Review
ISSN 2413-0516

Ruminant Gut Microbiota: Importance, Development, and Alternative Therapeutics for Dysbiosis

Nahlah Albakri[1,2], Reda Amasha[1], Magda M. Aly[1,3*]

[1]Department of Biology, College of Science, King Abdullaziz University, Jeddah, Saudi Arabia.
[2]Department of Biology, College of Science, Taibah University, Al-Medinah Al-Munawarh, Saudi Arabia.
[3]Botany and Microbiology Department, Faculty of Science, Kafrelsheikh University, Kafrelsheikh , Egypt.
*Correspondence to: Magda M. Aly (E-mail: mmmohammad@kau.edu.sa)

(Submitted: 08 November 2022 – Revised version received: 28 November 2022 – Accepted: 03 January 2023 – Published online: 26 February 2023)

Abstract

The microbiome is a population of microbes that colonized in mammalian gut. During the first few years of life, the gut microbiome undergoes alteration and is very diverse in adulthood, depends upon various of circumstances. Gut microbes, particularly gut flora in ruminants, are receiving more and more attention. Intestinal microbes, particularly ruminant microorganisms, have attracted an increasing amount of attention as high-throughput sequencing technology has improved and costs have decreased, whether in the fundamental research or application fields. The ruminant microbiome changes in conjunction with its host and it is influenced by inter-microbial interactions, environmental exposures, and host properties. However, any organism's core functional microbiome is much more conventional. Unfortunately, the fragile growth ratio of the microbial culture is susceptible to incursions under illness circumstances, which may affect the abundance of various microbial species, resulting to dysbiosis. As a result, the purpose of this review is to provide a broad summary of the relevance of ruminant gut microorganisms, as well as to investigate variables that influence the microbiota and alternative therapeutics such as probiotics, prebiotics, fecal transplantation, and rumen transfiguration, all of which have been shown to be effective in addressing dysbiosis.

Keywords: Gastrointestinal microbiome, alternative therapeutics, dysbiosis

Introduction

The gut microbiota is a diverse collection of microorganisms that occur in the gastrointestinal tract of mammals. This microbial community has a host-specific composition that is continually changing and responsive to both external and endogenous changes. The importance of this "organ's" structure and function in health and illness has been emphasized by increased attention to its structure and function. The intestinal microbiota, a complex ecosystem, contains around 1000 species of Firmicutes, Bacteroidetes, Actinomycetes, Proteophylum, and Verrucomicrobia.[1,2]

From nutritional condition to behavior and stress response, the microbiota is closely connected to many characteristics of normal host physiology. They might also be a main or secondary cause of a variety of diseases that affect both neighboring and distant organ systems. The presence or absence of significant species accomplished of causing particular responses, as well as the overall balance of the gut microbial community, are crucial in maintaining homeostasis or deficiency thereof in the intestinal mucosa and beyond. The mechanisms concluded which the microbiota exerts its valuable or detrimental effects are currently unknown. However, they contain both intestinal epithelial and mucosal immune cells developing signalling molecules and identifying bacterial epitopes. Advances in gut microbiota modelling and analysis will help us better understand their role in health and illness, allowing us to tailor present and future therapeutic and prophylactic approaches.[3,4]

Very complicated biological materials, such as taxonomic and useful identification of microbial groups that almost fill all present ecological niches, may now be easily examined thanks to technological advances in mass spectrometry, next-generation sequencing and bioinformatics. Metaproteomic techniques give operational data on the microbiota examined, as well as structural data collected via metagenomic research. Combining the major Omics technologies (metabolomics, transcriptomics, proteomics, and genomics) in living science offers very accurate data on the study object and aids in the understanding of molecular changes in response to externaland internalecological stimuli. The microbial communities that colonized animals' gastrointestinal tracts have an essential role in their metabolism as well as their physiology and health. Veterinarians, animal nutritionists, and microbiologists are interested in the microbiotas of cattle and ruminants.[5]

Between 2008 and 2014, just 20 papers were published yearly, a ratio of smaller than five per year, and there was no relevant literature before to 2008. With more than 10 papers produced per year after 2014, research entered a new era of fast expansion. The microbial diversity of the rumen or omasum and reticulum of giraffes, moose, bovine and kangaroos, lambs, steers, Musk Deer, goats, sheep, geese, Muskoxen, yark, camel, swine, grazing primate.[6]

Definition of Microbiome

The microbiome is a community of microorganisms that live or are present on the bodies of animals (viruses, archaea, bacteria including fungi, protozoa, and bacteriophages) (skin, urogenital tract, oral cavity, gastrointestinal tract and respiratory tract). The microbiome is also defined as the genetic information of microbes that inhabit in a certain environment, which includes species whose genomes are the only thing that distinguishes them.[7,8] Members of the microbiome might be commensal (without harming various types that benefit from one another), symbiotic (both helpful species benefiting from one another), pathogenic, or parasitic.[9]

Rumen Microbiome

The four components of the ruminal stomach (actual stomach) are the reticulum, rumen, omasum (pre-stomach), and abomasum.[10] Because the rumen is the stomach's most important portion, its microbial ecology enables it to use complex carbohydrates and fiber-rich diets,[11] resulting in the digestion of around 70% of the cellulose consumed.[12] The most abundant prokaryotes are bacteria, accounting for more than 95% of the ruminal microbiota.[13] In the rumen, the phylum Bacteroidetes is the most abundant, accounting for 45–57 percent 16S rRNA patterns and 90% of the Bacteroidetes population (with the genus *Prevotella* accounting for 45–57% 16S rRNA patterns and 90% of the Bacteroidetes population). Followed by Firmicutes accounting for 28 percent. Moreover, *Dialister, Succiniclasticum, Mitsuokella, Butyrivibrio*, and *Ruminococcus* made up over 1% of all bacterial species found in the rumen.[14,15]

Small Intestine Microbiome

Carbohydrates and proteinabsorptionis thecore function of the small intestine,[12] and its three sections (duodenum, jejunum, and ileum) have distinct roles and microbial ecosystems. According to a report, the phylum Firmicutes was more prevalent in all compartments of the cow gastrointestinal system except the jejunum that were dominated by Proteobacteria. In the jejunum, *Ruminococcus*, *Acetitomaculum*, and *Lachnospiraceae* were frequent, whereas Enterobacteriaceae were prevalent in the small intestine.[16] The relative abundance of the phylum Bacteroidetes reduced dramatically (0.4–1.1 percent) as compared to the rumen, while the comparative abundance of the phylum Firmicutes increased significantly (0.4–1.1%) (up to 80 percent of total relative abundance). Tenericutes (0.4–4%), Proteobacteria (0.8–5.8%), and Actinobacteria (6–13%) are examples of low-abundance taxa that have been investigated. Propionibacterium, *Bulleidia, Mogibacterium, Lactobacillus, Mitsuokella, Ruminococcus,* and *Butyrivibrio*are some of the other major genera found in the small intestine.[14,15]

Large Intestine Microbiome

In the rectum, colon, and cecum, bacterial concentrations vary from 10^{12} to 10^{14} cells per millilitre.[12] The large intestine is important for water digestion and absorption since it is responsible for 30 % of cellulose digestion.[12,17] Various parts of the large intestine have different amounts of microbial abundunce and diversity in the corresponding microbiota. The phylum Firmicutes have been shown to be the most abundant in the cecum, accounting for up to 81% of all phyla, with Bacteroidetes accounting for 18–26%. *Tenericutes*, *Actinobacteria* and *Spirochetes* have all been discovered in the cecum. *Oscillospira, Ruminococcus,Coprococcus, Turicibacter, Dorea, Blautia, Clostridium,* and *Prevotella* were the most common taxa in the cecum.[14] Firmicutes makes up 81% of the colon's relative microbial abundance, with Bacteroidetes accounting for 21–33%. Furthermore, of the remaining 23 phyla, The most common bacteria were *Fibrobacteria, Tenericutes, Spirochetes, Proteobacteria,* and *Actinobacteria*. The most prevalent genera were *Coprococcus, Dorea, Oscillospira, Ruminococcus, Turicibacter, Blautia, Parabacteroides,* and *Prevotella*.[14,18] The phylum Firmicutes has invaded the rectum in a similar fashion. The major genera in the rectum were *Clostridium, Prevotella, Turicibacter, Succinivibrio, Ruminococcus, Roseburia, Coprococcus, Bacteroides,* and *Osillospira*.[19]

Importance of the Rumen in Digesting Forages

The rumen and associated microorganisms, such as fungi, archaea, bacteria, and protozoa, may help mammalian enzymes use substrates that aren't easily available to them.[20,21] As a result, the host ruminant has substrates that may be absorbed.[22] Feeds become increasingly well-known for microbial colonisation after a physical breakdown during ingestion, rumination, and in the rumen.[23,24] Microorganisms consume simple carbohydrates to make VFAs such acetate (for fatty acid synthesis), propionate (for glucose synthesis), and butyrate (for butyrate synthesis), which are largely used as energy sources in the ruminant body. Microbiome composition[25,26] and ruminal circumstances influence the amount of various VFAs in the rumen. Intake rate, dietary forage to concentrate ratio, and diet type all impact ruminal conditions (e.g., breakdown rate, molecular structure). Acetate is produced more quickly in forage-dominated diets, whereas propionate is produced more easily in concentrate-based diets. Feeds heavy in starch and protein stimulate propionate synthesis, whereas hemicellulose and simple sugars raise butyrate production and cellulose increases acetate production.[27] Feed must be maintained long enough in the reticulorumen for microorganisms to adequately break down and ferment plant fibre. The supply of energy and protein in the rumen influences the efficiency and quantity of microbial protein production.[28] Ruminantanimals have a filter between the reticulum and the omasum that serves to prolong the ruminal retention time for neutral detergent fibre, which is an important component of forage.[29] Carbohydrates are bacteria's primary source of energy, but they may also serve as carbon skeletons for protein synthesis when combined with amino acids, ammonia, or short peptides.[30,31] During protein breakdown, peptides and amino acids are generated, which may be utilized by microbes (transamination) or deaminated to form VFAs, CO_2, and ammonia.[30,32] Ammonia that exceeds the ruminal wall's microbial growth capabilities is ingested, transformed to urea, and then returned to the rumen through saliva or urine.[33]

Morphological and Microbial Development of the Rumen

The rumen's development and microbe colonization are a two-way interaction between the host and microbial colonies. Rumen morphological development is aided by solid feed consumption. VFA synthesis and absorption as fermentation end-products aid the development of ruminal papillae, allowing for their absorption and subsequent epithelial metabolism.[34,35] Butyrate is the most efficient epithelial length and function activator, followed by propionate. Roughages, on the other hand, have a physical structure that increases ruminal volume, aids muscle growth,[36,37] and promotes rumen rumination and saliva flow.[38] The rumen's principal enzymatic activities of ruminal microbiota (proteolysis, fibrolysis, ureolysis, and amylolysis) have been reported from four to ten days of life.[39,40] During the early stages of life, more than 60 glycoside hydrolase microbial genes were found in the rumen, suggesting a high capacity for plant carbohydrate metabolism even in the absence of regular plant cell wall consumption.[41] Because 60–80% of all VFAs are absorbed across the ruminal wall and with 75–90% of absorbed butyrate being metabolised by the ruminal epithelium, the ketogenic capacity of the rumen must develop, as a calf grows, to that of a mature rumen.

After birth, microbial inoculation of the rumen began with contact with the vaginal canal, faeces, colostrum, the dam's skin, and saliva. The presence of methanogens, fibrinolytic bacteria, and Proteobacteria in the rumen of calves less than 20 minutes after birth has previously been investigated.[42] Inoculation may happen before birth, with rapid changes in the early days of life as initial colonising aerobic or facultative anaerobic bacteria from the biotype for the later fully anaerobic microbes.[43,44] Proteobacteria were found in >90% of newborn goat sequences, showing that the rumen and epidural microbial communities are formed in the same manner.[45] This might be because of their ability to scavenge oxygen from the capillary network, allowing anaerobic colonies to develop more easily. Many studies[41,44,46] have shown that the prewarned rumen has the same dominating phyla as the more developed post weaned rumen, namely Bacteroidetes, Proteobacteria, and Firmicutes, with relative abundance varying with age. Firmicutes numbers grow after weaning, however Bacteroidetes, notably *Prevotella*, are more reliant on solid food intake than milk elimination, reaching a stable abundance at 7 weeks and solid food consumption topping 100 g per day, respectively.[46–48] This demonstrates that the earlier a calf begins to eat solid food, the sooner a mature ruminal bacterial community arises.[49] looked at the effects of birth mode (natural vs. caesarean) and diet on the ruminal microbiome's development, as well as random factors in early life. Others[50,51] have revealed host genetic influences on the ruminal microbiome. The importance of defining ruminal function in young ruminants before, during, and after weaning was highlighted by all of these genetic and early-life effects.

Factors Influencing the Microbiota-Host Interaction

In reaction to environmental changes, the rumen microbiota alters its composition and function. Many scientists have studied the variables that influence the rumen microbiota throughout the past few decades. Various methods, ranging from demographic fingerprinting to high-throughput sequencing, were used. Diet, environment, and age all influence the rumen microbiota.

Diet Effects on the Rumen Microbiota

Rumen function, which is governed by interactions between the environment andhost genes, leads to changes in rumen microbial ecology, has a significant impact on ruminant production. By modifying microbial populations and fermentation activity, the type of diet may have a significant influence on rumen function.[52–55] Roughage has a large influence on rumen growth, and VFA absorption is aided by gene expression in rumen epithelial cells. As a result, one of the most critical features of large ruminant feeding operations has been modified to enhance feed efficiency. Ruminants have acquired a digestive mechanism that can digest roughages during millions of years of evolution. When ruminant animals are fed fiber-deficientor high-grain diets, the rapid breakdown of highly fermentable carbohydrates produces a large amount of VFA, lowering ruminal pH and causing acidosis, which may disturb physiological balance and change microbial ecology. Different kinds of roughages and the forage-to-concentrate ratio may have an impact on the ruminal metabolism and fermentation. Dairy cows given a mixture of *Leymus chinensis* hay, alfalfa hay, and corn silage produce more valerate, acetate, methylamine, and hydro cinnamate, but less glycine, glucose, isovalerate, and propionate, than dairy cows fed corn stover.[56]

The thickness of the stratum spinosum, stratum granulosum, stratum basale, and stratum corneum, as well as the size of the rumen papilla, are all affected by roughage. Changes in TLR gene expression in dietary components have a comparable effect. Dietary compositions and types have been demonstrated to impact ruminal microbiota, rumen epithelial tissue shape, and receptors in several investigations. Ruminant farmers would benefit greatly from a good understanding of the interaction between rumen epithelial cells and rumen microbes when using dietary treatments.

Age Effects on the Rumen Microbiota

Another element that influences rumen microbes is the age of the host. Rumen microbes vary from newborn to 2-year-old cows.[44] This might be due to dietary changes, in part (milk, colostrum, milk-supplemented rations for calves, and total mixed rations for adult cows). The host's development is a crucial determinant in GIT microbiota modifications since the microbiota of cows given the same diet differs with age.[41] It's most likely due to changes in the rumen and metabolites as the animals become older. These findings imply that as the host ages, alterations in the rumen microbiome may occur. However, there is a lack of knowledge on how the rumen microbiota and the hosts interact at different ages. More research is needed to provide the knowledge needed to build innovative techniques to increasing animal production at different phases.

External Environment Effects on the Rumen Microbiota

The rumen microbiota and hist interaction is influenced by the external living environment, including as temperature, climate, herd management, humidity, geography, and geography. The impact of the living environment on the comparability of ruminal microbiomes in cattle and bison.[57] As a consequence, the microbial genomes in the GIT change as the hosts' living environments change. The gut microorganisms and microbial activity of a ill person may vary from that of a healthy one.[58] Identifying the causes of microbial diversity changes and calculating the host-microbiota interaction is difficult due to the complexity of the GIT environment.[54]

Despite the need for further study across species, nutrition has the greatest impact on the ruminal microbiota. Using today's omics technology, scientists might rapidly identify the microbial makeup, host-microbe interactions, variables impacting the GIT microbiota, androles in the GIT. Future study should concentrate on the mechanisms that support the host-microbe relationship, such as dietary impacts on the GIT microbiota and epithelial cells, as well as their coordinated control.[59]

Altered Microbiota: Dysbiosis

A microbiome is an interacting and changing micro-ecosystem defined by the genetic components, structures, and metabolites of unique microbiota. The microbiota may be found in a variety of environments, including among eukaryotic hosts. Many studies have identified the microbiome as a neglected niche in the maintenance of physiological functioning in eukaryotic host settings.[12] The microbiome's influence on ruminant growth and immunity has been extensively researched.[13] The commensal microbiota contributes to animal health in a variety of ways, including helping in the digestion of indigestible plant fibre.[60] It also supplies the host with sustenance and energy (volatile fatty acids), building components (lipids, peptides, and carbohydrates), and immune system modification (antibodies and cytokines).[61] The microbiome, which competes with pathogens for adhesion sites and nutrition, separates infections and immune cells.[62,63] Furthermore, antimicrobial compounds such as hydrogen peroxide, organic acids, biosurfactants, and bacteriocins are produced by these microbes, limiting pathogenic development.[15] Dysbiosis is a breakdown or imbalance in the gastrointestinal tract's natural microbiota. Dysbiosis may be caused by an increase or decrease in the number of commensal bacteria, the introduction of pathogenic organisms, or the development of opportunistic microorganisms. Because the microbiota is a metabolically active "organ," dysbiosis may impact the production of essential nutrients or metabolites like short-chain fatty acids or secondary bile acids. Significant dysbiosis has been associated to acute diarrhoea (infectious, non-infectious, and hemorrhagic), chronic diarrhea (food or antibiotic response and IBD), GI motility problems, EPI, antibiotics, and gastric acid reducers. Despite the limited evidence, dysbiosis seems to be a significant component in both acute and chronic feline and canine diarrhoea. Fatty acid, biotin, tryptophan, ascorbate, and glycosphingolipid metabolism in the microbiota are all affected by changes in GI bacterial groups.[64]

Alternative Therapeutics Ways

The use of Probiotics

Probiotics are living associated to human and animal health that have a therapeutic effect on health when given in proper proportions.[65] Probiotics' positive benefits may be produced in a variety of ways.[66] Pathogens competing for adhesion sites and nutrients may affect the host's microbiota.[67] In addition, probiotics aid in the maintenance of intestinal homeostasis, which improves barrier function. They may create antimicrobial metabolites such as lactic acid and diacetyl, as well as antimicrobial peptides such as bacteriocins.[68] By interacting directly with host cells, probiotics have the ability to affect the immune system.[69,70] The most prevalent probiotic microorganisms are food-grade bacteria from the families Bifidobacterium, *Lactobacillus*, and *Lactobacillus*. Probiotics also include microorganisms such as *enterococcus* and *streptococcus*.[71]

Studies injecting probiotics to treat rumen acidosis were a realistic option due to the importance of dairy cattle. According to Goto et al.,[72] adding a probiotic cocktail including *C. butyricum, E. faecium*, and *L. plantarum* for seven days improved pH and lactic acid levels. Yeast has also been used in cow probiotics after many studies shown that it reduces ruminal acidity.[73,74] According to Mohammed et al.,[73] a diet supplemented with Saccharomyces cerevisiae decreased subacute rumen acidosis but not acute acidosis. Researchers have used probiotics as a viable alternative for preventing and managing mastitis in conjunction with global efforts to reduce antibiotic consumption.[75,76] Probiotics based on LAB have been proven to increase the host immune response effectively, suggesting that they might be approved as a non-antibiotic mastitis treatment.[66]

The use of Prebiotics

Prebiotics are natural compounds that are complexed by an animal's superior gastrointestinal tract enzymes but can be digested, developed, and operate more efficiently by one or a small group of gut bacteria. The cumulative effect increases the host's health.[77,78] The most often used prebiotics in animals are manno-, fructose-, and trans galacto-oligosaccharides. In cattle, prebiotics have been demonstrated to reduce harmful bacteria adhesion and enhance immunological response.[79] In the research, prebiotics were introduced to the Holstein Friesian diet, which reduced the incidence of *E. coli*.[80]

Fecal Microbiota Transplantation

The therapeutic transplantation of faecal microbiota from a healthy person into an ill person is known as "faecal microbiota transplantation," or FMT. During the FMT procedure, all species that contribute to an entire complex ecosystem of the gastrointestinal microbiota are transplanted, including viruses, bacteria, fungi, archaea, and protozoa, as well as minute particulate feedstuffs, colonocytes, and metabolites.[81] FMT has a long history of usage in humans, dating back to at least the 4th century in China when it was used to treat gastroenteritis and diarrhea.[82] FMT administered by colonic enemas was shown to be a successful treatment approach in four human instances of pseudomembranous enterocolitis caused by Staphylococcus aureus in an early case report published in the United States.[83] FMT has been more commonly employed in hospitals and clinics in recent years as a very successful treatment option for recurrent Clostridium difficile infections that are resistant to antimicrobials.[84] Although C. difficile infections are the most common ailment now treated with FMT in the modern era, many other disorders have shown a favourable response to experimental FMT treatment, includingidiopathic thrombocytopenic purpura, insulin sensitivity, and chronic fatigue syndrome in patients with metabolic syndrome.[85–87] The actual mechanism behind FMT's success in the majority of disorders is unknown. Increased microbial diversity, larger numbers of beneficial microbial communities, and immune system modulation are most likely to be responsible.

The most common historical use of FMT in animals is in ruminants, where it is used to return microbes to the ruminal contents of cattle. It's commonly used for digestive or metabolic issues, such as inappetence or ruminal hypomotility.[88] Ruminant transformation has a lengthy history, dating back to the 17th century in Italy, when it was initially noted as a way for restoring correct rumination.[89] For millennia, Sweden has employed regurgitated digesta or cud as a method for microbial transplantation to treat ruminal indigestion, with cud being described to as a "living thing"[90] FMT has lately gained popularity as a treatment and prevention method in other animals including household pets.

Although the FMT efficacy exact mechanism in animals, the majority of ailments is unclear, many possibilities have been offered. One of the most well-documented mechanisms of action is restoring normal flora by repopulating the gut with a full diverse population of microorganisms.[91,92] Transformation in ruminants, for example, is thought to be advantageous because it recolonizes the rumen with beneficial anaerobes, restoring normal fermentation function. Furthermore, increasing the variety of the microbiome enhances the host's capacity to absorb complex carbohydrates, which aids digestion. FMT is believed to have a role in gastrointestinal pathogen competitive inhibition by recolonizing normal bacteria, where beneficial microbes outcompete all the pathogens infection steps.[93,94] FMT has recently emerged as a viable therapy option for those afflicted with multidrug-resistant bacteria including vancomycin-resistant Enterococcus faecalis and methicillin-resistant *Staphylococcus aureus*.[95–97]

Rumen Transfaunation

The rumen's symbiotic microbiota provides nutrition and energy to the host by digesting ingesta and decomposing plant materials into different volatile fatty acids (VFAs), ammonia, and other chemicals. As a result, improved rumen microbial digesting ability may improve feed efficiency and yield. Many factors have been used in previous techniques to target the rumen microbiota. Various studies have looked at changing animal diets,[1] lowering rumen pH,[98] reducing rumen protozoa,[99] and other approaches. However, none of the aforementioned procedures have consistently positive effects, suggesting that long-term ways for increasing animal performance by altering rumen microbiota have yet to be identified.[100]

Rumen transformation is the process of transferring rumen fluid from healthy animals to animals that have a wide variety of microbes. The transplanted rumen fluid provides energy and nutrients to the rumen microbial population.[101] VFA, microbial proteins, amino acids, vitamins, enzymes and minerals are among the nutrients found in rumen fluid.[102,103] Small quantities (1 L) of rumen fluid transformed, which enhances rumen function and feed intake in cows, may also be used to treat feed indigestion in cows.[104] Microbial intervention in young calves may also be intentionally induced, affecting calf health and rumen microbiota development. Inoculating newborn animals with rumen fluid from adult animals (fresh, lyophilized, or autoclaved) improved feed efficiency and weight gain.[105,106] Inoculating newborn lambs with mature lyophilized rumen fluid dramatically increased growth performance during and after weaning and starter meal digestibility, according to a recent sheep study.[107] Vaccination also raised ruminal propionate concentrations and rumen amylase activity, as well as lowering the acetate/propionate ratio.

The usage of mature lyophilized rumen fluid increased the population of *Streptococcus ruminantium*, which is linked to starch consumption.[108] Similarly, in young calves fed exogenous rumen fluid obtained from an adult cow, the relative abundance of eight bacterial genera (*Acidiphilium, Sporosarcina, Polaribacte, Bdellovibrio, Microbacterium, Pseudodesulfo vibrio, Sporosarcina* and *Jeotgalibaca*) belonging to four phyla Actinobacteria, Proteobacteria, Bacteroidetes, and Firmicutes.[109] According to a recent study,[110] inoculating fresh rumen fluid from adult goats promotes early rumen colonisation through the strong protozoal population, resulting in enhanced rumen absorption, feed intake and VFA production during the preweaning period. The immune systems of suckling dairy calves were improved by spray-dried rumen fluid containing 1% maltodextrin, as seen by lower interleukin-6 blood concentrations.[111] These findings suggest that providing exogenous rumen fluid to young ruminants enhances weight gain while also altering feed health, immunity, and digestibility.[112]

Conclusion

Recently, gut microbiota has received more attention from scientists. The numbers of researches about intestinal microbiota, epically in ruminant gut, are increased. Biotechnological improvement processes have positive roles in this field. Gut microbiota is a symbiotic complex ecosystem that played key roles in the host health and immune system function. These key roles are affected by both external and internal factors. Any alteration of these factors led to imbalance in the gut microbiota which is associated with dangerous diseases like dysbiosis. Probiotics, prebiotics, fecal transplantation, and rumen transfiguration are success therapeutics ways for treating several gastrointestinal diseases. ■

References

1. Chai, L., Dong, Z., Chen, A., & Wang, H. (2018). Changes in intestinal microbiota of Bufogargarizans and its association with body weight during metamorphosis. Archives of Microbiology, 200(7), 1087–1099.
2. Meng, X., Zhang, G., Cao, H., Yu, D., Fang, X., de Vos, W. M., & Wu, H. (2020). Gut dysbacteriosis and intestinal disease: mechanism and treatment. Journal of Applied Microbiology, 129(4), 787–805.
3. Sekirov, I., Tam, N. M., Jogova, M., Robertson, M. L., Li, Y., Lupp, C., & Finlay, B. B. (2008). Antibiotic-induced perturbations of the intestinal microbiota alter host susceptibility to enteric infection. Infection and Immunity, 76(10), 4726–4736.
4. Sekirov, I., Russell, S. L., Antunes, L. C. M., & Finlay, B. B. (2010). Gut microbiota in health and disease. Physiological Reviews.
5. Deusch, S., Tilocca, B., Camarinha-Silva, A., & Seifert, J. (2015). News in livestock research—use of Omics-technologies to study the microbiota in the gastrointestinal tract of farm animals. Computational and Structural Biotechnology Journal, 13, 55–63.
6. Ming, W., & Ding, L. (2021). A brief history of ruminant gut microbiological research. Environment, Resource and Ecology Journal, 5(2), 23–28.
7. Martinez, K. B., Leone, V., & Chang, E. B. (2017). Microbial metabolites in health and disease: Navigating the unknown in search of function. Journal of Biological Chemistry, 292(21), 8553–8559.
8. Desselberger, U. (2018). The mammalian intestinal microbiome: composition, interaction with the immune system, significance for vaccine efficacy, and potential for disease therapy. Pathogens, 7(3), 57.
9. Matijašić, M., Meštrović, T., ČipčićPaljetak, H., Perić, M., Barešić, A., &Verbanac, D. (2020). Gut microbiota beyond bacteria—Mycobiome, virome, archaeome, and eukaryotic parasites in IBD. International Journal of Molecular Sciences, 21(8), 2668.
10. Membrive, C.M.B. Anatomy and Physiology of the Rumen. In Rumenology; Millen, D.D., Arrigoni, M.B., Pacheco, R.D.L., Eds.; Springer: Basel, Switzerland, 2016; pp. 1–38.
11. Petri, R. M., Neubauer, V., Humer, E., Kröger, I., Reisinger, N., &Zebeli, Q. (2020). Feed additives differentially impact the epimural microbiota and host epithelial gene expression of the bovine rumen fed diets rich in concentrates. Frontiers in Microbiology, 11, 119.

12. O'Hara, E., Neves, A. L., Song, Y., & Guan, L. L. (2020). The role of the gut microbiome in cattle production and health: driver or passenger?. Annual Review of Animal Biosciences, 8, 199–220.
13. Cammack, K. M., Austin, K. J., Lamberson, W. R., Conant, G. C., & Cunningham, H. C. (2018). RUMINNAT NUTRITION SYMPOSIUM: Tiny but mighty: the role of the rumen microbes in livestock production. Journal of Animal Science, 96(2), 752–770.
14. Myer, P. R., Freetly, H. C., Wells, J. E., Smith, T. P. L., & Kuehn, L. A. (2017). Analysis of the gut bacterial communities in beef cattle and their association with feed intake, growth, and efficiency. Journal of Animal Science, 95(7), 3215–3224.
15. Khalil, A., Batool, A., &Arif, S. (2022). Healthy Cattle Microbiome and Dysbiosis in Diseased Phenotypes. Ruminants, 2(1), 134–156.
16. Mao, S., Zhang, M., Liu, J., & Zhu, W. (2015). Characterising the bacterial microbiota across the gastrointestinal tracts of dairy cattle: membership and potential function. Scientific Reports, 5(1), 1–14.
17. Harfoot, C. G. (1981). Anatomy, physiology and microbiology of the ruminant digestive tract. Lipid Metabolism in Ruminant Animals, 1–19.
18. Myer, P. R., Wells, J. E., Smith, T. P., Kuehn, L. A., & Freetly, H. C. (2015). Microbial community profiles of the colon from steers differing in feed efficiency. Springerplus, 4(1), 1–13.
19. Durso, L. M., Miller, D. N., Schmidt, T. B., & Callaway, T. (2017). Tracking bacteria through the entire gastrointestinal tract of a beef steer. Agricultural & Environmental Letters, 2(1), 170016.
20. Van Nevel, C. J., & Demeyer, D. I. (1996). Control of rumen methanogenesis. Environmental Monitoring and Assessment, 42(1), 73–97.
21. Walker, W. F., & Liem, K. F. (1994). Functional anatomy of the vertebrates: an evolutionary perspective.
22. Bergman, E. N. (1990). Energy contributions of volatile fatty acids from the gastrointestinal tract in various species. Physiological Reviews, 70(2), 567–590.
23. Cheng, K. J., Fay, J. P., Howarth, R. E., & Costerton, J. W. (1980). Sequence of events in the digestion of fresh legume leaves by rumen bacteria. Applied and Environmental Microbiology, 40(3), 613–625.
24. McAllister, T. A., Bae, H. D., Jones, G. A., & Cheng, K. J. (1994). Microbial attachment and feed digestion in the rumen. Journal of Animal Science, 72(11), 3004–3018.
25. Henderson, G., Cox, F., Ganesh, S., Jonker, A., Young, W., & Janssen, P. H. (2015). Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. Scientific Reports, 5(1), 1–15.
26. Seshadri, R., Leahy, S. C., Attwood, G. T., Teh, K. H., Lambie, S. C., Cookson, A. L., ... & Kelly, W. J. (2018). Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 36(4), 359–367.
27. Bannink, A., Kogut, J., Dijkstra, J., France, J., Kebreab, E., Van Vuuren, A. M., &Tamminga, S. (2006). Estimation of the stoichiometry of volatile fatty acid production in the rumen of lactating cows. Journal of Theoretical Biology, 238(1), 36–51.
28. Tedeschi, L. O., Fox, D. G., & Russell, J. B. (2000, October). Accounting for ruminal deficiencies of nitrogen and branched-chain amino acids in the structure of the Cornell net carbohydrate and protein system. In Proceedings of Cornell Nutrition Conference for Feed Manufacturers (pp. 224–238). New York: Cornell University.
29. Van Soest, P. J. (1996). Allometry and ecology of feeding behavior and digestive capacity in herbivores: a review. Zoo Biology: Published in affiliation with the American Zoo and Aquarium Association, 15(5), 455–479.
30. Bach, A., Calsamiglia, S., & Stern, M. D. (2005). Nitrogen metabolism in the rumen. Journal of Dairy Science, 88, E9–E21.
31. Lanzas, C., Broderick, G. A., & Fox, D. G. (2008). Improved feed protein fractionation schemes for formulating rations with the Cornell Net Carbohydrate and Protein System. Journal of Dairy Science, 91(12), 4881–4891.
32. Tamminga, S. (1979). Protein degradation in the forestomachs of ruminants. Journal of Animal Science, 49(6), 1615–1630.
33. Cheng, L., Cantalapiedra-Hijar, G., Meale, S. J., Rugoho, I., Jonker, A., Khan, M. A., ... & Dewhurst, R. J. (2021). Markers and proxies to monitor ruminal function and feed efficiency in young ruminants. Animal, 15(10), 100337.
34. Sander, E. G., Warner, R. G., Harrison, H. N., &Loosli, J. K. (1959). The stimulatory effect of sodium butyrate and sodium propionate on the development of rumen mucosa in the young calf. Journal of Dairy Science, 42(9), 1600–1605.
35. Suárez, B. J., Van Reenen, C. G., Beldman, G., Van Delen, J., Dijkstra, J., &Gerrits, W. J. J. (2006). Effects of supplementing concentrates differing in carbohydrate composition in veal calf diets: I. Animal performance and rumen fermentation characteristics. Journal of Dairy Science, 89(11), 4365–4375.
36. Tamate, H., McGilliard, A. D., Jacobson, N. L., & Getty, R. (1962). Effect of various dietaries on the anatomical development of the stomach in the calf. Journal of Dairy Science, 45(3), 408–420.
37. Stobo, I. J. F., Roy, J. H. B., & Gaston, H. J. (1966). Rumen development in the calf: 1. The effect of diets containing different proportions of concentrates to hay on rumen development. British Journal of Nutrition, 20(2), 171–188.
38. Hodgson, J. (1971). The development of solid food intake in calves 4. The effect of the addition of material to the rumen, or its removal from the rumen, on voluntary food intake. Animal Science, 13(4), 581–592.
39. Sahoo, A., Kamra, D. N., & Pathak, N. N. (2005). Pre-and postweaning attributes in faunated and ciliate-free calves fed calf starter with or without fish meal. Journal of Dairy Science, 88(6), 2027–2036.
40. Kmet, V., Flint, H. J., & Wallace, R. J. (1993). Probiotics and manipulation of rumen development and function. Archives of Animal Nutrition, 44(1), 1–10.
41. Li, R. W., Connor, E. E., Li, C., Baldwin, VI, R. L., & Sparks, M. E. (2012). Characterization of the rumen microbiota of pre-ruminant calves using metagenomic tools. Environmental Microbiology, 14(1), 129–139.
42. Guzman, C. E., Bereza-Malcolm, L. T., De Groef, B., & Franks, A. E. (2015). Presence of selected methanogens, fibrolytic bacteria, and proteobacteria in the gastrointestinal tract of neonatal dairy calves from birth to 72 hours. PloS One, 10(7), e0133048.
43. Malmuthuge, N., Griebel, P. J., & Guan, L. L. (2015). The gut microbiome and its potential role in the development and function of newborn calf gastrointestinal tract. Frontiers in Veterinary Science, 2, 36.
44. Jami, E., Israel, A., Kotser, A., & Mizrahi, I. (2013). Exploring the bovine rumen bacterial community from birth to adulthood. The ISME Journal, 7(6), 1069–1079.
45. Wang, Z., Elekwachi, C., Jiao, J., Wang, M., Tang, S., Zhou, C., ... & Forster, R. J. (2017). Changes in metabolically active bacterial community during rumen development, and their alteration by rhubarb root powder revealed by 16S rRNA amplicon sequencing. Frontiers in Microbiology, 8, 159.
46. Meale, S. J., Li, S., Azevedo, P., Derakhshani, H., Plaizier, J. C., Khafipour, E., & Steele, M. A. (2016). Development of ruminal and fecal microbiomes are affected by weaning but not weaning strategy in dairy calves. Frontiers in Microbiology, 7, 582.
47. Meale, S. J., Morgavi, D. P., Cassar-Malek, I., Andueza, D., Ortigues-Marty, I., Robins, R. J., ... &Cantalapiedra-Hijar, G. (2017). Exploration of biological markers of feed efficiency in young bulls. Journal of Agricultural and Food Chemistry, 65(45), 9817–9827.
48. Rey, M., Enjalbert, F., Combes, S., Cauquil, L., Bouchez, O., & Monteils, V. (2014). Establishment of ruminal bacterial community in dairy calves from birth to weaning is sequential. Journal of Applied Microbiology, 116(2), 245–257.
49. Furman, O., Shenhav, L., Sasson, G., Kokou, F., Honig, H., Jacoby, S., ... & Mizrahi, I. (2020). Stochasticity constrained by deterministic effects of diet and age drive rumen microbiome assembly dynamics. Nature Communications, 11(1), 1–13.
50. Roehe, R., Dewhurst, R. J., Duthie, C. A., Rooke, J. A., McKain, N., Ross, D. W., ... & Wallace, R. J. (2016). Bovine host genetic variation influences rumen microbial methane production with best selection criterion for low methane emitting and efficiently feed converting hosts based on metagenomic gene abundance. PLoS Genetics, 12(2), e1005846.
51. Wallace, R. J., Sasson, G., Garnsworthy, P. C., Tapio, I., Gregson, E., Bani, P., ... & Mizrahi, I. (2019). A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances, 5(7), eaav8391.
52. Bevans, D. W., Beauchemin, K. A., Schwartzkopf-Genswein, K. S., McKinnon, J. J., & McAllister, T. A. (2005). Effect of rapid or gradual grain adaptation on subacute acidosis and feed intake by feedlot cattle. Journal of Animal Science, 83(5), 1116–1132.
53. Auffret, M. D., Dewhurst, R. J., Duthie, C. A., Rooke, J. A., John Wallace, R., Freeman, T. C., ... &Roehe, R. (2017). The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle. Microbiome, 5(1), 1–11.
54. Liu, K., Xu, Q., Wang, L., Wang, J., Guo, W., & Zhou, M. (2017). The impact of diet on the composition and relative abundance of rumen microbes in goat. Asian-Australasian Journal of Animal Sciences, 30(4), 531.
55. Pandit, R. J., Hinsu, A. T., Patel, S. H., Jakhesara, S. J., Koringa, P. G., Bruno, F., ... & Joshi, C. G. (2018). Microbiota composition, gene pool and its expression in Gir cattle (Bosindicus) rumen under different forage diets using metagenomic and metatranscriptomic approaches. Systematic and Applied Microbiology, 41(4), 374–385.

56. Zhao, S., Zhao, J., Bu, D., Sun, P., Wang, J., & Dong, Z. (2014). Metabolomics analysis reveals large effect of roughage types on rumen microbial metabolic profile in dairy cows. Letters in Applied Microbiology, 59(1), 79–85.
57. Ribeiro, G. O., Oss, D. B., He, Z., Gruninger, R. J., Elekwachi, C., Forster, R. J., ... & McAllister, T. A. (2017). Repeated inoculation of cattle rumen with bison rumen contents alters the rumen microbiome and improves nitrogen digestibility in cattle. Scientific Reports, 7(1), 1–16.
58. Clavel, T., Gomes-Neto, J. C., Lagkouvardos, I., & Ramer-Tait, A. E. (2017). Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. Immunological Reviews, 279(1), 8–22
59. Liu, K., Zhang, Y., Yu, Z., Xu, Q., Zheng, N., Zhao, S., ... & Wang, J. (2021). Ruminal microbiota–host interaction and its effect on nutrient metabolism. Animal Nutrition, 7(1), 49–55.
60. Firkins, J. L., & Yu, Z. (2015). Ruminant nutrition symposium: how to use data on the rumen microbiome to improve our understanding of ruminant nutrition. Journal of Animal Science, 93(4), 1450–1470.
61. van den Broek, M. F., De Boeck, I., Kiekens, F., Boudewyns, A., Vanderveken, O. M., &Lebeer, S. (2019). Translating recent microbiome insights in otitis media into probiotic strategies. Clinical Microbiology Reviews, 32(4), e00010–18.
62. Karstrup, C. C., Klitgaard, K., Jensen, T. K., Agerholm, J. S., & Pedersen, H. G. (2017). Presence of bacteria in the endometrium and placentomes of pregnant cows. Theriogenology, 99, 41–47.
63. Moore, S. G., Ericsson, A. C., Poock, S. E., Melendez, P., & Lucy, M. C. (2017). Hot topic: 16S rRNA gene sequencing reveals the microbiome of the virgin and pregnant bovine uterus. Journal of Dairy Science, 100(6), 4953–4960
64. Webb, C. B. (2019). Fecal Microbiota Transplantation: from theory to practice
65. Hill, C., Guarner, F., Reid, G., Gibson, G. R., Merenstein, D. J., Pot, B., ... & Sanders, M. E. (2014). The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. Nature Reviews Gastroenterology & Hepatology, 11(8), 506–514.
66. Krishnan, D., Al-Harbi, H., Gibson, J., Olchowy, T., & Alawneh, J. (2020). On the use of probiotics to improve dairy cattle health and productivity. Microbiology Australia, 41(2), 86–90.
67. Wan, M. L. Y., Forsythe, S. J., & El-Nezami, H. (2019). Probiotics interaction with foodborne pathogens: a potential alternative to antibiotics and future challenges. Critical Reviews in Food Science and Nutrition, 59(20), 3320–3333.
68. Gao, J., Li, Y., Wan, Y., Hu, T., Liu, L., Yang, S., ... & Cao, H. (2019). A novel postbiotic from Lactobacillus rhamnosus GG with a beneficial effect on intestinal barrier function. Frontiers in Microbiology, 10, 477.
69. Anas, M., Ahmed, K., &Mebrouk, K. (2014). Study of the antimicrobial and probiotic Effect of Lactobacillus Plantarum isolated from raw goat's milk from the region of Western Algeria. World Applied Sciences Journal, 32(7), 1304–1310.
70. Sanders, M. E., Merenstein, D. J., Reid, G., Gibson, G. R., & Rastall, R. A. (2019). Probiotics and prebiotics in intestinal health and disease: from biology to the clinic. Nature Reviews Gastroenterology & Hepatology, 16(10), 605–616.
71. Suryadi, U., Nugraheni, Y. R., Prasetyo, A. F., & Awaludin, A. (2019). Evaluation of effects of a novel probiotic feed supplement on the quality of broiler meat. Veterinary World, 12(11), 1775.
72. Goto, H., Qadis, A. Q., Kim, Y. H., Ikuta, K., Ichijo, T., & Sato, S. (2016). Effects of a bacterial probiotic on ruminal pH and volatile fatty acids during subacute ruminal acidosis (SARA) in cattle. Journal of Veterinary Medical Science, 16–0211.
73. Mohammed, R., Vyas, D., Yang, W. Z., & Beauchemin, K. A. (2017). Changes in the relative population size of selected ruminal bacteria following an induced episode of acidosis in beef heifers receiving viable and non-viable active dried yeast. Journal of Applied Microbiology, 122(6), 1483–1496.
74. Ogunade, I., Pech-Cervantes, A., & Schweickart, H. (2019). Metatranscriptomic analysis of sub-acute ruminal acidosis in beef cattle. Animals, 9(5), 232.
75. Rainard, P., & Foucras, G. (2018). A critical appraisal of probiotics for mastitis control. Frontiers in Veterinary Science, 251.
76. Angelopoulou, A., Warda, A. K., Hill, C., & Ross, R. P. (2019). Non-antibiotic microbial solutions for bovine mastitis–live biotherapeutics, bacteriophage, and phage lysins. Critical Reviews in Microbiology, 45(5-6), 564–580.
77. Frizzo, L. S., Signorini, M. L., & Rosmini, M. R. (2018). Probiotics and prebiotics for the health of cattle. In Probiotics and prebiotics in animal health and food safety (pp. 155–174). Springer, Cham.
78. Smulski, S., Turlewicz-Podbielska, H., Wylandowska, A., & Włodarek, J. (2020). Non-antibiotic possibilities in prevention and treatment of calf diarrhoea. Journal of Veterinary Research, 64(1), 119–126
79. Singh, A., Kerketta, S., Yogi, R., Kumar, A., & Ojha, L. (2017). Prebiotics: the new feed supplement for dairy calf. Int J Livest Res, 7, 1–17.
80. Grispoldi, L., Bertero, F., Franceschini, S., Mastrosimone, F., Sechi, P., Iulietto, M. F., ... & Cenci-Goga, B. T. (2017). Prevalence and characterisation of shigatoxigenic Escherichia coli isolated from beef cattle fed with prebiotics. Italian Journal of Food Safety, 6(4).
81. Bojanova, D. P., &Bordenstein, S. R. (2016). Fecal transplants: what is being transferred?. PLoS Biology, 14(7), e1002503.
82. Zhang, F., Luo, W., Shi, Y., Fan, Z., & Ji, G. (2012). Should we standardize the 1,700-year-old fecal microbiota transplantation?. The American Journal of Gastroenterology, 107(11), 1755-author.
83. EISEMAN, B., Silen, W., Bascom, G. S., & Kauvar, A. J. (1958). Fecal enema as an adjunct in the treatment of pseudomembranous enterocolitis. Surgery, 44(5), 854–859.
84. Hota, S. S., Surangiwala, S., Paterson, A. S., Coburn, B., & Poutanen, S. M. (2018). Regional variability in fecal microbiota transplantation practices: a survey of the Southern Ontario Fecal Microbiota Transplantation Movement. Canadian Medical Association Open Access Journal, 6(2), E184–E190.
85. Borody, T., Nowak, A., Torres, M., Campbell, J., Finlayson, S., & Leis, S. (2012). Bacteriotherapy in Chronic Fatigue Syndrome (CFS): A Retrospective Review: 1481. Official journal of the American College of Gastroenterology| ACG, 107, S591–S592.
86. Vrieze, A., Van Nood, E., Holleman, F., Salojarvi, J., Kootte, R. S., Bartelsman, J. F., ... & Nieuwdorp, M. (2012). Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome. Gastroenterol 143 (4): 913–916. e7.
87. Allegretti, J. R., Kassam, Z., Hurtado, J., Marchesi, J. R., Mullish, B. H., Chiang, A., ... & Cummings, B. P. (2021). Impact of fecal microbiota transplantation with capsules on the prevention of metabolic syndrome among patients with obesity. Hormones, 20(1), 209–211.
88. Mandal, R. S. K., Joshi, V., Balamurugan, B., Gautam, D., Chethan, G. E., & Lekshman, A. (2017). Rumen transfaunation an effective method for treating simple indigestion in ruminants. North-East Veterinarian, 17(1), 31–33.
89. Borody, T. J., Warren, E. F., Leis, S. M., Surace, R., Ashman, O., & Siarakas, S. (2004). Bacteriotherapy using fecal flora: toying with human motions. Journal of Clinical Gastroenterology, 38(6), 475–483.
90. Brag, S., & Hansen, H. J. (1994). Treatment of ruminal indigestion according to popular belief in Sweden. Revue scientifique et technique (International Office of Epizootics), 13(2), 529–535.
91. Allegretti, J. R., & Hamilton, M. J. (2014). Restoring the gut microbiome for the treatment of inflammatory bowel diseases. World Journal of Gastroenterology: WJG, 20(13), 3468.
92. Liu, S. X., Li, Y. H., Dai, W. K., Li, X. S., Qiu, C. Z., Ruan, M. L., ... & Shu, S. N. (2017). Fecal microbiota transplantation induces remission of infantile allergic colitis through gut microbiota re-establishment. World Journal of Gastroenterology, 23(48), 8570.
93. Collado, M., Grześkowiak, Ł., & Salminen, S. (2007). Probiotic strains and their combination inhibit in vitro adhesion of pathogens to pig intestinal mucosa. Current Microbiology, 55(3), 260–265.
94. Khoruts, A., & Sadowsky, M. J. (2016). Understanding the mechanisms of faecal microbiota transplantation. Nature Reviews Gastroenterology & Hepatology, 13(9), 508–516.
95. Cohen, N. A., & Maharshak, N. (2017). Novel indications for fecal microbial transplantation: update and review of the literature. Digestive Diseases and Sciences, 62(5), 1131–1145.
96. Niederwerder, M. C. (2018). Fecal microbiota transplantation as a tool to treat and reduce susceptibility to disease in animals. Veterinary Immunology and Immunopathology, 206, 65–72.
97. Takáčová, M., Bomba, A., Tóthová, C., Micháľová, A., &Turňa, H. (2022). Any Future for Faecal Microbiota Transplantation as a Novel Strategy for Gut Microbiota Modulation in Human and Veterinary Medicine?. Life, 12(5), 723.
98. Bevans, D. W., Beauchemin, K. A., Schwartzkopf-Genswein, K. S., McKinnon, J. J., & McAllister, T. A. (2005). Effect of rapid or gradual grain adaptation on subacute acidosis and feed intake by feedlot cattle. Journal of Animal Science, 83(5), 1116–1132.
99. Mosoni, P., Martin, C., Forano, E., &Morgavi, D. P. (2011). Long-term defaunation increases the abundance of cellulolytic ruminococci and in methanogens but does not affect the bacterial and methanogen diversity the rumen of sheep. Journal of Animal Science, 89(3), 783–791.
100. Zhou, M., Peng, Y. J., Chen, Y., Klinger, C. M., Oba, M., Liu, J. X., & Guan, L. L. (2018). Assessment of microbiome changes after rumen transfaunation:

implications on improving feed efficiency in beef cattle. Microbiome, 6(1), 1–14.

101. DePeters, E. J., & George, L. W. (2014). Rumen transfaunation. Immunology Letters, 162(2), 69–76.
102. Elfaki, M. O., & Abdelatti, K. A. (2018). Rumen content as animal feed: a review. Journal of Veterinary Medicine and Animal Production, 7(2).
103. Sarteshnizi, F. R., Benemar, H. A., Seifdavati, J., Greiner, R., Salem, A. Z., & Behroozyar, H. K. (2018). Production of an environmentally friendly enzymatic feed additive for agriculture animals by spray drying abattoir's rumen fluid in the presence of different hydrocolloids. Journal of Cleaner Production, 197, 870–874.
104. Steiner, S., Linhart, N., Neidl, A., Baumgartner, W., Tichy, A., & Wittek, T. (2020). Evaluation of the therapeutic efficacy of rumen transfaunation. Journal of Animal Physiology and Animal Nutrition, 104(1), 56–63.
105. Muscato, T. V., Tedeschi, L. O., & Russell, J. B. (2002). The effect of ruminal fluid preparations on the growth and health of newborn, milk-fed dairy calves. Journal of Dairy Science, 85(3), 648–656.
106. Zhong, R. Z., Sun, H. X., Li, G. D., Liu, H. W., & Zhou, D. W. (2014). Effects of inoculation with rumen fluid on nutrient digestibility, growth performance and rumen fermentation of early weaned lambs. Livestock Science, 162, 154–158.
107. Yu, S., Zhang, G., Liu, Z., Wu, P., Yu, Z., & Wang, J. (2020). Repeated inoculation with fresh rumen fluid before or during weaning modulates the microbiota composition and co-occurrence of the rumen and colon of lambs. BMC Microbiology, 20(1), 1–15.
108. Wang, M., Wang, R., Liu, M., Beauchemin, K. A., Sun, X. Z., Tang, S. X., ... & He, Z. X. (2019). Dietary starch and rhubarb supplement increase ruminal dissolved hydrogen without altering rumen fermentation and methane emissions in goats. Animal, 13(5), 975–982.
109. Li, W., Edwards, A., Riehle, C., Cox, M. S., Raabis, S., Skarlupka, J. H., ... & Suen, G. (2019). Transcriptomics analysis of host liver and meta-transcriptome analysis of rumen epimural microbial community in young calves treated with artificial dosing of rumen content from adult donor cow. Scientific Reports, 9(1), 1–11.
110. Belanche, A., Palma-Hidalgo, J. M., Nejjam, I., Jiménez, E., Martín-García, A. I., &Yáñez-Ruiz, D. R. (2020). Inoculation with rumen fluid in early life as a strategy to optimize the weaning process in intensive dairy goat systems. Journal of Dairy Science, 103(6), 5047–5060.
111. Sarteshnizi, F. R., Abdi-Benemar, H., Seifdavati, J., Khalilvandi-Behroozyar, H., Seyedsharifi, R., & Salem, A. Z. M. (2020). Influence of spray-dried rumen fluid supplementation on performance, blood metabolites and cytokines in suckling Holstein calves. Animal, 14(9), 1849–1856.
112. Arshad, M. A., Hassan, F. U., Rehman, M. S., Huws, S. A., Cheng, Y., & Din, A. U. (2021). Gut microbiome colonization and development in neonatal ruminants: Strategies, prospects, and opportunities. Animal Nutrition, 7(3), 883–895.