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Adaptive Mechanisms of Rumen Microbiota to High-Fiber Diets: Mystery of Fiber Degradation and Nutrient Utilization for Improved Host Performance

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Abstract

The rumen microbiota plays a critical role in the digestion of plant fibers, enabling herbivores to derive essential nutrients from fibrous feed sources. The adaptation of these microbial communities to high-fiber diets is crucial for optimizing fiber degradation and nutrient utilization. This study explores the mechanisms by which rumen microbes adjust to handle the complex structure of fibrous materials such as cellulose, hemicellulose, and lignin. Through an integrated approach, we examine key processes such as the upregulation of cellulolytic and fibrolytic bacteria, enzymatic production, shifts in microbial diversity, and the role of fungi in breaking down lignocellulosic compounds. Additionally, we explore microbial interactions, such as cross-feeding between fiber-degrading bacteria and methanogens, and how these symbiotic relationships enhance fermentation efficiency. The study highlights how microbial biofilm formation and buffering compounds protect against the acidic by-products of fermentation, supporting sustained microbial activity. Moreover, we investigate microbial–host interactions, focusing on how the rumen microbiota influences nutrient absorption and overall host performance. Understanding these adaptive mechanisms provides valuable insights into improving livestock nutrition, particularly under conditions of high-fiber feeding. By enhancing fiber fermentation, these microbial adaptations contribute to improved energy production, optimal nutrient absorption, and overall animal performance, offering potential strategies for more efficient and sustainable livestock management.

Keywords: Adaptation, biofilm formation, cellulolytic bacteria, enzymatic activity, fiber degradation, microbial diversity, microbial–host interaction

INTRODUCTION

The rumen microbiota is integral to the efficient digestion of fibrous plant materials, which are otherwise indigestible by the host [1, 2]. High-fiber diets, rich in cellulose, hemicellulose, and lignin, present a challenge for rumen microbes due to the complex and recalcitrant nature of these compounds [3, 4]. The microbial communities in the rumen have evolved numerous strategies to degrade these fibrous components, enabling herbivores to access the energy stored in plant cell walls [5, 6]. These mechanisms include the upregulation of specific microbial populations capable of breaking down fiber and the production of various enzymes like cellulases, xylanases, and lignases [7]. The adaptability of the rumen microbiota to such challenging feedstuffs ensures continued nutrient availability for the host animal.

As fiber fermentation is a complex process involving various microbial species, understanding how the rumen microbiota adapts to high-fiber diets is crucial for optimizing feed utilization [8]. Studies

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have highlighted several microbial strategies, including the increased presence of cellulolytic bacteria, fungi, and other microorganisms that work synergistically to enhance fiber breakdown [9, 10]. The production of volatile fatty acids (VFAs), the primary energy source for the host, depends on efficient microbial activity, which is influenced by changes in microbial composition, enzymatic production, and interactions within the rumen ecosystem [11, 12]. Furthermore, the ability of the rumen microbiota to produce buffering compounds and adjust to changes in pH is essential for maintaining an environment conducive to fermentation.

The novelty of this study lies in its comprehensive examination of the adaptive mechanisms of the rumen microbiota to high-fiber diets. While previous research has focused on individual microbial processes or specific fiber-degrading microbes, this study integrates various aspects of microbial adaptation, including enzymatic activity, microbial population shifts, biofilm formation, and the interplay between fiber-degrading bacteria and methanogens. By exploring these factors collectively, this study provides a holistic understanding of how rumen microbes optimize fiber degradation and nutrient utilization. The insights gained from this research have important implications for improving livestock feed efficiency and sustainability, contributing to the development of more efficient and cost-effective feeding strategies.

INCREASED CELLULOLYTIC BACTERIA

In response to high-fiber diets, the population of cellulolytic bacteria in the rumen, particularly species, such as Ruminococcus and Fibrobacter, significantly increases [1, 13]. These bacteria play a crucial role in the breakdown of complex plant fibers, such as cellulose and hemicellulose, which are major components of fibrous feed. The enzymes produced by these bacteria, including cellulases and hemicellulases, break down the long-chain polysaccharides into simpler sugars that can be further fermented by other microbial groups [14, 15]. As fiber content in the diet rises, these bacteria thrive by adapting to the increased substrate availability. Their enhanced activity facilitates more efficient fiber degradation, leading to the production of volatile fatty acids (VFAs) like acetate, propionate, and butyrate, which are utilized by the host animal for energy [15]. The shift in microbial population towards fiber-degrading bacteria thus enables more effective utilization of fibrous materials, supporting the animal's nutritional requirements while improving rumen health.

Enhanced Enzymatic Activity

In response to high-fiber diets, microbial enzymes, such as cellulases, xylanases, and amylases, are upregulated to efficiently degrade the complex carbohydrates present in fibrous feed [2, 16]. Cellulases are primarily responsible for breaking down cellulose, a major component of plant cell walls, into simpler sugars like glucose. Xylanases target hemicellulose, another structural polysaccharide, while amylases act on starches found in certain fibrous materials. The increased production of these enzymes allows rumen microbes to effectively decompose tough plant fibers, converting them into fermentable sugars that can be further metabolized [8, 17–20]. This enzymatic activity is crucial for improving the overall digestibility of fibrous feeds, leading to greater production of volatile fatty acids (VFAs), such as acetate, propionate, and butyrate, which provide energy to the host animal. The upregulation of these enzymes in response to fiber intake enhances the efficiency of rumen fermentation and nutrient utilization.

Microbial Population Shifts

High-fiber diets induce significant microbial population shifts in the rumen, promoting the growth of specific bacteria and fungi that are specialized in fiber fermentation [9, 21–23]. These microbes, including cellulolytic bacteria like Ruminococcus and Fibrobacter, and fiber-degrading fungi, are particularly adept at breaking down complex carbohydrates such as cellulose and hemicellulose into simpler compounds [8, 20]. As fiber intake increases, these microbes become more abundant, allowing for more efficient fermentation of plant materials. The breakdown of fiber results in the production of volatile fatty acids (VFAs), such as acetate, propionate, and butyrate, which serve as primary energy sources for the host animal. Additionally, the shift in microbial composition helps maintain rumen pH and improves fiber digestion efficiency. This adaptive response not only enhances the overall fermentation process but also supports the animal's nutritional needs by increasing the digestibility of otherwise indigestible fiber.

Adaptation of Microbial Diversity

As animals consume higher levels of fiber, the rumen microbiome adapts by becoming more diverse, allowing it to handle the increased availability of complex fiber components [8, 24]. This increased microbial diversity includes a broader range of bacteria, fungi, and protozoa that specialize in the degradation of various fibrous substrates [12]. Each group of microbes contributes differently to fiber breakdown, with some bacteria focusing on cellulose degradation, while others specialize in breaking down hemicellulose, lignin, or starch. The expanded microbial diversity enhances the rumen's ability to ferment a variety of fibrous materials, optimizing the release of fermentable sugars and other metabolites [25–27]. This diversity also supports the production of volatile fatty acids (VFAs), which are essential for providing energy to the host animal. Furthermore, a diverse microbiome improves the rumen's resilience to changes in diet and environmental conditions, ensuring efficient fermentation and better overall digestion of fiber-rich feeds.

FUNGI INVOLVEMENT

Fungi, particularly Neocallimastix, play an increasingly vital role in the breakdown of lignin and cellulose in the rumen, especially on high-fiber diets [28]. These fungi produce a range of enzymes, including cellulases and lignases, that enable them to break down the complex plant cell wall components, such as cellulose and lignin, which are otherwise resistant to microbial degradation [29]. Neocallimastix and other rumen fungi degrade the lignocellulosic matrix of plant fibers, liberating fermentable sugars that are then further processed by other microorganisms [30]. Their ability to degrade lignin, which is structurally challenging for bacteria, is particularly crucial for enhancing fiber digestion. This fungal activity contributes to the overall efficiency of fiber fermentation, leading to the production of volatile fatty acids (VFAs) that provide energy to the host animal [31]. The increased presence of these fungi in response to fiber intake ensures more complete fiber breakdown, improving nutrient availability and enhancing the rumen's overall digestive capacity.

Synthesis of Hydrolytic Enzymes

The increased synthesis of hydrolytic enzymes in response to high-fiber diets plays a crucial role in the breakdown of lignocellulosic compounds, which are key components of plant cell walls. These enzymes, such as cellulases, hemicellulases, and lignases, are produced by rumen microbes, including bacteria, fungi, and protozoa, to degrade complex carbohydrates like cellulose, hemicellulose, and lignin [17]. Cellulases target cellulose, breaking it down into glucose, while hemicellulases act on hemicellulose to release xylose and other sugars. Lignases are essential for breaking down lignin, a highly resistant compound that binds the fiber structure [32]. The synthesis of these enzymes is upregulated as fiber intake increases, allowing the rumen microbiota to effectively process tough plant materials [33, 34]. This enzymatic breakdown releases fermentable sugars, which are further metabolized into volatile fatty acids (VFAs) that provide energy to the host animal. The enhanced production of these hydrolytic enzymes thus improves fiber digestion efficiency and nutrient utilization.

Alteration of Microbial Metabolites

Alteration of microbial metabolites occurs as a result of metabolic shifts within the rumen microbiota in response to high-fiber diets [10]. As fiber is fermented, the microbial communities adapt by increasing the production of short-chain fatty acids (SCFAs), particularly acetate and butyrate. These SCFAs are critical end products of fiber fermentation and serve as major energy sources for the host animal. Acetate, produced primarily by cellulolytic bacteria, is utilized by the animal for fat synthesis and energy storage [35]. Butyrate, produced by both cellulolytic bacteria and fungi, supports the health of the rumen epithelium and provides energy for cell regeneration [36]. The increased production of these metabolites indicates a more efficient breakdown of fiber, enhancing overall fermentation [37]. This metabolic shift not only improves the digestibility of complex fibrous feeds but also contributes to the host's energy balance, promoting better growth, reproduction, and overall health. Thus, these altered metabolic pathways optimize fiber utilization in the rumen.

Microbial Adaptation to pH Changes

Microbial adaptation to pH changes is a key mechanism for maintaining efficient fermentation on high-fiber diets. As fiber is fermented in the rumen, the process produces volatile fatty acids (VFAs), which acidify the rumen environment, causing the pH to decrease. This lower pH can be detrimental to many microbes, but certain rumen microorganisms have adapted to tolerate more acidic conditions [38]. These adapted microbes, including acid-tolerant bacteria like Lactobacillus and Prevotella, are able to maintain their metabolic activity in the more acidic rumen environment, ensuring continued fermentation of fiber. These microbes often produce buffering compounds or modify their internal pH to counteract the acidity. As a result, the fermentation process remains efficient, leading to consistent production of VFAs, such as acetate, propionate, and butyrate, which are essential for energy production in the host. This microbial adaptation to pH fluctuations enables the rumen to effectively process high-fiber diets without compromising overall fermentation efficiency.

Increased Efficiency of Fiber Utilization

Increased efficiency of fiber utilization occurs as the rumen microbiota adapts to high-fiber diets, optimizing the fermentation process to release more energy from fibrous feeds. This adaptation involves a combination of enhanced microbial activity, including the upregulation of fiber-degrading enzymes and shifts in microbial populations that are specialized for fiber fermentation [17, 39, 40]. As a result, more of the fiber in the diet is broken down into fermentable sugars, which are then converted into volatile fatty acids (VFAs), primarily acetate, propionate, and butyrate. These VFAs are utilized by the host animal for energy production. Additionally, the microbes increase their ability to adhere to fiber particles and maintain prolonged fermentation, further improving the breakdown of fiber [41–43]. This enhanced efficiency allows the host to derive more energy from fibrous feeds, improving overall feed conversion and supporting better growth, milk production, and reproduction in ruminants. Therefore, microbial adaptation leads to greater energy yield from fiber-rich diets, enhancing the animal's nutritional status.

IMPROVED FIBER ADHERENCE

Improved fiber adherence is a crucial adaptation by rumen microbes to enhance the fermentation and breakdown of fibrous feed. As animals consume more fiber, microbes evolve mechanisms that enable them to more effectively adhere to fiber particles, such as the production of extracellular polymeric substances (EPS), that create a sticky biofilm around the fibers [44]. This biofilm allows microbes to remain attached to the fiber surface for longer periods, ensuring continuous fermentation. The enhanced adherence improves the contact between microbes and fiber particles, allowing for more thorough breakdown of complex carbohydrates like cellulose and hemicellulose [45, 46]. As a result, fiber is degraded more efficiently, releasing fermentable sugars that can be converted into volatile fatty acids (VFAs) like acetate, propionate, and butyrate, which provide energy to the host. This adaptation supports prolonged fermentation in the rumen, optimizing fiber utilization and improving overall energy extraction from fibrous feeds.

Cross-Feeding Among Microbes

Cross-feeding among microbes plays a critical role in enhancing fiber degradation in the rumen. As different microbial species, such as cellulolytic bacteria, fungi, and protozoa, work together, they transfer breakdown products like sugars, amino acids, and other metabolites [47]. For example, cellulolytic bacteria break down complex fibers into simpler sugars, which can then be utilized by other microbial species like lactate-producing bacteria or methanogens [4]. This collaborative metabolic process improves overall fermentation efficiency, ensuring that more of the fiber is broken down into volatile fatty acids (VFAs), which provide energy to the host animal [48–50]. Cross-feeding interactions optimize nutrient utilization by promoting synergy among microbial communities, facilitating more complete digestion of fibrous materials.

Strain-Specific Adaptations

Strain-specific adaptations refer to the unique evolutionary adjustments made by individual microbial strains to better utilize fiber, thus enhancing the overall fiber degradation capacity of the rumen. These adaptations can involve the production of specialized enzymes, such as more efficient cellulases, hemicellulases, or lignases, that break down complex plant fibers into simpler, fermentable sugars [9, 11, 51]. Some strains may also evolve to tolerate the lower pH environments created by increased fiber fermentation, enabling them to continue their activity in more acidic conditions. Additionally, certain strains may develop mechanisms to adhere more effectively to fiber particles, ensuring prolonged fermentation and breakdown. These strain-specific traits allow for a more efficient microbial ecosystem, optimizing fiber utilization in the rumen. As a result, the animal benefits from increased energy production in the form of volatile fatty acids (VFAs), improving overall nutrient absorption, growth, and performance.

Microbial Scavenging of Ammonia

Microbial scavenging of ammonia is an important adaptation in the rumen, especially when animals consume high-fiber diets. As fiber is fermented, microbes break it down into simpler compounds, leading to the production of ammonia, a by-product of protein and nitrogen metabolism. Elevated ammonia levels can be detrimental to the rumen environment, affecting microbial health and overall fermentation efficiency [35, 52, 53]. To counteract this, certain microbial strains have evolved mechanisms to better utilize or detoxify ammonia, thereby improving nitrogen balance. These microbes, such as Ruminococcus and Prevotella, are capable of incorporating ammonia into microbial protein through assimilation pathways, reducing its accumulation in the rumen. Additionally, other microbes may convert ammonia into less toxic compounds like urea, which is absorbed and processed by the liver. By efficiently managing ammonia levels, these microbes help maintain a stable rumen environment, support optimal fermentation, and enhance protein utilization, ultimately improving the animal's nitrogen balance and overall performance.

Increased Biofilm Formation

Increased biofilm formation is a key adaptation by rumen microbes that enhances fiber digestion efficiency. Biofilms are complex layers of microbial cells and extracellular polymeric substances (EPS) that adhere to the surface of fiber particles in the rumen. These biofilms provide several benefits to the microbial community. They allow microbes to remain attached to fiber surfaces for longer periods, increasing the time available for fermentation and breakdown of fibrous materials like cellulose and hemicellulose [54–56]. This prolonged attachment improves the microbial degradation of complex carbohydrates, leading to more complete fermentation. Furthermore, biofilm formation protects microbes from harsh rumen conditions, such as low pH and competition for substrates, ensuring continuous microbial activity. The biofilm also serves as a barrier, facilitating the efficient transfer of breakdown products, such as sugars and amino acids, between microbes. This enhanced interaction supports optimal fiber digestion and promotes the production of volatile fatty acids (VFAs), which provide energy to the host animal.

SYMBIOTIC RELATIONSHIPS

Symbiotic relationships between fiber-degrading bacteria and methanogens play a crucial role in enhancing fiber fermentation efficiency in the rumen. Fiber-degrading bacteria, such as Ruminococcus and Fibrobacter, break down complex carbohydrates like cellulose and hemicellulose into simpler compounds, producing hydrogen gas (H_2) as a by-product of fermentation [10]. This hydrogen production creates an opportunity for cooperation with methanogens, a group of archaea that use hydrogen to reduce carbon dioxide (CO_2) into methane (CH_4) [51]. In this symbiotic relationship, methanogens consume the excess hydrogen produced by fiber fermenters, preventing hydrogen accumulation, which could inhibit microbial fermentation. In turn, the methane produced by methanogens is expelled from the rumen, helping to maintain a stable rumen environment [57–59]. This cooperation enhances the efficiency of fiber digestion by optimizing hydrogen utilization and supporting continuous fermentation, ultimately improving energy production in the form of volatile fatty acids (VFAs) for the host animal.

Adapting to Slow Digestion

Adapting to slow digestion involves changes in microbial populations that allow the rumen microbiota to effectively process tough, fibrous material over extended periods. High-fiber diets, such as those rich in cellulose and lignin, require slower fermentation rates due to the complex and resistant nature of these plant materials [60, 61]. To accommodate this, certain microbial species evolve mechanisms that enhance their ability to degrade fibers more gradually. For example, cellulolytic bacteria and fungi adapt by producing more efficient enzymes and extending their fermentation activity to break down cellulose and lignin over longer timescales. Additionally, these microbes may form biofilms on fiber particles, maintaining prolonged contact with the fibrous material [62]. The slower fermentation rate allows for a more steady and sustained release of fermentable sugars, which are then converted into volatile fatty acids (VFAs). This adaptation optimizes nutrient release and energy production, ensuring efficient digestion even with fibrous and less readily digestible feed.

Higher Rumen Motility

Higher rumen motility plays a key role in optimizing fiber fermentation by enhancing the mixing and contact between fiber particles and microbial populations. As fiber-rich diets are consumed, the rumen undergoes changes in motility to facilitate more efficient digestion. Increased rumen contractions help to mix the ingested feed more thoroughly, ensuring that fiber particles are evenly distributed throughout the rumen and come into closer contact with the microorganisms responsible for fermentation [63]. This enhanced mixing improves microbial access to fibrous materials, promoting more efficient breakdown of complex carbohydrates such as cellulose and hemicellulose. Additionally, improved motility helps prevent fiber particles from settling and promotes their movement towards the areas of the rumen where microbial populations are most active. The overall effect is a more uniform and prolonged fermentation process, leading to better nutrient breakdown and the production of volatile fatty acids (VFAs), which provide energy for the host animal.

Production of Buffering Compounds

Production of buffering compounds is an essential adaptation by rumen microbes to manage the increased acidity resulting from fiber fermentation. As fibrous materials like cellulose and hemicellulose are broken down, volatile fatty acids (VFAs) such as acetate, propionate, and butyrate are produced, leading to a decrease in rumen pH. To counteract this acidity, certain microbes have developed mechanisms to produce buffering compounds, including bicarbonates and organic acids [30, 64–67]. These buffers neutralize excess hydrogen ions, stabilizing the rumen environment and preventing a drop in pH that could hinder microbial function. By maintaining a more neutral pH, these adapted microbes ensure that fiber fermentation can continue efficiently without disrupting the overall microbial ecosystem. The increased buffering capacity not only supports microbial activity but also prevents the occurrence of ruminal acidosis, promoting optimal fiber degradation and enhancing the production of volatile fatty acids (VFAs), which are vital for the host animal's energy supply.

SELECTION OF FIBROLYTIC STRAINS

Selection of fibrolytic strains is a crucial mechanism by which the rumen microbiota adapts to high-fiber diets. As animals consume more fibrous feed, natural selection favors the proliferation of microbial strains with enhanced fibrolytic capabilities. These fibrolytic strains, including specific bacteria, fungi, and protozoa, are more efficient in breaking down complex fibrous materials such as cellulose, hemicellulose, and lignin into simpler, fermentable sugars [9, 66, 68–70]. Over time, strains that produce more effective enzymes, such as cellulases and xylanases, are selected for, as they facilitate the breakdown of tough plant fibers. This selective pressure ensures that the microbial community becomes better suited to handle high-fiber diets, improving the overall efficiency of fiber fermentation. The increased abundance of these fibrolytic strains leads to higher production of volatile fatty acids (VFAs), providing more energy for the host animal, and optimizing nutrient utilization from fibrous feed sources.

Microbe–Host Interaction Adjustments

Microbe–host interaction adjustments involve the adaptation of rumen microbes to optimize their relationship with the host, thereby improving nutrient absorption and enhancing fermentation efficiency. As the rumen microbiota evolves to handle high-fiber diets, certain microbial strains strengthen their interactions with the host's digestive system. This adaptation may involve the production of specific metabolites, such as volatile fatty acids (VFAs), that are directly absorbed by the host for energy. Additionally, microbes may secrete enzymes that help break down complex carbohydrates into simpler sugars, which are more easily absorbed by the host's intestinal cells [2, 7, 10, 71]. Some microbes also enhance the host's ability to absorb nutrients by influencing the structure and function of the rumen epithelium, increasing surface area for absorption. Furthermore, these microbes may affect the host's immune system, promoting a balanced immune response that supports healthy digestion. Overall, these adjustments improve the fermentation process, increase energy production from fiber, and optimize nutrient absorption, benefiting the host animal's health and performance.

CONCLUSION

The adaptive mechanisms of rumen microbiota to high-fiber diets play a critical role in optimizing fiber degradation and enhancing nutrient utilization for the host. The upregulation of cellulolytic and fibrolytic microorganisms, along with the production of specific enzymes, enables the efficient breakdown of complex fibers. Additionally, microbial interactions, biofilm formation, and the ability to adapt to pH fluctuations contribute to sustained fermentation activity. The insights from this study underscore the importance of microbial diversity and adaptability in ensuring optimal fiber digestion. Understanding these mechanisms provides valuable knowledge for improving livestock nutrition, promoting better feed utilization, and contributing to more sustainable and efficient livestock farming practices.

Future Direction

Future research should focus on further unraveling the specific microbial strains and enzymes responsible for the degradation of various fiber types in the rumen, with particular attention to the genetic and biochemical pathways involved. Investigating the role of fungi and other non-bacterial microorganisms in fiber breakdown could offer insights into enhancing fiber fermentation efficiency. Moreover, exploring the interaction between microbial populations and host physiology, including how microbial shifts influence gut health and nutrient absorption, warrants deeper investigation. Understanding the impact of different high-fiber diets on rumen microbiota adaptation across various livestock species would provide valuable information for species-specific feeding strategies. Additionally, the development of targeted microbial inoculants or feed additives designed to optimize fiber degradation and improve fermentation efficiency holds potential for enhancing livestock productivity. Finally, integrating omics technologies, such as metagenomics and metabolomics, could provide a comprehensive understanding of microbial adaptation and its effects on overall animal performance.

REFERENCES

1. Shi H, Guo P, Wang Z, Zhou J, He M, Shi L, et al. Cellulase enhancing rumen microbiome of Tan sheep indicates plastic responses to seasonal variations of diet in the typical steppe. BMC Microbiol. 2025 Mar 18;25(1):154. doi: 10.1186/s12866-025-03799-7.
2. Pu G, Hou L, Zhao Q, Liu G, Wang Z, Zhou W, et al. Interactions between gut microbes and host promote degradation of various fiber components in Meishan pigs. mSystems. 2025 Feb 18;10(2): e01500–24. doi: 10.1128/msystems.01500-24.
3. Li T, Raja BR, Liao J, Zheng L, Yin F, Gan S, et al. The characteristics, influence factors, and regulatory strategies of growth retardation in ruminants: A review. Front Vet Sci. 2025 Mar 26;12:1566427. doi: 10.3389/fvets.2025.1566427.
4. Wang F, Xie B, Ji H, Xia J, Hao Y, Cao Z, et al. Temporal modulation of duodenal microbiota in dairy cows: Effects of dietary shift from high forage to high concentration. Front Vet Sci. 2025 Apr 4;12:1551327. doi: 10.3389/fvets.2025 .1551327.

5. Wang Y, Yin X, Hao K, Wang C, Wei W, Li Y, et al. Consumption of steam explosion and fermentation-pretreated corn stover affects the growth performance of sheep by shifting the rumen microbiota community structure. Front Microbiol. 2025 Apr 3;16:1532746. doi: 10.3389/fmicb.2025.1532746.
6. Wang S, Kong F, Dai D, Li C, Hao Y, Wang E, et al. Deterministic succession patterns in the rumen and fecal microbiome associate with host metabolic shifts in peripartum dairy cattle. GigaScience. 2025;14:giaf042. doi: 10.1093/gigascience /giaf042.
7. Fu R, Han L, Li Q, Li Z, Dai Y, Leng J. Studies on the concerted interaction of microbes in the gastrointestinal tract of ruminants on lignocellulose and its degradation mechanism. Frontiers in Microbiology. 2025 May 9;16:1554271. [Online]. Available: https://pmc.ncbi.nlm.nih.gov/articles/PMC12098361/.
8. Li B, Jia G, Wen D, Zhao X, Zhang J, Xu Q, et al. Rumen microbiota of indigenous and introduced ruminants and their adaptation to the Qinghai–Tibetan plateau. Front Microbiol. 2022 Oct 10;13: 1027138. doi: 10.3389/fmicb.2022.1027138.
9. Zhu W, Chang L, Shi S, Lu N, Du S, Li J, et al. Gut microbiota reflect adaptation of cave-dwelling tadpoles to resource scarcity. ISME J. 2024 Jan 1;18(1):wrad009. doi: 10.1093/ismejo/wrad009.
10. Chen Q, Sha Y, Liu X, He Y, Chen X, Yang W, et al. Unique rumen micromorphology and microbiota–metabolite interactions: Features and strategies for Tibetan sheep adaptation to the plateau. Front Microbiol. 2024 Oct 9;15:1471732. doi: 10.3389/fmicb.2024.1471732.
11. Hu B, Wang J, Li Y, Ge J, Pan J, Li G, et al. Gut microbiota facilitates adaptation of the plateau zokor (Myospalax baileyi) to the plateau living environment. Front Microbiol. 2023 Feb 24;14: 1136845. doi: 10.3389/fmicb.2023.1136845.
12. Zhao J, Yao Y, Dong M, Xiao H, Xiong Y, Yang S, et al. Diet and high altitude strongly drive convergent adaptation of gut microbiota in wild macaques, humans, and dogs to high altitude environments. Front Microbiol. 2023 Feb 23;14:1067240. doi: 10.3389/fmicb.2023 .1067240.
13. Chang S, Ma Y, Cheng Y, Kong X, Li H, Li C, et al. Mannan oligosaccharides enhance rumen cellulose degradation by modulating microbial composition and glycoside hydrolase expression. J Biotech Res. 2024;19:230–41 . Available: https://www.btsjournals.com/assets/2024v19p230-241.pdf
14. Liang Y, Wang F, Jia R, Li J, Wang L, Li Y, et al. Cellulase activity and age-based variation of intestinal microbiota in Hezuo pigs. Front Microbiol. 2025 May 9;16:1599847. doi: 10.3389/fmicb.2025.1599847.
15. Weimer PJ, Waghorn GC, Odt CL, Mertens DR. Effect of diet on populations of three species of ruminal cellulolytic bacteria in lactating dairy cows. J Dairy Sci. 1999;82(1):122–34. doi: 10.3168 /jds.S0022-0302(99)75216-1.
16. Zhang Y, Wang Y, Wanyan R, Yao B, Tan Z, Wang R, et al. The influence of multi-generational high-fiber diet on the gut microbiota of root voles (Microtus oeconomus). 2024 Aug. doi: 10.21203/rs.3.rs-4858686/v1.
17. Ran T, Saleem AM, Shen Y, Ribeiro GO Jr, Beauchemin KA, Tsang A, et al. Effects of a recombinant fibrolytic enzyme on fiber digestion, ruminal fermentation, nitrogen balance, and total tract digestibility of heifers fed a high forage diet. J Anim Sci. 2019 Jul 30;97(8):3578–87. doi: 10.1093/jas/skz216.
18. Miccoli FE, Pérez CD, Vargas-Bello-Perez E, Danelón JL, Cantet JM, Martínez R, et al. Effects of high fiber energy supplements on production performance, milk composition and milk fatty acid profile from dairy ewes fed fresh cut Lolium multiflorum. Small Rumin Res. 2022 Apr 1;209:106640. doi: 10.1016/j.smallrumres.2022.106640.
19. Le Sciellour M, Labussière E, Zemb O, Renaudeau D. Effect of dietary fiber content on nutrient digestibility and fecal microbiota composition in growing-finishing pigs. PLoS One. 2018 Oct 24;13(10):e0206159. doi: 10.1371/journal .pone.0206159.
20. Baniel A, Amato KR, Beehner JC, Bergman TJ, Mercer A, Perlman RF, et al. Seasonal shifts in the gut microbiome indicate plastic responses to diet in wild geladas. Microbiome. 2021 Jan 23;9(1):26. doi: 10.1186/s40168-020-00977-9.

21. Zhao X, Zhang Y, Rahman A, Chen M, Li N, Wu T, et al. Rumen microbiota succession throughout the perinatal period and its association with postpartum production traits in dairy cows: A review. Anim Nutr. 2024 Sep 1;18:17–26. doi: 10.1016/j.aninu.2024.04.013.
22. Li K, Shi B, Na R. The Colonization of Rumen Microbiota and Intervention in Pre-Weaned Ruminants. Animals. 2023;13(6). doi: 10.3390/ani13060994.
23. Hu C, Ding L, Jiang C, Ma C, Liu B, Li D, et al. Effects of management, dietary intake, and genotype on rumen morphology, fermentation, and microbiota, and on meat quality in yaks and cattle. Front Nutr. 2021 Nov 11;8:755255. doi: 10.3389/fnut.2021.755255.
24. Fan Q, Cui X, Wang Z, Chang S, Wanapat M, Yan T, et al. Rumen microbiota of Tibetan sheep (Ovis aries) adaptation to extremely cold season on the Qinghai-Tibetan Plateau. Front Vet Sci. 2021 May 25;8:673822. doi: 10.3389/fvets.2021.673822.
25. Zou H, Li Q, Liu J, Wang X, Gao Q, Yang Y, et al. Fecal microbiota reveal adaptation of herbivores to the extreme environment of the Qinghai–Tibet Plateau. Grassl Res. 2024 Jun;3(2):155–70. doi: 10.1002/glr2.12075.
26. Wang Y, Zhou R, Yu Q, Feng T, Li H. Gut microbiome adaptation to extreme cold winter in wild plateau pika (Ochotona curzoniae) on the Qinghai-Tibet Plateau. FEMS Microbiol Lett. 2020 Aug;367(16):fnaa134. doi: 10.1093/femsle/fnaa134.
27. Xiao K, Liang X, Lu H, Li X, Zhang Z, Lu X, et al. Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. ISME J. 2022 Aug;16(8):1980–92. doi: 10.1038/s41396-022-01247-2.
28. Yan XT, Yan BY, Ren QM, Dou JJ, Wang WW, Zhang JJ, et al. Effect of slow-release urea on the composition of ruminal bacteria and fungi communities in yak. Anim Feed Sci Technol. 2018 Oct 1;244:18–27. doi: 10.1016/j.anifeedsci.2018 .07.016.
29. Liang Z, Zhang J, Ahmad AA, Han J, Gharechahi J, Du M, et al. Forage lignocellulose is an important factor in driving the seasonal dynamics of rumen anaerobic fungi in grazing yak and cattle. Microbiol Spectr. 2023 Oct 17;11(5):e00788–23. doi: 10.1128 /spectrum.00788-23.
30. Xue F, Nan X, Sun F, Pan X, Guo Y, Jiang L, et al. Metagenome sequencing to analyze the impacts of thiamine supplementation on ruminal fungi in dairy cows fed high-concentrate diets. AMB Express. 2018 Oct 3;8(1):159. doi: 10.1186/s13568-018-0680-6.
31. Langda S, Zhang C, Zhang K, Gui B, Ji D, Deji C, et al. Diversity and composition of rumen bacteria, fungi, and protozoa in goats and sheep living in the same high-altitude pasture. Animals (Basel). 2020 Jan 22;10(2):186. doi: 10.3390/ani10020186.
32. Li M, Zi X, Yang H, Ji F, Tang J, Lv R, et al. Effects of king grass and sugarcane top in the absence or presence of exogenous enzymes on the growth performance and rumen microbiota diversity of goats. Trop Anim Health Prod. 2021 Mar;53(1):106. doi: 10.1007/s11250-020-02544-8.
33. Kala A, Kamra DN, Kumar A, Agarwal N, Chaudhary LC, Joshi CG. Impact of levels of total digestible nutrients on microbiome, enzyme profile and degradation of feeds in buffalo rumen. PLoS One. 2017 Feb 16;12(2):e0172051. doi: 10.1371/journal.pone.0172051.
34. Song SD, Chen GJ, Guo CH, Rao KQ, Gao YH, Peng ZL, et al. Effects of exogenous fibrolytic enzyme supplementation to diets with different NFC/NDF ratios on the growth performance, nutrient digestibility and ruminal fermentation in Chinese domesticated black goats. Anim Feed Sci Technol. 2018 Feb 1;236:170–7. doi: 10.1016/j .anifeedsci.2017.12.008.
35. Phungviwatnikul T, Lee AH, Belchik SE, Suchodolski JS, Swanson KS. Weight loss and high-protein, high-fiber diet consumption impact blood metabolite profiles, body composition, voluntary physical activity, fecal microbiota, and fecal metabolites of adult dogs. J Anim Sci. 2022;100(2). doi: 10.1093/jas/skab379.
36. Wang Y, Zhao Y, Tang X, Nan X, Jiang L, Wang H, et al. Nutrition, gastrointestinal microorganisms and metabolites in mastitis occurrence and control. Anim Nutr. 2024 Jun 1;17:220-31. doi: 10.1016/j.aninu.2024.01.010.
37. Liu M, Zhang Y, Liu Y, Li Y, Wang Z, Ge G, et al. Effect of fermented total mixed rations on rumen microbial communities and serum metabolites in lambs. Grassl Res. 2024 Sep;3(3):249–63. doi: 10.1002/glr2.12095.

38. Vargas JE, López-Ferreras L, Andrés S, Mateos I, Horst EH, López S. Differential diet and pH effects on ruminal microbiota, fermentation pattern and fatty acid hydrogenation in RUSITEC continuous cultures. Fermentation. 2023 Mar 23;9(4):320. doi: 10.3390/fermentation9040320.
39. Xu H, Wang G, Gao Q, Liu Z, Jia J, Xu Y, et al. Microbial insights into ruminal fiber degradation and feed efficiency of Hu sheep. Front Microbiol. 2025 Apr 22;16:1561336. doi: 10.3389/fmicb.2025.1561336.
40. Justice KE, Smith FA. A model of dietary fiber utilization by small mammalian herbivores, with empirical results for Neotoma. Am Nat. 1992;139(2):398–416. doi: 10.1086/285333.
41. Wu J, Yang D, Gong H, Qi Y, Sun H, Liu Y, et al. Multiple omics analysis reveals that high fiber diets promote gluconeogenesis and inhibit glycolysis in muscle. BMC Genomics. 2020 Sep 24;21(1):660. doi: 10.1186/s12864-020-07048-1.
42. Gao Q, Sun G, Duan J, Luo C, Yangji C, Zhong R, et al. Alterations in gut microbiota improve SCFA production and fiber utilization in Tibetan pigs fed alfalfa diet. Front Microbiol. 2022 Oct 21;13:969524. doi: 10.3389/fmicb.2022.969524.
43. Zhou Z, Zhou X, Li J, Zhong Z, Li W, Liu X, et al. Transcriptional regulation and adaptation to a high-fiber environment in Bacillus subtilis HH2 isolated from feces of the giant panda. PLoS One. 2015;10(2):e0116935. doi: 10.1371/journal.pone.0116935.
44. Elghandour MM, Tan ZL, Abu Hafsa SH, Adegbeye MJ, Greiner R, Ugbogu EA, et al. Saccharomyces cerevisiae as a probiotic feed additive to non and pseudo-ruminant feeding: A review. J Appl Microbiol. 2020;128(3):658–674. doi: 10.1111/jam.14416.
45. Jouany JP, Medina B, Bertin G, Julliand V. Effect of live yeast culture supplementation on hindgut microbial communities and their polysaccharidase and glycoside hydrolase activities in horses fed a high-fiber or high-starch diet. J Anim Sci. 2009;87(9):2844–2852. doi: 10.2527/jas.2008-1602.
46. Patel V, Patel AK, Parmar NR, Patel AB, Reddy B, Joshi CG. Characterization of the rumen microbiome of Indian Kankrej cattle (Bos indicus) adapted to different forage diet. Appl Microbiol Biotechnol. 2014;98(23):9749–9761. doi: 10.1007/s00253-014-6153-1.
47. Bian G, Yu S, Cheng C, Huang H, Liu J. Ruminal microbiota-host crosstalks promote ruminal epithelial development in neonatal lambs with alfalfa hay introduction. mSystems. 2024;9(2). doi: 10.1128/msystems.01034-23.
48. Hou L, Ma Y, Li J, Yang Y, Duan P, Guo T. Effects of dietary supplementation with different amounts of Lycium ruthenicum (black goji berry) branch roughage on plasma biochemical indices and rumen microflora of sheep. Front Microbiol. 2025 Apr 8;16:1556724. doi: 10.3389/fmicb.2025.1556724.
49. Gao Z, Liu B, La S, Li D, Zhu X, Sun H, et al. Alfalfa hay substitution for wheat straw improves beef quality via rumen microflora alteration. Heliyon. 2023 Oct 1;9(10). doi: 10.1016/j.heliyon.2023.e20803.
50. Coates LC, Storms D, Finley JW, Fukagawa NK, Lemay DG, Kalscheur KF, et al. A low-starch and high-fiber diet intervention impacts the microbial community of raw bovine milk. Curr Dev Nutr. 2022 Jun 1;6(6):nzac086. doi: 10.1093/cdn/nzac086.
51. Cui X, Wang Z, Guo P, Li F, Chang S, Yan T, et al. Shift of feeding strategies from grazing to different forage feeds reshapes the rumen microbiota to improve the ability of Tibetan sheep (Ovis aries) to adapt to the cold season. Microbiol Spectr. 2023;11(2). doi: 10.1128/spectrum.02816-22.
52. Marques RD, Cooke RF. Effects of ionophores on ruminal function of beef cattle. Animals (Basel). 2021 Sep 30;11(10):2871. doi: 10.3390/ani11102871.
53. Hu R, Zou H, Wang H, Wang Z, Wang X, Ma J, et al. Dietary energy levels affect rumen bacterial populations that influence the intramuscular fat fatty acids of fattening yaks (Bos grunniens). Animals (Basel). 2020 Aug 22;10(9):1474. doi: 10.3390/ani10091474.
54. Yang S, Zheng J, Mao H, Vinitchaikul P, Wu D, Chai J. Multiomics of yaks reveals significant contribution of microbiome into host metabolism. npj Biofilms Microbiomes. 2024 Nov 21;10(1):133. doi: 10.1038/s41522-024-00609-2.
55. Li Q, Fei HL, Luo ZH, Gao SM, Wang PD, Lan LY, et al. Gut microbiome responds compositionally and functionally to the seasonal diet variations in wild gibbons. npj Biofilms Microbiomes. 2023 Apr 21;9(1):21. doi: 10.1038/s41522-023-00388-2.

56. Zhao J, Yao Y, Li D, Zhu W, Xiao H, Xie M, et al. Metagenome and metabolome insights into the energy compensation and exogenous toxin degradation of gut microbiota in high-altitude rhesus macaques (Macaca mulatta). npj Biofilms Microbiomes. 2023 Apr 20;9(1):20. doi: 10.1038/s41522-023-00387-3.
57. Zhao MA, Chu J, Feng S, Guo C, Xue B, He K, et al. Immunological mechanisms of inflammatory diseases caused by gut microbiota dysbiosis: A review. Biomed Pharmacother. 2023 Aug 1;164:114985. doi: 10.1016/j.biopha.2023.114985.
58. Wen Y, Li S, Wang Z, Feng H, Yao X, Liu M, et al. Intestinal microbial diversity of free-range and captive yak in Qinghai Province. Microorganisms. 2022 Mar 31;10(4):754. doi: 10.3390/ microorganisms10040754.
59. Keum GB, Pandey S, Kim ES, Doo H, Kwak J, Ryu S, et al. Understanding the Diversity and Roles of the Ruminal Microbiome. J Microbiol. 2024;62(3):217–230. doi: 10.1007/s12275-024-00121-4.
60. Yan L, Tang L, Zhou Z, Lu W, Wang B, Sun Z, et al. Metagenomics reveals contrasting energy utilization efficiencies of captive and wild camels (Camelus ferus). Integr Zool. 2022;17(3):333–345. doi: 10.1111/1749-4877.12585.
61. Mu Y, Qi W, Zhang T, Zhang J, Mao S. Multi-omics analysis revealed coordinated responses of rumen microbiome and epithelium to high-grain-induced subacute rumen acidosis in lactating dairy cows. mSystems. 2022;7(1). doi: 10.1128/msystems.01490-21.
62. Jia T, Zhang W, Zhu W, Fan L. Intermittent fasting driven different adaptive strategies in Eothenomys miletus (red-backed vole) at different altitudes: based on the patterns of variations in intestinal microbiota. BMC Microbiol. 2025 Mar 31;25(1):185. doi: 10.1186/s12866-025-03934-4.
63. Wang K, Ren A, Zheng M, Jiao J, Yan Q, Zhou C, et al. Diet with a high proportion of rice alters profiles and potential function of digesta-associated microbiota in the ileum of goats. Animals (Basel). 2020 Jul 24;10(8):1261. doi: 10.3390/ani10081261.
64. Fan G, Su N, He Y, Yuan C, Zhao C, Hu X, et al. Carbonate buffer mixture alleviates subacute rumen acidosis induced by long-term high-concentrate feeding in dairy goats by regulating rumen microbiota. Microorganisms. 2025 Apr 19;13(4):945. doi: 10.3390/microorganisms13040945.
65. Wang X, Guo C, Xu X, Zhang L, Li S, Dai D, et al. Effect of Alkaline Mineral Complex Buffer Supplementation on Rumen Fermentation, Rumen Microbiota and Rumen Epithelial Transcriptome of Newborn Calves. Fermentation. 2023;9(11). doi: 10.3390/fermentation9110973.
66. Elmhadi ME, Ali DK, Khogali MK, Wang H. Subacute ruminal acidosis in dairy herds: Microbiological and nutritional causes, consequences, and prevention strategies. Anim Nutr. 2022;10:148–155. doi: 10.1016/j.aninu.2021.12.008.
67. Metzler BU, Mosenthin R. A review of interactions between dietary fiber and the gastrointestinal microbiota and their consequences on intestinal phosphorus metabolism in growing pigs. Asian-Australas J Anim Sci. 2008;21(4):603–615. doi: 10.5713/ajas.2008.r.03.
68. Li QS, Wang R, Ma ZY, Zhang XM, Jiao JZ, Zhang ZG, et al. Dietary selection of metabolically distinct microorganisms drives hydrogen metabolism in ruminants. ISME J. 2022;16(11):2535–2546. doi: 10.1038/s41396-022-01294-9.
69. Yang R, Guo Y, Zhang S, Hao Q, Duan C, Wang Y, et al. Effect of Dioscorea opposite waste supplementation on antioxidant capacity, immune response and rumen microbiome in weaned lambs. Fermentation. 2023 Mar 4;9(3):256. doi: 10.3390 /fermentation9030256.
70. Zhong Z, Sun P, Zhang Y, Li L, Han D, Pan X, et al. Differential responses of rumen and fecal fermentation and microbiota of Liaoning cashmere goats after 2-hydroxy-4-(methylthio) butanoic acid isopropyl ester supplementation. Sci Rep. 2024 Apr 12;14(1):8505. doi: 10.1038/s41598-024-58581-y.
71. Na SW. Understanding the role of rumen epithelial host-microbe interactions in cattle feed efficiency. Anim Nutr. 2022 Sep 1;10:41–53. doi: 10.1016/j.aninu.2022.04.002.