

Digestive Dynamics: Microbes and Metabolites as Functions of Canine Gastrointestinal Wellbeing

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Abstract

The GI (Gastrointestinal) tract, or digestive system, is the primary emphasis of this article, which investigates the specifics of the canine microbiome. It analyzes the wide range of microbes that inhabit the gut and the significant impact that diet has the structure and operation of the microbiome in preserving the general health of canines. Furthermore, this review delves into the organization, strength, and degeneration of the microbiome in the gut over various stages of a canine's living, providing insights into the variables that impact microbial resilience and variety. Developing solutions to support and preserve an appropriate canine microbiome requires a comprehension of these interactions. Focusing on the consequences of disturbances in the effect of gastrointestinal bacteria on the well-being of canines, this article looked at the intricate link between the microbiome as well as GI disorders in canines. It enhances our knowledge of the microbiome's function in illness origin and development by examining microbial changes linked to a variety of GI ailments. The paper also discusses the influence of canine GI illnesses on the microbiota and therapeutic approaches for them. In the context of managing disease, an examination of therapeutic interventions such as food alterations, probiotics, and antibiotics offers knowledge on such strategies influence on the gut microbiota composition and function. This review's main objective is to enhance comprehension of the complex connection between canines' microbiome and general well-being by combining existing research on the microbiome in normal canines and its changes in illness states.

Keywords: Canines, Digestive System, Gastrointestinal (GI), Well-Being, Microbiota, and Therapeutic Approaches

INTRODUCTION

The health and wellbeing of canines depend heavily on their microbiome. The term "microbiome" relates to the number of bacterium which live in different regions of a canine's body, usually the gastrointestinal system, just like the term "human microbiome" does. Canine digestion, immunity, and overall health are significantly impacted by this intricate bacterial community (1).

In canines, the microbiota, or gastrointestinal microbiome, in the stomach plays a critical role. It is composed of billions of bacteria that support immune system maintenance, vitamin synthesis, and the digestion and absorption of nutrients. For healthy digestion, food absorption, and infection prevention, a diverse and balanced gut flora is required (2).

The makeup of a canines' microbiome is impacted by several variables, including age, genetics, diet, as well as environment. A healthy microbiome may be attained by eating a diet rich in nutrients and well-balanced to encourage the growth of beneficial bacteria in the stomach. Stress, antibiotics, and other medications can upset the balance of the microbiome, which may result in digestive issues and weakened immunity (3).

It's important to keep the canine's microbiome healthy for good digestion, but it also affects the pet's general health. A rich and varied microbiome has been associated with immune response, inflammation, and even

mental well-being. Scholars are progressively investigating the connections among the stomach and other physiological systems, clarifying the complex interaction between the microbiome and the general health of a pet (4).

Pet owners should think about feeding their pets a balanced, nutritionally sound food, adding probiotics and prebiotics, and lowering stress levels that might harm the microbiome in order to preserve the microbiome and enhance overall health. Frequent trips to the doctor may also help monitor and treat any irregularities in the microbiome, keeping the canine's digestive tract and general health in excellent condition (5).

Improving general canine well-being requires an understanding of and commitment to the microbiome of canines. In order to ensure that their pets have happy and active lives, pet owners may promote their pets' health by providing them with a balanced diet, good cleanliness, and medical care (6).

HEALTHY CANINE MICROBIOME

Variations Along the Gastrointestinal GITract

Lab investigations and genetic techniques indicate that the number and variety of bacteria in the gut are growing. An early bacteriological investigation found that the small intestine of a healthy canine had a smaller bacterial population than the colon, with a range of CFU (colonial-forming units) per gram of luminal material (7). The total microbial burden in the canine gastrointestinal system has been estimated to be around ten times as many host cells thanks to the development of molecular technologies.

The distinct microbial compositions in various segments of the gut reflect unique microenvironments and physiological activities found in each area. Unlike the colon, dominated by anaerobic bacteria, the small intestine is inhabited by a mix of facultative and aerobic anaerobic bacterial species, including Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, and Proteobacteria (8).

Differing metabolites are produced and consumed along the GI tract, reflecting differences in taxonomic abundance. Metabolomics, a relatively young domain of study (9), intends to examine the metabolic interactions among the host and as well as the microbiome. Although samples from specific gut sections are challenging to collect, most clinical research relies on canine fecal samples, which exhibit the majority of relevant taxa, unlike in humans. This may be connected to the structure of the canine digestive system, it is shorter than humans and travels faster, allowing researchers to investigate canine gut microorganisms.

While there are composition differences between studies, major bacterial species are found in healthy canines' feces samples, demonstrating a fundamental fecal bacterial community. Fusobacterium, Bacteroidetes, and Firmicutes co-dominate the fecal microbiota of healthy canines. However, it's crucial to note significant variation in bacterial taxa proportions, attributed to evolving data analysis and sequencing methods (10). Individual differences in microbiota profiles also exist and should be considered when evaluating results from small sample sets.

Many important core bacterial species ecosystem, Firmicutes are members of the phylum Firmicutes with the Clostridia class among the most numerous taxa. Bacilli and Erysipelotrichi were common groups in Firmicutes, while the Lactobacillales order dominates the class Bacilli. Bacteroidetes, another prevalent phylum, includes genera such as Bacteroides, Prevotella, and Megamonas, with Bacteroides and Prevotella significantly varying in abundance among canines (11).

Fusobacterium, connected with healthy control canines, increases in canines with outdoor access, and higher levels are reported in other carnivore species. Actinobacteria and Proteobacteria, generally small intestine colonists are found in lower quantities in fecal samples under physiological settings. Members of the Enterobacteriaceae family, Anaerobic facultatives, present in feces, are linked to various disorders. Actinobacteria, connected to the small intestine, include families like Corynebacteriaceae and Coriobacteriaceae (12).

Diet Effect

Canines, natural carnivorous scavengers, tend to consume a variety of available food, even though they have a preference for a high-meat diet. The predominant focus of canine microbiome research (13) has been on extruded diets, such as kibble, comprising canines' dry food, up to 95% of it. Traditionally, high carbohydrate levels in these diets are achieved using vegetable components for the extrusion process. However, recent industrial methods have introduced kibble with higher protein and lower carbohydrate content as shown in Table (1). Additionally, there is a growing popularity of uncooked meals, both frozen and dried in a freezer, which prioritize meat and generally have minimal to no carbohydrate content.

Table (1). Comparative Nutritional Profiles for canines' Diets Normal Protein vs High Protein

Nutrition	Normal protein (%)	High protein (%)
Protein	30 - 40	18 - 25
Fat	15 - 20	10 - 15
Carbohydrates	30 - 40	40 - 50
Fiber	2 - 5	3 - 5
Calcium	1 - 1.5	0.5 - 1
Phosphorus	0.8 - 1.2	0.6 - 1
Sodium	0.2 - 0.5	0.2 - 0.4

It has been established that the composition of an animal's meal, especially notable differences in macronutrients between the diets of carnivores and herbivores, affects the gut microbiomes of different species (14). Even a quick consumption of animal products or plant-based diets can alter microbial community structures in omnivores including humans by surpassing individual differences in microbial gene expression. Omnivores are capable of flourishing on both extremes of the dietary range. In humans higher levels of vegetable fiber in extruded meals in canines are connected with higher Firmicute abundances and lower amounts of Fusobacteria and Proteobacteria.

The consequences of high-meat diets have been studied (15) by comparing the gut microbiomes of healthy canines' fed raw meat against those given kibble. Bones and Raw Food Prepared at Home (BARF) meals, made up of veggies, meaty bones, organs, and raw flesh, were fed to the canines participating in the experiments. Generally speaking, BARF meals had lower amounts of fiber and carbs and greater quantities of protein and fat than the kibble-fed control group.

The relationship between the butyrate kinase butyrate-synthesis is a pathway in carnivores and the clostridiaceae family, and *Clostridium perfringens* was highlighted in a recent study (16). Because this method allows butyrate to be created from protein, it is uncertain if bacteria that are specialists in carbohydrate fermentation would benefit carnivore gastrointestinal tracts in the same way that they do omnivores.

Dynamics of Gut Microbiome: Formation, Stability, and Decline

Mammals of all species experience Gut Microbiome (GI) tract colonization even before the infant leaves the birth canal (17). The mode of parturition and nutrition are reflected in the first colonization which differs and the established microbiome will become more diverse with time. In humans, infants born vaginally are exposed to the mother's vaginal microbiota, whereas babies born by cesarean section inherit germs from the mother's skin.

Although there isn't any research on canines delivered via cesarean, the dam's tongue exposes the pups to her fecal and vaginal microbiota, which may lessen the effect of the delivery technique.

Canine microbiomes, like human microbiomes, develop throughout weaning to look more like adult microbiomes. Several microbiomes were discovered in the first few weeks of a research with pups (18), aged one week to one year, with Proteobacteria the most frequent microbiota. At nine weeks, the levels of Proteobacteria had decreased, but those of both *Clostridium hiranonis* and *Faecalibacterium* spp. had dramatically increased, reaching levels comparable to those of healthy adult canines.

The environment, particularly other household members has the potential to affect the gut microbiota. A study of canines (19) and their owners discovered a significant exchange of the skin microbiome among pet owner pairings compared to non-household members. The fecal microbiome had a little impact as well. Due to possible zoonotic consequences, families with immunocompromised persons should take this microbiota exchange into account, even if its total impact is probably minimal.

There is a correlation between aging and decreased cognitive performance and a decline in the variety of gut microbes in other animals. Inflammaging, a chronic low-grade inflammatory condition indicated by dysbiosis within the microbiome has been associated with elderly people undergoing immunosenescence.

Disease of Gut Microbiome

Age, food, and environment contribute to maintaining the microbiome in a healthy state, but the modifications they cause minimal in comparison to the profound changes that occur in sick animals. Dysbiosis is related to several illnesses, both systemic and localized, that impacted by the gut microbiota. The gut transcriptome, proteome, or metabolome of microorganisms can vary due to dysbiosis, which is typified by alterations in the gut microbiota's composition. Higher than normal levels of bacteria with facultative anaerobic metabolism that belong to the Enterobacteriaceae family are a common sign of dysbiosis, and this is also occurring in canines (20).

Speculations have suggested that oxygen may play a part in the compositional alterations in the microbiota that occur during dysbiosis. Because oxygen, either alone or understanding how changes in gut homeostasis lead to dysbiosis, Increases the prevalence of Enterobacteriaceae in the large intestine is crucial when combined along with additional respiratory electron acceptors. Furthermore, the demographics of the gut microbiota regulates the localized manufacture of antibodies and has a substantial influence on immune function. Although the glycocalyx and the inner mucous layer prevent gut bacteria from getting into direct contact with enterocytes, dendritic cells in the intestine can reach within the stomach lumen. With their dendrites to collect microbiota samples. While B cells are exposed to the most invasive germs, macrophages also destroy some of them. IgA (Immunoglobulin A) is subsequently produced by B cells and released into the lumen, where it binds to bacteria and starts to destroy them.

Both humans and canines have been shown to have intestinal inflammation, which might be caused by gut dysbiosis that results in bile acid dysmetabolism (21). Bile acids (BA) have anti-inflammatory qualities and are essential for the digestion of lipids. Dysbiosis impairs secondary BA synthesis by interfering with gut bacteria's capacity to deconjugate and dehydroxylate BA. Chronic gastrointestinal disease can reduce the Comprising the apical sodium-dependent bile acid transporter (ASBT), a necessary component of linked primary BA resorption. As a result, intestinal inflammation is exacerbated by dysbiosis and inflammation, which impair BA metabolism. While a connection with dysbiosis has been found in several illnesses, a causal effect is frequently lacking, and Dysbiosis could not be the cause of the illness, but rather one of its symptoms.

GI Disorders and The Gut Microbiome

Gastrointestinal dysfunctions have an intense connection to gut dysbiosis. Both acute and chronic diarrhea have been correlated with changes to the gut microbiome. Investigations involving canines with GI disorders indicate

varied percentages of taxonomic abundance, similar to observations in healthy canines. Nonetheless, within the same illness manifestation, a similar pattern of increased or reduced taxa is frequently found.

When canines have acute uncomplicated diarrhea (AD), there is a marked dysbiosis that is typified by a reduction in the number of microorganisms that produce short-chain fatty acids (SCFAs), including *Turicibacter* spp., *Blautia* spp., *Ruminococcus* spp., *Faecalibacterium praunitzii* along with an increase in the genus *Clostridium*. As a result, there is a reduction in the variety of microorganisms, and the makeup of microbiological communities differs from healthy canines.

Despite its modest clinical manifestation, AD is linked to dysbiosis of the feces, which profoundly changes blood and urine metabolite profiles in addition to fecal SCFA profiles. This suggests that acute episodes of diarrhea affect the host's entire metabolic profile. According to research (22) there was a decrease in the quantity of bacteria that produce squalin in the feces of canines suffering from AD. Interestingly, the concentration of propionate showed a considerable drop, even if the total levels of SCFA decreased. Butyrate levels were discovered to be higher in canine feces samples suffering from AD. The authors speculate that the apparent paradox may result from decreased enterocyte use of butyrate or decreased absorption of butyrate.

Canines suffering from hemorrhagic gastroenteritis (HGE), another name for acute hemorrhagic diarrhea syndrome (AHDS) have microbiological changes that are comparable to those seen in AD cases. Despite having differing clinical symptoms, both illnesses contain a decreased amount of *Ruminococcaceae* and *Faecalibacterium* spp. Canines with AD and AHDS had lower levels of these bacterial groups than healthy canines. Research (23) connects *Clostridium perfringens* to AHDS, yet fecal samples from AHDS patients do not contain its enterotoxin.

Canines that have recovered from parvovirus infection have developed chronic enteropathies (CE), which is consistent with a human pattern. Dysbiosis and decreased concentrations of SCFA-producing bacteria are shared features between acute diarrhea and CE, as demonstrated by human and canine studies (24). It is necessary to do further research to assess the extended impacts of severe diarrhea and how it may contribute to CE. Antibiotic-responsive diarrhea (ARD), Food-responsive diarrhea (FRD), and immunosuppressive-responsive diarrhea, Inflammatory Bowel Disease (IBD) are three types of diarrhea. The three types of canine chronic enteropathies are classified based on how well they respond to therapy. All canines with chronic enteropathies, regardless of categorization, have different levels of intestinal inflammation, which results in dysbiotic microbiomes that are shared with healthy canines.

Before therapy, canines with IBD and FRD show comparable overall richness, diversity, and microbial composition. Their reaction to therapy differs even with these commonalities. Following therapy, the helpful bacteria *Bacteroides* are more prevalent in the colons of both FRD and IBD canines, indicating a change toward a healthy microbiome. However, several taxa of bacteria have varying abundances in FRD and IBD.

In a study (25) involving canines with FRD, the microbiome diversity was normalized and nearly matched healthy controls after a vegetable protein exclusion diet treatment. Furthermore, the richness increased. Unlike FRD, canines receiving immunosuppressive therapy for inflammatory bowel disease IBD may not, even with additional therapies like antibiotics, have a concomitant restoration of their microbiota as they recover clinically. They found that after three weeks of treatment, the diversity indices showed a tendency for further decline, all canines' clinical conditions had improved.

Canines with FRD and IBD respond to therapy, and this difference can be attributed to different pathogenic processes underlying their enteropathies. Canines' IBD is a combination of environmental variables and genetic susceptibility, whereas FRD is caused by prolonged exposure to food antigens. Resolving FRD mostly entails removing the causal antigen from the diet, which lowers inflammation and restores the balance of the microbiota.

The Impact of Treatment Methods on the Microbiome

Antibiotics are used to treat both acute and chronic gastrointestinal diseases to eradicate harmful bacteria. However, there is insufficient evidence to support antibiotic usage, which can have significant impacts on the gut microbiome. A controlled, randomized experiment with non-septic canine found no appreciable differences between the antibiotic and control groups in terms of overall result, hospitalization time, clinical symptom intensity, or death rate in instances like Acute Hemorrhagic Diarrhea Syndrome (AHDS). Antibiotics are commonly used to treat chronic diarrhea, yet research (26) showed no difference in the clinical recovery between canines treated with metronidazole plus prednisone and those treated with prednisone alone.

Antibiotics tylosin and metronidazole are utilized and have a significant influence on the gut microbiota for treating gastrointestinal disorders. Antibiotic treatment can cause gut dysbiosis, when broad-spectrum antibiotics are used. This results in Taxonomic richness rapidly and significantly declining, variety, and consistency. While many bacterial species return after antibiotic treatment is stopped, it is rare for the original composition to be fully restored (27). The effects of antibiotic use are well known, and probiotics, prebiotics, and synbiotics have received more attention. Beneficial bacteria that are already present in the host are encouraged to flourish by prebiotics, which include non-digestible dietary ingredients like fiber. Probiotics, give the host an outside source of living bacteria. Products with both combination are referred as synbiotics.

When probiotic bacteria try to through the gut, they usually run into conflict with the pre-existing microbiota. A synbiotic comprising seven probiotic species temporarily increased the population of *Enterococcus* and *Streptococcus* species in healthy canines, but this effect returned to baseline levels when treatment was stopped. Even if probiotics do not directly affect the abundance of certain microbial taxa, they can nevertheless provide benefits by producing metabolites and antimicrobial peptides (28).

These bioactive substances influence and interact with the immunological system and the local host's microbiome (29). A product made with sour milk comprising three *Lactobacillus* species developed from canines was given to canines with Atopic Dermatitis (AD) in a controlled clinical trial, which used a double-blind placebo design. By using this sour-milk product, the frequency of a toxin-producing organism strain of *Clostridium perfringens* and *Enterococcus faecium* both bacteria that cause diarrhea classified as possible enteropathogens was reduced and stool consistency quickly returned to normal.

Fecal microbiota transplantation (FMT) therapy for parvovirus-infected puppies resulted in a shorter hospital stay and quicker recovery than usual treatment, according to a rare case-control study in canines (30). Weaning-associated diarrhea was not prevented by FMT, and no improvement in fecal scores was noted in a laboratory environment when puppies received oral FMT. Sixteen canines in a case series had inflammatory bowel disease (IBD) was the subject of a different research, which revealed encouraging, albeit temporary, results. Canines who received daily oral doses of frozen donor stool after FMT showed signs of prolonged remission.

Though optimistic, further research is needed to discover the optimal technique to use when employing FMT to treat dysbiosis and associated illnesses in canines. Because of the preservation of donor materials, the manner and timing of administration, and anatomical and physiological differences between humans and canines, Human research findings may not be applicable to canines. Perhaps more studies will enable researchers to examine the inherent and possible restrictions of FMT's use in the management of gastrointestinal disorders.

CONCLUSION

The microbiome of a canines' stomach influences their overall health. In adult healthy canines, the gut microbiome is stable, although age, food, and a variety of other environmental variables can impact maintaining the microbiota in good shape. Changes detected in sick animals are evident, and whether they influence the metabolome, transcriptome, or proteome, they are referred as dysbiosis. When there is GI tract pathology, imbalance should be examined. Microbiota composition recovery does not always correspond with clinical healing, as well as the long-term ramifications of such residual changes are unclear. The discovery of bacteria-

derived materials and bacteria-taxa substances implicated in the development of both acute and long-term GI illnesses may contribute to the evolution of novel medicinal and diagnostic techniques and should be considered. There is a lack of knowledge on particular bacteria roles in canine GI health. Investigating targeted therapies and individualized diets to improve the digestive dynamics of canines.

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