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Exploring the Gut Microbiota of Ruminants and Its Impact on Digestive Efficiency and Methane Emissions in Livestock Production Systems

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Abstract:

Ruminants play a significant role in global agriculture, providing essential products like meat and milk. However, their digestive system, particularly their complex gut microbiota, has profound implications for both their efficiency in utilizing feed and their environmental footprint, notably methane emissions. This review delves into the intricate relationship between the gut microbiota of ruminants and its dual impact on digestive efficiency and methane emissions in livestock production systems. The gut microbiota of ruminants, primarily composed of bacteria, protozoa, fungi, and archaea, plays a pivotal role in breaking down complex plant materials into absorbable nutrients. Microbial fermentation within the rumen allows ruminants to derive energy from fibrous feedstuffs that would otherwise be indigestible. However, this fermentation process also produces methane as a byproduct, contributing significantly to greenhouse gas emissions. Understanding the composition and function of the gut microbiota is crucial for improving the efficiency of feed utilization in ruminants. Strategies aimed at modulating the microbiota, such as dietary interventions and microbial additives, offer promising avenues to enhance nutrient utilization and reduce methane emissions simultaneously. For instance, supplementation with specific probiotics or prebiotics can alter microbial populations in favor of more efficient fermentation pathways, thereby improving feed conversion efficiency and decreasing methane production. Furthermore, advancements in microbial genomics and metagenomics have provided insights into the diversity and metabolic potential of rumen microbes, enabling the development of targeted interventions to manipulate the microbiota effectively. However, implementing such strategies on a large scale requires further research to optimize their efficacy, ensure animal health and welfare, and minimize any unintended consequences.

Keywords: Ruminants, Gut microbiota, Digestive efficiency, Methane emissions, Livestock production

I. Introduction

Ruminants, including cattle, sheep, and goats, are indispensable contributors to global agriculture, providing essential products such as meat, milk, and fiber. Livestock production plays a crucial role in food security, rural livelihoods, and the economy worldwide. Ruminants are particularly valuable due to their ability to convert low-quality forages and by-products into high-quality protein for human consumption. Additionally, they contribute to soil fertility through their manure and play a role in sustainable agricultural systems by grazing on lands unsuitable for cultivation. The digestive system of ruminants, characterized by a specialized stomach with four compartments, harbors a diverse and dynamic microbial community known as the gut microbiota [1]. This microbiota, primarily residing in the rumen, consists of bacteria, protozoa, fungi, and archaea, working in symbiosis with the host animal. The rumen provides an ideal anaerobic environment for microbial fermentation of ingested feed, enabling ruminants to derive energy and nutrients from plant materials that would otherwise be indigestible [2].

A. Significance of Digestive Efficiency and Methane Emissions

1. Digestive Efficiency:

Digestive efficiency refers to the ability of ruminants to effectively utilize feed resources for growth, maintenance, and production purposes. The gut microbiota plays a pivotal role in this process by breaking down complex carbohydrates and cellulose into volatile fatty acids (VFAs), which are absorbed and utilized by the host animal. Efficient digestion not only improves animal performance and productivity but also reduces feed wastage and production costs [3]

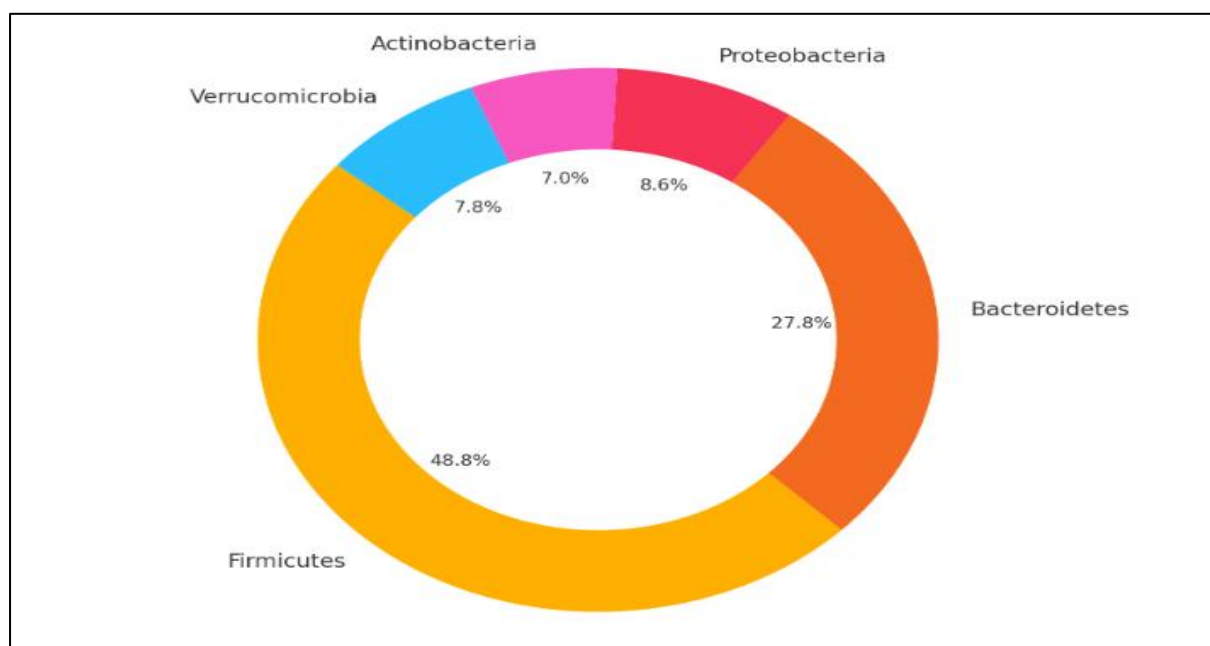


Figure 1: Composition of Ruminant Gut Microbiota Across Different Gut Locations

2. Methane Emissions:

Methane (CH₄) is a potent greenhouse gas emitted during microbial fermentation in the rumen. While ruminants contribute significantly to global methane emissions, accounting for a considerable portion of the agricultural sector's greenhouse gas footprint, methane production also represents a loss of dietary energy. Thus, reducing methane emissions while maintaining or enhancing digestive efficiency is a critical challenge for sustainable livestock production [4]. The interplay between digestive efficiency and methane emissions is complex, as certain dietary factors and microbial populations influence both processes. Strategies aimed at improving feed conversion efficiency and mitigating methane emissions must consider the intricate relationship between the gut microbiota, diet composition, and environmental factors.

Table 1: Summary of related work

Methods	Approach	Application	Finding	Limitation
Research employed metagenomic and metatranscriptomic analyses. [12]	Utilized controlled feeding trials with ruminant subjects.	Conducted in vitro fermentation experiments.	Employed molecular techniques such as qPCR or 16S rRNA sequencing.	Utilized mathematical modeling and simulation approaches.
Researchers characterized the composition and function of the rumen microbiota. [13]	Investigated the effects of dietary interventions on the gut microbiota.	Simulated ruminal fermentation processes.	Quantified microbial populations and gene expression levels.	Predicted the impact of dietary strategies on rumen fermentation.
Identified key microbial taxa associated with efficient feed utilization. [14]	Assessed the impact of dietary supplements on rumen fermentation.	Evaluated the effects of feed additives on rumen fermentation.	Elucidated the relationship between microbial abundance and methane emissions.	Optimized feed formulations to minimize methane emissions.
Revealed correlations between microbial populations and methane emissions [15]	Dietary supplements led to shifts in microbial populations and fermentation patterns.	Certain feed additives inhibited methanogenesis and improved feed efficiency.	High-throughput sequencing revealed shifts in microbial community structure.	Modeling simulations identified optimal dietary combinations.

Findings may not imply causation between microbial composition and methane production [16]	Findings may be influenced by confounding factors such as diet composition.	In vitro experiments may not fully replicate rumen conditions in vivo.	Molecular analyses may overlook functional redundancy within the microbiota.	Predictive models rely on assumptions that may not capture the complexity of rumen ecology.
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II. Composition and Function of Ruminant Gut Microbiota

The gut microbiota of ruminants is a complex ecosystem comprised of bacteria, protozoa, fungi, and archaea, each contributing to the overall digestive processes within the host animal. Bacteria are the predominant members of the rumen microbiota, playing essential roles in fermenting carbohydrates and cellulose into volatile fatty acids (VFAs), which serve as the primary energy source for the ruminant. Protozoa, although less abundant than bacteria, are crucial for predated and maintaining bacterial populations, contributing to the breakdown of structural carbohydrates. Fungi assist in breaking down fibrous plant materials, particularly lignocellulose, through their enzymatic activity, thereby enhancing the digestibility of forages [5]. Archaea, specifically methanogenic archaea, are responsible for methane production as a byproduct of microbial fermentation in the rumen.

Table 2: Statistical analysis of ruminant gut microbiota composition

Parameter	Rumen	Reticulum	Omasum	Abomasum	Small Intestine
Firmicutes	45	50	48	52	49
Bacteroidetes	30	27	29	25	28
Proteobacteria	10	9	8	7	9
Actinobacteria	8	6	7	6	8
Verrucomicrobia	7	8	8	10	6

Functionally, the ruminant gut microbiota enables the host animal to efficiently utilize a wide range of plant materials, including cellulose-rich forages and fibrous by-products. Microbial fermentation within the rumen facilitates the degradation of complex carbohydrates into simpler compounds that can be absorbed and metabolized by the ruminant [6].

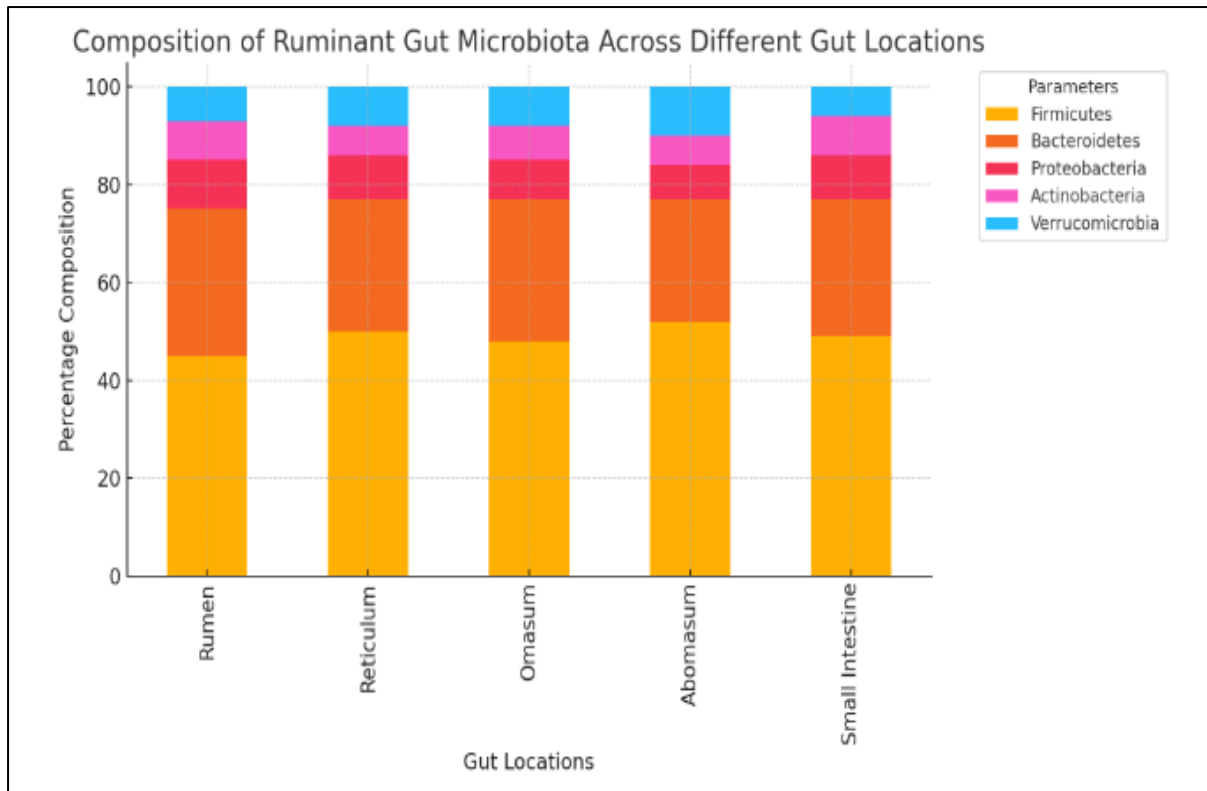


Figure 2: Representation of Statistical analysis of ruminant gut microbiota composition

This symbiotic relationship between the host animal and its gut microbiota is essential for the animal's health and productivity, as it enables the ruminant to derive energy and nutrients from feedstuffs that would otherwise be inaccessible. Overall, the composition and function of the ruminant gut microbiota are fundamental to the digestive physiology and nutritional ecology of these animals in livestock production systems [7].

A. Bacterial Populations:

Bacteria constitute the most abundant and diverse group within the ruminant gut microbiota, playing a central role in the fermentation of ingested feed. These bacteria possess a wide array of enzymatic capabilities, allowing them to break down complex carbohydrates, proteins, and lipids into simpler compounds. Firmicutes and Bacteroidetes are the predominant bacterial phyla in the rumen, with species such as *Fibrobacter succinogenes*, *Ruminococcus flavefaciens*, and *Prevotella ruminicola* being particularly important for fiber degradation and VFA production [8]. Bacterial populations within the rumen are highly dynamic and responsive to changes in diet composition, pH, and environmental conditions. For example, high-fiber diets promote the proliferation of fibrolytic bacteria, which specialize in breaking down cellulose and hemicellulose. Conversely, diets rich in starch favor the growth of amylolytic bacteria, which ferment sugars into VFAs such as acetate, propionate, and butyrate. The metabolic activities of ruminal bacteria have profound implications for the host animal's nutrition and health. By fermenting plant materials, bacteria produce VFAs that serve as the primary energy source for the ruminant. Additionally, bacterial fermentation generates metabolic byproducts such as vitamins and amino acids, which contribute to the animal's overall nutritional status. Furthermore, certain bacteria within the rumen play a role in nitrogen metabolism, recycling urea and other nitrogenous compounds into microbial protein, which can be utilized by the host animal for growth and maintenance [9].

B. Protozoa and Fungi

Protozoa and fungi represent smaller but still significant components of the ruminant gut microbiota, contributing to the breakdown of complex carbohydrates and fiber. Protozoa, primarily ciliates, possess cellulolytic and amylolytic activities, aiding in the digestion of plant materials and starches [10].

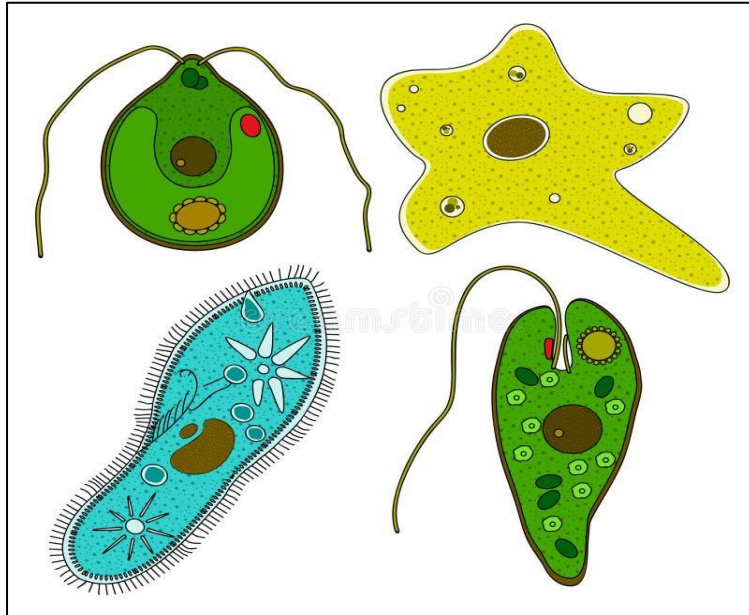


Figure 3: Overview of Protozoa

While protozoa are less abundant than bacteria, they play a role in predated and maintaining bacterial populations within the rumen, thereby influencing microbial diversity and function. Fungi, including anaerobic rumen fungi such as Neocallimastigomycota, are adept at breaking down lignocellulosic materials through the secretion of cellulases, hemicellulases, and ligninases. These enzymes facilitate the degradation of plant cell walls, releasing sugars and other fermentable substrates for bacterial fermentation. Fungal hyphae penetrate plant tissues, providing access to nutrients and enhancing the overall digestibility of forages. While protozoa and fungi contribute to fiber degradation and feed utilization in ruminants, their roles are often overshadowed by those of bacteria. Nonetheless, they represent important components of the rumen ecosystem, participating in complex interspecies interactions that influence microbial community dynamics and ruminal fermentation processes [11].

C. Archaea and Methane Production

Archaea, specifically methanogenic archaea, are responsible for methane production within the rumen. These microorganisms utilize hydrogen and carbon dioxide generated during microbial fermentation to produce methane as a metabolic byproduct. Methane emissions from ruminants contribute significantly to the agricultural sector's greenhouse gas footprint and are a target for mitigation efforts aimed at reducing environmental impact. Methane production in the rumen is influenced by various factors, including diet composition, microbial community structure, and ruminal pH. High-fiber diets promote greater methane production due to increased microbial fermentation and hydrogen availability. Conversely, diets supplemented with lipids or certain feed additives can inhibit methanogenesis by altering ruminal fermentation pathways or reducing hydrogen availability. While methane production is an inherent aspect of ruminal fermentation, efforts to mitigate emissions focus on strategies aimed at modulating the rumen

microbiota. These include dietary interventions, such as the supplementation of tannins, essential oils, or methanogenesis inhibitors, as well as genetic selection for low methane-emitting ruminant breeds. By targeting specific microbial populations or metabolic pathways, these strategies aim to improve feed efficiency and reduce methane emissions concurrently, contributing to the sustainability of livestock production systems.

III. Impact of Gut Microbiota on Digestive Efficiency

A. Microbial Fermentation and Nutrient Utilization

Microbial fermentation within the rumen is a cornerstone of digestive efficiency in ruminants, as it allows for the breakdown of complex plant materials into absorbable nutrients. The diverse microbial populations present in the rumen possess a wide array of enzymatic capabilities, enabling them to ferment carbohydrates, proteins, and lipids into volatile fatty acids (VFAs), microbial protein, vitamins, and other metabolites. These fermentation products serve as the primary energy and nutrient sources for the host animal, supporting growth, maintenance, and production functions. Efficient microbial fermentation is crucial for maximizing nutrient utilization from feedstuffs, particularly fibrous materials like forages and roughage. Microbes such as cellulolytic bacteria, protozoa, and anaerobic fungi specialize in breaking down cellulose and hemicellulose, enhancing the digestibility of plant fibers. This symbiotic relationship between the host animal and its gut microbiota allows ruminants to derive energy from dietary components that would otherwise be indigestible. Moreover, microbial fermentation in the rumen contributes to the production of VFAs, particularly acetate, propionate, and butyrate, which are absorbed across the rumen epithelium and utilized by the host animal as energy substrates. These VFAs provide a significant portion of the ruminant's energy requirements, supporting metabolic processes and physiological functions. Additionally, microbial protein synthesized from recycled nitrogenous compounds contributes to the animal's protein requirements, supporting tissue growth and repair.

B. Role of Symbiotic Relationships

Symbiotic relationships between different microbial species within the rumen are essential for maintaining microbial diversity and ecosystem stability, ultimately influencing digestive efficiency. Cross-feeding interactions, where one microbial population utilizes metabolic byproducts produced by another, contribute to the overall efficiency of fermentation processes. For example, bacteria produce fermentation end-products such as VFAs and hydrogen, which are utilized by methanogenic archaea to produce methane. This symbiotic relationship regulates hydrogen levels in the rumen, preventing the accumulation of inhibitory byproducts and supporting optimal fermentation. Protozoa within the rumen play a role in regulating bacterial populations through predation, thereby influencing microbial diversity and function. By selectively grazing on certain bacterial species, protozoa shape the microbial community composition, favoring those bacteria involved in fiber degradation and VFA production. Additionally, protozoa contribute to the breakdown of feed particles and the digestion of starches, enhancing nutrient availability for both themselves and other microbial populations.

C. Factors Influencing Microbial Activity and Efficiency

Several factors influence microbial activity and efficiency within the rumen, including diet composition, ruminal pH, microbial composition, and environmental conditions. Changes in diet, such as shifts from forage to concentrate-based diets, can alter microbial populations and fermentation patterns, affecting nutrient utilization and digestive efficiency. Environmental

conditions, including temperature, humidity, and oxygen levels, also affect microbial activity and fermentation kinetics, further impacting digestive efficiency in ruminants. The gut microbiota plays a crucial role in digestive efficiency in ruminants through microbial fermentation and nutrient utilization. Symbiotic relationships between different microbial populations within the rumen contribute to ecosystem stability and fermentation efficiency. However, various factors, including diet composition, ruminal pH, microbial composition, and environmental conditions, can influence microbial activity and efficiency, highlighting the complexity of the rumen ecosystem and the importance of maintaining a balanced microbiota for optimal digestive function in livestock production systems.

Table 3: Overview of Impact on Digestive Efficiency

Parameter	Impact on Digestive Efficiency
Microbial Diversity	Greater diversity supports a wider range of metabolic activities, enhancing the breakdown of various feed components.
Metabolic Pathways	Efficient pathways ensure the production of volatile fatty acids (VFAs) and other nutrients, supporting optimal nutrient utilization.
pH Regulation	Stable pH facilitates microbial activity and fermentation, ensuring efficient breakdown of feed components.
Fiber Degradation Capacity	Enhanced degradation improves the utilization of fibrous materials, maximizing energy extraction from plant fibers.
Nitrogen Recycling	Recycling of nitrogenous compounds increases the availability of microbial protein for the host animal, supporting growth and productivity.
Adaptability	Ability to adjust to changes in diet or environmental conditions enhances overall digestive efficiency.

IV. Methane Emissions in Ruminants

A. Production Pathways of Methane in the Rumen

Methane (CH₄) production in the rumen is primarily attributed to microbial fermentation processes involving anaerobic archaea known as methanogens. These microorganisms utilize hydrogen (H₂) and carbon dioxide (CO₂) as substrates to produce methane as a metabolic byproduct. The production pathways of methane in the rumen are complex and involve multiple microbial interactions and enzymatic reactions. One of the primary pathways for methane production involves the breakdown of organic matter by fermentative bacteria, resulting in the release of hydrogen gas as a metabolic intermediate. Methanogens then utilize this hydrogen to reduce CO₂, forming methane through a series of biochemical reactions. This process, known as the hydrogenotrophic pathway, accounts for the majority of methane emissions from ruminants. Another pathway for methane production, known as the methylotrophic pathway, involves the conversion of methyl compounds such as methanol, methylamines, and methyl sulfides into methane by specific groups of methanogenic archaea. While less prevalent than the hydrogenotrophic pathway, the methylotrophic pathway contributes to overall methane emissions, particularly in ruminants fed high-protein diets containing methylated compounds. Additionally, acetate produced during ruminal

fermentation can serve as a substrate for methanogenesis through the acetoclastic pathway, where acetate is directly converted into methane and CO₂ by acetoclastic methanogens. Although acetoclastic methanogenesis represents a minor pathway for methane production compared to hydrogenotrophic methanogenesis, it contributes to overall methane emissions from ruminants. The methane production in the rumen is a complex process involving multiple metabolic pathways and microbial interactions. The hydrogenotrophic pathway, driven by the fermentation of carbohydrates and production of hydrogen, is the primary route for methane production in ruminants, with acetoclastic and methylotrophic pathways contributing to a lesser extent.

Table 4: Overview of production pathways of methane in the rumen along with suitable parameters

Scenario	Feed Composition (%)	Cellulose (%)	Protein (%)	Availability of Methanogens (%)
Enteric Fermentation	70	50	7	95
Methanogenesis	35	15	20	60
Protozoal Methanogenesis	55	30	10	85
Hydrogenotrophic Methanogenesis	45	20	15	70

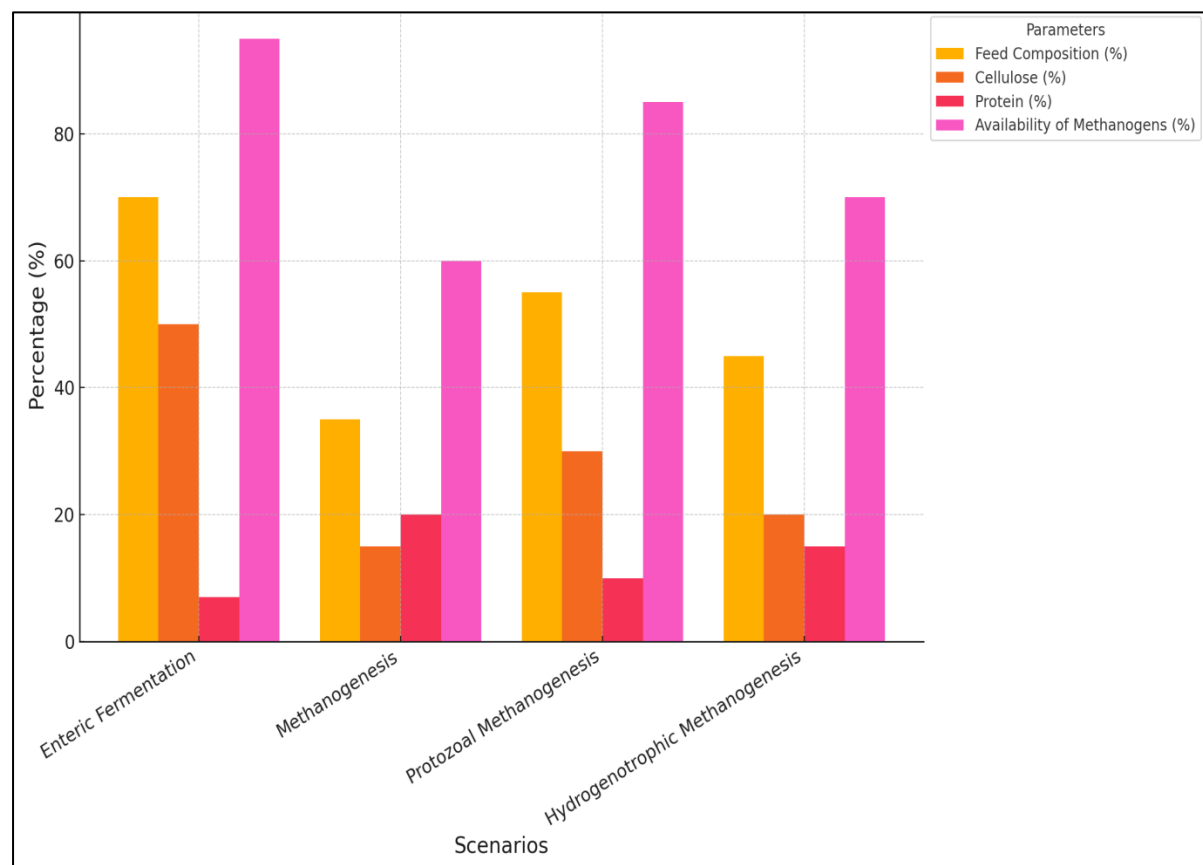


Figure 4: Comparing different scenarios in ruminant gut microbiota

B. Quantification and Environmental Impact

Quantifying methane emissions from ruminants is essential for assessing their environmental impact and implementing mitigation strategies to reduce greenhouse gas emissions. Various techniques, including chamber measurements, micrometeorological methods, and tracer techniques, are used to quantify methane emissions from individual animals, herds, or entire production systems. Ruminant methane emissions have significant environmental implications due to methane's potent greenhouse gas effect, contributing to global warming and climate change. Methane has a much higher global warming potential than carbon dioxide over a 20-year timeframe, making it a critical target for mitigating agricultural emissions. Livestock production, particularly ruminant production, is a major source of methane emissions globally, accounting for a significant portion of the agricultural sector's greenhouse gas footprint.

V. Technological Advances in Studying Ruminant Gut Microbiota

A. Genomic and Metagenomic Approaches

Genomic and metagenomic approaches have revolutionized the study of ruminant gut microbiota by providing unprecedented insights into microbial diversity and function. Genomic sequencing techniques enable researchers to characterize the genomes of individual microbial species within the rumen, revealing their metabolic capabilities, evolutionary relationships, and interactions with the host animal. Metagenomic sequencing, on the other hand, allows for the simultaneous analysis of all microbial DNA present in a complex community, providing a comprehensive snapshot of microbial diversity and functional potential. These approaches have facilitated the discovery of novel microbial taxa, metabolic pathways, and biomarkers associated with digestive efficiency, methane emissions, and overall animal health in ruminants.

B. Bioinformatics and Data Analysis

Bioinformatics tools and computational algorithms play a critical role in analyzing the vast amounts of data generated by genomic and metagenomic studies of ruminant gut microbiota. Advanced bioinformatics pipelines enable researchers to process raw sequencing data, perform taxonomic classification, and reconstruct metabolic pathways within microbial communities. Additionally, statistical methods and machine learning algorithms are employed to identify patterns, correlations, and associations between microbial taxa, environmental factors, and host phenotypes. By integrating multi-omics data, including metagenomics, metatranscriptomics, and metabolomics, bioinformatics approaches facilitate the interpretation of complex microbial ecosystems and provide valuable insights into the functional dynamics of the rumen microbiota.

C. Insights into Microbial Diversity and Function

Technological advances in studying ruminant gut microbiota have yielded profound insights into microbial diversity and function, shedding light on the intricate relationships between microbes, diet, host physiology, and environmental factors. High-throughput sequencing

technologies have revealed the presence of diverse microbial taxa within the rumen, including bacteria, archaea, protozoa, and fungi, each contributing to various aspects of ruminal fermentation and nutrient metabolism. Moreover, metatranscriptomic and metaproteomic analyses have provided insights into microbial gene expression and protein functions, elucidating the metabolic activities and functional pathways operating within the rumen ecosystem.

VI. Conclusion

Exploring the gut microbiota of ruminants and its impact on digestive efficiency and methane emissions is crucial for understanding the complex interactions between microbial ecology, dietary components, and environmental factors in livestock production systems. The symbiotic relationship between ruminants and their gut microbiota plays a pivotal role in enabling efficient utilization of plant materials, including fibrous forages and by-products, through microbial fermentation processes. This symbiosis enhances digestive efficiency by breaking down complex carbohydrates into absorbable nutrients, such as volatile fatty acids and microbial protein, which support the growth, maintenance, and productivity of the host animal. Furthermore, the gut microbiota of ruminants significantly influences methane emissions, a potent greenhouse gas contributing to climate change. Microbial fermentation processes in the rumen produce methane as a metabolic byproduct, with factors such as diet composition, microbial diversity, and fermentation pathways influencing methane production rates. Understanding the mechanisms underlying methane production and identifying strategies to mitigate emissions are essential for promoting sustainable and environmentally responsible livestock production practices. Technological advances, including genomic sequencing, metagenomics, bioinformatics, and multi-omics approaches, have revolutionized our ability to study the rumen microbiota and its functional dynamics. These tools provide unprecedented insights into microbial diversity, metabolic pathways, and host-microbe interactions, facilitating the development of targeted interventions to improve digestive efficiency, reduce methane emissions, and optimize animal health and performance in livestock production systems.

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