *et al.*, 2023). A healthy microbiome also influences the regulation of systemic immunity, affecting how the animal responds to infections, vaccinations, and stressors, all of which can influence phenotype in terms of health, longevity, and productivity (Li *et al.*, 2025).

One of the well-known impacts of the gastrointestinal microbiome on ruminant phenotype is the production of methane during fermentation in the rumen. Methanogenic archaea in the rumen produce methane as a byproduct of digesting plant material, and this methane is released by the animal through belching. Hydrogenotrophic methanogenesis is the predominant pathway in the rumen and is carried out mainly by *Methanobrevibacter* species, which typically account for more than 90% of archaeal 16S rRNA gene reads (Hristov *et al.*, 2012), though several other less abundant methanogen species are also found in the rumen (Tapio *et al.*, 2017). The amount of methane produced varies significantly between individual ruminants, influenced by the microbial community composition. Methane emission has both economic and environmental implications, as it represents an energy loss for the animal and a greenhouse gas emission. Therefore, the microbiome also influences the animal's environmental impact, with implications for breeding strategies aimed at reducing methane production.

In dairy ruminants, the microbiome has a profound effect on milk yield and composition. Metabolism of nitrogen-containing compounds (including peptides, ammonia, and urea) by the rumen microbiota is also vital in the provision of microbial proteins to the host for muscle and milk synthesis (Bach *et al.*, 2005). The fermentation process in the rumen affects the synthesis of milk precursors like fatty acids, proteins, and lactose. Changes in the microbiome can impact the fatty acid composition in milk, influencing its quality (e.g., fat content and unsaturated fatty acid profile) (Bach *et al.*, 2005).

CONCLUSION

The gastrointestinal microbiome profoundly influences ruminant phenotype by affecting digestion, nutrient absorption, immune function, methane production, and other metabolic processes. The microbial communities in the rumen interact with the host in complex ways, and their composition can be shaped by genetic,

environmental, and dietary factors. Advances in microbiome research hold the potential to optimize ruminant production systems by selecting for desirable microbiome profiles that improve feed efficiency, health, and reduce environmental impact. Understanding these relationships is critical for breeding and management strategies that aim to enhance ruminant productivity in sustainable ways.

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