



Effects of Dietary Intervention on Intestinal Microflora and Common Diseases in Horses

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Abstract. Dietary interventions based on gut microbiome regulation show important application potential in the management of common diseases in horses. As monogastric herbivores, horses are highly dependent on the stability of hindgut microbial communities for their health. Intestinal flora imbalance is closely related to the occurrence and development of common diseases such as colitis, metabolic syndrome and abdominal colic. The occurrence of these diseases is often accompanied by the decline of microbial diversity, depletion of beneficial flora and proliferation of conditional pathogens, which destroy intestinal barrier function and trigger local or systemic inflammatory reactions. Diet is the most direct and effective external factor regulating intestinal microbiota. Targeted dietary adjustments such as optimizing dietary fiber sources and controlling non-structural carbohydrate intake can guide microbial community succession in beneficial directions. Supplementing specific functional additives such as prebiotics and probiotics can further support the restoration and stabilization of the intestinal ecosystem. These results suggest that microbially targeted dietary intervention strategies can improve intestinal environment, enhance host immune homeostasis and regulate energy metabolism, providing new ideas for prevention and auxiliary management of common diseases in horses.

Keywords: Horse Intestinal Microbiota, Dietary Intervention, Flora Imbalance, Common Diseases, Nutritional Management

1 Introduction

With the continuous development of modern equestrian industry and competitive sports, horse health management has been paid more and more attention [1]. Common diseases such as colic, metabolic disorders and digestive system dysfunction not only affect the performance and welfare of horses, but also bring significant economic losses. Traditional treatments tend to focus on symptom relief, with relatively limited intervention in its underlying causes. In recent years, gut microbiota, as a key link linking host health and disease, has demonstrated a central regulatory role in a variety of animal models. Horses are monogastric herbivores, and their complex hindgut fermentation system is highly dependent on a stable microbial community. The imbalance of

this community is closely related to the occurrence and development of the above diseases.

Diet is one of the most direct and effective external factors regulating the composition and function of intestinal microbiota. Through targeted adjustment of feed ingredients, nutritional structure and feeding methods, beneficial regulation of intestinal flora may be achieved, thereby improving intestinal environment, enhancing immune homeostasis and promoting metabolic health. This approach provides new ideas for the prevention and auxiliary management of common horse diseases [2]. At present, the research on the relationship between intestinal microorganisms and specific diseases in horses is still in the development stage, and the precise diet intervention strategy based on microbial regulation has not yet formed a systematic theory and practice system. Therefore, it is of important theoretical and application value to deeply explore the interaction mechanism between diet, microorganisms and horse health.

The aim of this study was to clarify the role of intestinal microbiota in the occurrence of critical diseases in horses and systematically elaborate the potential role of microbial-based dietary intervention strategies in order to provide theoretical basis for nutritional management of horse diseases.

2 Characteristics of Intestinal Microbial Community in Horses

Intestinal microbial community is the core biological system of horse digestion and health, and its composition and dynamic balance have profound effects on the physiological functions of the host. A thorough understanding of the core composition of intestinal microbiota and its influencing factors in healthy horses is an important basis for exploring dietary intervention to regulate microbiota to manage diseases. Intestinal microflora of healthy horses is a complex and relatively stable ecosystem, and its core components show specific distribution and functional characteristics in different intestinal segments [3]. The core composition of the gut microbiota of healthy horses and their main functions are shown in Table 1.

Table 1. Core Composition and Function of Intestinal Microbes in Healthy Horses

Microbial Category	Primary Colonization Site	Key Functions
Firmicutes	Throughout the intestinal tract, especially enriched in the hindgut	Participates in the fermentation of fibrous polysaccharides, producing volatile fatty acids, and serves as the primary energy supplier.
Bacteroidetes	Throughout the intestinal tract, a key member in the hindgut	Involved in the metabolism of complex carbohydrates and proteins; its abundance is correlated with fiber digestion capacity.
Spirochaetes	Cecum and colon	Some members possess fiber-degrading capabilities; their ecological roles are diverse and closely related to health status.

Microbial Category		Primary Colonization Site	Key Functions
Fibrobacteres		Hindgut	Obligate anaerobes that play a specific role in the degradation of plant cell wall polysaccharides.
Methanogenic chaea	Ar-	Hindgut	Participate in hydrogen metabolism, help maintain the stability of the anaerobic fermentation environment, and influence overall fermentation efficiency.

In the gastrointestinal tract of horses, the distribution of microorganisms has obvious compartmentalization characteristics. Due to digestive juice, the number and diversity of microorganisms in stomach and forepart of small intestine were relatively low, mainly facultative anaerobic bacteria and some acid-resistant bacteria. The caecum and colon form a large anaerobic fermenter populated with a dense and diverse microbial community, with Firmicutes and Bacteroides usually dominating. These two phyla contain most of the bacterial populations that degrade plant structural polysaccharides (such as cellulose and hemicellulose) through complex enzyme systems that break down cellulose into volatile fatty acids that can be absorbed and utilized by the host, mainly acetic acid, propionic acid and butyric acid. These short-chain fatty acids are not only an important source of energy for horse life support, especially for maintaining the health of colonic epithelial cells, but also participate in host immunity and metabolic regulation as signal molecules.

In addition, the intestinal microbial community also undertakes the functions of synthesizing essential vitamins, promoting mineral absorption, metabolizing nitrogen-containing compounds, and constituting a biological barrier against pathogen colonization. A structurally stable and functionally coordinated core microbial community is essential for maintaining environmental homeostasis in the horse gut, supporting normal digestive physiology and overall health.

3 The Mechanism of Association Between Intestinal Flora Imbalance and Common Diseases of Horses

As a complex and dynamic ecosystem in horses, the homeostasis of intestinal microflora is critical to maintaining the health of the host. This imbalance of the ecosystem, namely intestinal flora imbalance, has been proved to be closely related to the occurrence and development of many common diseases in horses. Microflora imbalance not only directly affects the local intestinal environment, but also causes systemic effects through microbial metabolites, immune regulation and signal molecule transmission, thus participating in various pathological states such as digestive system diseases, metabolic disorders and inflammatory processes. Dissecting the mechanisms of association between intestinal flora disorders and specific diseases is key to understanding the pathophysiological basis of disease and developing microbiome-based intervention strategies.

3.1 Colitis and Digestive Disorders

Colitis manifests itself in a variety of ways, including infectious colitis caused by specific pathogens such as *Salmonella*, antibiotic-associated diarrhea caused by the use of broad-spectrum antibiotics that disrupt normal flora, and idiopathic or unexplained colitis of more complex etiology. Despite differences in predisposing factors, gut microbiota in these disease states often exhibit highly consistent dysregulated features. The most significant change was an overall decline in microbial diversity, reflecting a simplification of community structure and a weakening of ecological resilience [4]. At the same time, some conditional pathogens gain competitive advantage and proliferate abnormally, while some functional bacteria beneficial to host health, such as bacteria involved in dietary fiber fermentation and short-chain fatty acids production, are significantly depleted.

This specific microflora structural change exacerbates intestinal pathological damage in a variety of ways. The reduction of beneficial bacteria directly leads to insufficient production of short-chain fatty acids, which are not only the main energy source of colonic epithelial cells, but also play an important role in maintaining the integrity of intestinal epithelial barrier, inhibiting inflammatory response and regulating immune cell function. Its absence weakens the intestinal barrier function [5]. The excessive proliferation of pathogenic bacteria or conditional pathogens will directly invade epithelial cells, or release specific toxins and metabolites, further damaging the mucosal layer. Disrupting the gut barrier allows bacteria and their products, such as lipopolysaccharides, to translocate into the submucosa and even the blood circulation, activating the innate immune system, triggering and continuing to amplify local inflammatory responses in the gut. This inflammation and barrier destruction are mutually causal, forming a vicious circle, leading to diarrhea, mucosal necrosis and other clinical manifestations. Therefore, intestinal flora imbalance is not only a concomitant phenomenon of disease, but an important link that drives the occurrence and persistence of intestinal inflammation.

3.2 Foot Inflammation and Horse Metabolic Syndrome

Equine metabolic syndrome is a metabolic disorder characterized by obesity, regional fat deposition and insulin resistance. Insulin resistance leads to impaired glucose utilization by the body, increasing the risk of metabolic abnormalities. Gut microbes play a key role in the development of this syndrome. Long-term feeding of diets rich in unstructured carbohydrates is common practice in modern horse management, but this may exceed the full digestive absorption capacity of the small intestine. A large amount of undigested starch and carbohydrates enter the hindgut, disturbing the hindgut microbial ecosystem dominated by fiber fermentation. Part of the microbial community turns to ferment these unstructured carbohydrates, producing large amounts of lactic acid, resulting in rapid acidification of hindgut contents [6]. This acidic environment not only inhibited the activity of normal fiber-degrading bacteria, resulting in a decrease in beneficial metabolites, but also induced an increase in the release of lipopolysaccharide, a cell wall component of Gram-negative bacteria. Lipopolysaccharide (LPS) is a potent

inflammatory trigger that penetrates the compromised intestinal barrier into the portal circulation, triggering a low-grade chronic inflammatory state in the liver and systemically. This persistent systemic inflammation is thought to be an important pathological basis linking insulin resistance, obesity and metabolic syndrome. Intestinal microorganisms mediate this inflammatory process and directly affect the energy metabolism balance and insulin sensitivity of the host. The pathological process described above, driven by a high non-structural carbohydrate diet and flora imbalance, is a classic pathway for the induction of acute laminitis [7]. Dermatitis is a painful disease characterized by severe inflammation and ischemia of the hoof lobules. From hindgut acidification, microbial flora disorder, endotoxin release and systemic inflammatory reaction, finally leading to hoof microcirculation disorder and tissue damage, constitute a coherent causal chain. The gut is therefore considered the primary pathological trigger for many cases of laminitis, highlighting the close link between gut health and disease of distant organs.

3.3 Abdominal Colic

In addition to the above diseases, intestinal flora disorders are important potential factors for inducing or exacerbating colic (ie, colic in horses). The etiology of abdominal colic is complex, but its occurrence is closely related to abnormal physical properties of intestinal contents, excessive fermentation gas production and intestinal dynamic disorder, which are deeply affected by microbial community status.

Abnormal gas production and mechanical colic: When the flora is out of balance, especially when the non-structural carbohydrates that are easy to ferment enter the hindgut in excess, it can lead to excessive proliferation and abnormal fermentation of certain gas-producing bacteria, producing a large amount of gas. The rapid accumulation of gas in the intestine not only causes pain directly, but may also develop into more serious mechanical obstruction such as displacement or torsion.

Changes in Digestive Properties and Obstructive Colic: Microflora imbalance may affect the efficiency of cellulose degradation and water absorption, resulting in dense, dry or thin chyme. Dry chyme clumps tend to clog narrow intestinal tracts, causing food cramp.

Metabolite and functional colic: Metabolite products of intestinal microbiota can affect the function of the intestinal nervous system and smooth muscle. Microflora dysregulation may result in a decrease in beneficial metabolites or an increase in harmful metabolites, interfere with the normal peristaltic rhythm of the intestine, and cause spasmodic or flaccid dyskinesia.

Endotoxins and inflammatory pain: dysbacteriosis can lead to impaired intestinal barrier and endotoxin translocation. Locally produced inflammatory mediators can significantly increase the sensitivity of intestinal pain nerves and reduce pain thresholds.

Therefore, maintaining the stability and balance of intestinal microbial community is of great significance to prevent various abdominal colic caused by gas production, changes in chyme physical properties, dynamic disorders and low-grade inflammation.

4 Dietary Intervention Strategies for Horse Diseases Based on Microbial Regulation

Dietary intervention, as an important means of regulating intestinal microbial community, has potential application value in the prevention and management of common diseases in horses. According to the pathogenesis and clinical characteristics of different diseases, dietary intervention programs need to be individually designed and adjusted.

For colitis and other digestive disorders, dietary management needs to be dynamically adjusted according to the stage of the disease. During acute episodes, priority should be given to providing low-residue, highly digestible feeds aimed at reducing the burden on intestinal digestion and reducing the risk of fermentation gas production and osmotic pressure disturbances [8]. During the recovery and long-term management phases, dietary strategies should shift towards re-establishing stable and beneficial microbial ecosystems. Specific fiber sources, such as alfalfa and beet meal, can be introduced gradually to selectively stimulate the growth of certain beneficial microorganisms. At the same time, prebiotics such as oligosaccharides and mannan oligosaccharides can provide exclusive substrates for beneficial bacteria such as bifidobacteria and lactic acid bacteria. Direct supplementation with probiotic preparations, including specific yeast strains and lactic acid bacteria, facilitates rapid introduction of beneficial bacteria into the gut, competitive inhibition of pathogens, and synergistic promotion of repair of intestinal barrier function.

When dealing with laminitis and equine metabolic syndrome, the core of diet control is to correct the imbalance of energy metabolism and reduce systemic inflammation. Limiting non-structural carbohydrate intake is a key measure, which involves selecting forage grass with low non-structural carbohydrate content and significantly adjusting concentrate composition and feed quantity [9]. At the same time, improving the quality and quantity of structured carbohydrates in the diet is crucial. Increasing the proportion of high-quality roughage not only provides long-lasting energy release, but also promotes the proliferation of cellulose-degrading bacteria and increases the production of short-chain fatty acids, which has a positive effect on maintaining intestinal epithelial health and systemic insulin sensitivity. In addition, under the premise of strict control of non-structural carbohydrates, moderate supplementation of fat as an alternative energy source may have a certain impact on the composition of microbial communities and provide high-density energy for the body, which helps to meet energy requirements without aggravating blood glucose fluctuations.

Dietary prevention strategies for colic focus on optimizing the digestive environment through feeding management to avoid abnormal physical properties of intestinal contents or abrupt changes in fermentation processes. Maintaining a highly regular feeding program is essential to help microbial communities establish stable metabolic rhythms. Increase the proportion of roughage in the diet, ensure adequate chewing and saliva secretion, and can form a good chyme structure, conducive to normal gastrointestinal motility [10]. Reducing the high intake of fast-fermenting carbohydrates is an important step in reducing the risk of abnormal gas production and acidosis in the cecum and colon, thus preventing some types of abdominal colic at source. Table 2 summarizes the recommended dietary interventions for different diseases in order to provide clarity.

Table 2. Summary of Recommended Dietary Intervention Plans for Different Common Equine Diseases

Disease Name	Core Intervention Objective	Core Dietary Measures	Recommended Supplements
Colitis and Digestive Disorders	Reduce burden, restore microbiota and gut barrier	Acute phase: Low-residue, highly digestible feed. Recovery phase: Gradually add specific fibers like alfalfa, beet pulp.	Prebiotics (e.g., fructooligosaccharides) Probiotics (e.g., yeast)
Laminitis and Metabolic Syndrome	Improve insulin sensitivity, regulate energy metabolism	Restrict non-structural carbohydrate (NSC) intake (low-NSC forage, limit concentrates). Increase proportion of high-quality roughage. Supplement fat as an alternative energy source.	Botanicals or minerals with metabolic regulatory functions
Colic (Prevention)	Maintain motility and fermentation balance	• Consistent feeding schedule. • Increase roughage proportion. • Avoid abrupt feed changes. • Reduce highly fermentable carbohydrates.	Additives beneficial for maintaining gastrointestinal environment (e.g., electrolytes)

5 Conclusions

This study systematically illustrates the central role of gut microbes in the development of critical diseases in horses and demonstrates the effectiveness of dietary intervention strategies based on microbial regulation. The results showed that intestinal flora homeostasis was an important basis for maintaining digestive health, metabolic balance and overall physiological function of horses, and its imbalance was closely related to colitis, metabolic syndrome and abdominal colic. Through targeted adjustment of dietary structure, such as optimizing fiber sources, controlling non-structural carbohydrate intake and adding functional components, it can effectively guide the succession of intestinal microbial communities in beneficial directions, thereby improving intestinal environment, enhancing barrier function and regulating systemic inflammatory response. This microbially targeted approach to nutrition management provides a more precise and fundamental approach to the prevention and adjuvant treatment of common diseases in horses. Future research could be devoted to exploring the construction of individualized precision nutrition protocols.

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