

In sickness and in health: the intestinal microbiome of dogs

Na saúde e na doença: os efeitos do microbioma intestinal no cão

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ABSTRACT

Studies on the interactions between the intestinal microbiome and its host have strengthened in the last decade. However, publications on this topic in dogs still need to be made available, reinforcing the need for new studies and literary data for consultation. Given this, this review aims to describe the intestinal microbiome and its interactions with the canine host, which can contribute to both health and morbid conditions in these animals. The definition of microbiome encompasses the collective genome of all microorganisms that live in a defined habitat (intestine). It is known that the dog's intestinal microbiota is varied, composed of bacteria, archaea, viruses, fungi, and protozoa. Under normal conditions, there is commensalism between some of these microorganisms and the host, which promotes critical physiological relationships and interactions that contribute to homeostasis and the consequent health of the animal. With this in mind, it is expected that the disturbances associated with the microbiome will result in imbalances in this commensal relationship and thus precipitate the development of diseases and aggravation of other diseases, thus characterizing intestinal dysbiosis.

Keywords: Dog. Dysbiosis. Microbiota. Intestine.

RESUMO

Os estudos sobre as interações entre o microbioma intestinal e o seu hospedeiro ganharam força na última década. Entretanto, as publicações acerca de tal temática em cães ainda são escassas, o que reforça a necessidade de novos estudos e dados literários para consultas. Frente a isso, o objetivo da presente revisão é descrever sobre o microbioma intestinal e suas interações e principais efeitos no cão, os quais podem contribuir tanto para a higidez quanto para quadros mórbidos desses animais. A definição de microbioma engloba o genoma coletivo de todos os microrganismos que vivem em habitat definido (intestino). É sabido que a microbiota intestinal do cão é muito variada, sendo composta por bactérias, arqueas, vírus, fungos e protozoários. Em condições normais, há o comensalismo entre alguns desses microrganismos e o hospedeiro, o que promove importantes relações e interações fisiológicas que contribuem sobremaneira para a homeostasia e consequente saúde do animal. Ciente disso, é de se esperar que os distúrbios associados ao microbioma resultarão em desequilíbrios nessa relação comensal e, assim, precipitar o desenvolvimento de doenças e/ou agravamento de outras moléstias, caracterizando, assim, a disbiose intestinal.

Palavras-chave: Cão. Disbiose. Microbiota. Intestino.

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Received: October 18, 2022

Approved: May 29, 2023

How to cite: Varallo GR, Bueno GM, Brandão CC, Sanches L, Oliveira IBD. In sickness and in health: the intestinal microbiome of dogs. *Braz J Vet Res Anim Sci.* 2023;60:e203612. <https://doi.org/10.11606/issn.1678-4456.bjvras.2023.203612>.

Introduction

From one perspective, a mammal can be considered a multispecies organism concerning cell composition according to the following criteria: cell composition, genetic diversity, and metabolic capacity. This plurality is guaranteed by the microbiota that lives in symbiosis and balances with this animal, i.e., the host, as well as by its genomic and physiological characteristics (Barko et al., 2018). About microbiota, it is essential to emphasize that different parts of the body - oral cavity, skin, nasal cavity - hold their community of microorganisms. In quantitative terms, the largest resides in the intestines (Mondo et al., 2019), whose total microbial load is estimated to be between 10^{12} to 10^{14} microorganisms (Suchodolski, 2011a, 2011b).

Microbiota is the set of microorganisms inhabiting a given environment (Hernandez et al., 2022). In this context, a dog's gastrointestinal tract (GIT) is colonized by a complex and diverse community of microorganisms composed of bacteria, archaea, viruses, fungi, and protozoa. Most of this microbiota is composed of bacteria (Pilla & Suchodolski, 2020). These different microbial populations play complex roles in host health by providing nutritional substrates, modulating the immune system, and aiding in defense against intestinal pathogens (Tal et al., 2021).

The term microbiome is defined in this review as the collective genome of all microorganisms that live in or in a defined habitat (Jergens, 2017; Lederberg & McCray, 2001; Pilla & Suchodolski, 2020; Schmitz & Suchodolski, 2016). Due to its influence and interactions with the host, the gastrointestinal microbiome is recognized as a metabolic and immune organ, starting in the oral cavity and ending in the rectum (Wernimont et al., 2020; Ziese & Suchodolski, 2021).

This review describes the intestinal microbiome, its interactions, and its main effects on dogs, which can contribute to both health and morbid conditions in these animals (*Canis lupus familiaris*).

Acquisition and Maturation of the Intestinal Microbiome

Studies on the acquisition and development of the canine intestinal microbiome are incipient (Barko et al., 2018). In addition to the physiological condition of each animal, the preliminary colonization of the digestive system is also influenced by external factors, including maternal, social, environmental, and nutritional. These factors help in the development and establishment of the intestinal microbiota in the puppy, as well as favoring the generation of a stable, balanced, and personalized microbial profile (Garrigues et al., 2022; Guard et al., 2017). As in humans, it is suggested that the beginning of colonization occurs during birth, through direct contact with maternal (vertical transmission, by licking) and environmental microorganisms (Barko et al., 2018; Jergens, 2017).

Thus, the type of parturition can influence the newborn's intestinal microbiota composition. In a vaginal birth, a human's baby microbiota is composed of bacteria in the mother's vagina and intestine (Dominguez-Bello et al., 2010; Mackie et al., 1999). In the cesarean section, bacteria are present on the mother's skin and mouth (Backhed et al., 2015; MacIntyre et al., 2015). However, in dogs, the amniotic membrane remains intact after birth, and in unassisted birth, the bitches' teeth break the sac. For this reason, it is inferred that the vaginal canal in dogs should not contribute significantly to the neonatal microbiota of puppies, which is influenced by lactation and the environment (Balouei et al., 2023). In addition, the type of parturition can also influence the composition of the microbiota of dam's milk. One study found greater bacterial richness in the colostrum of female dogs that had normal delivery (vaginally) when compared to those submitted to cesarean section. The identical bacterial specimens detected in the mothers' colostrum were isolated from the meconium of neonates delivered vaginally. Moreover, they also observed that the bacteria in the mother's milk were present in the intestine, meconium, and feces of newborn puppies. However, the origin of the intestinal microbiota in colostrum is unclear (Garrigues et al., 2022; Kajdič et al., 2021). Therefore, the potential for microbial colonization by external agents at this stage of life is favored by low microbial abundance and diversity (Garrigues et al., 2022). The opportunistic colonization of specific species acquires the emergence of commensal bacteria due to random environmental encounters.

These first-chance bacteria can modulate the gene expression of intestinal epithelial cells, which creates a favorable environment for microbiota development and prevents the growth of other bacteria that will be introduced later (Jergens, 2017). In mice and humans, such symbiosis is driven by interactions between microorganisms and the host's immune signaling pathways, which promotes immune tolerance and niche colonization (Round et al., 2011; Stockinger et al., 2011).

In dogs, as in humans, microbiome maturation occurs at weaning (Pilla & Suchodolski, 2020). A diverse composition, functional diversity, and dynamic interactions characterize the mature intestinal microbiome. Another feature is its stability in healthy adult animals over time. Although no long-term studies exist in dogs, the canine intestinal microbiome is believed to achieve such stability (Barko et al., 2018; Pilla & Suchodolski, 2020).

Composition of the Intestinal Microbiota

Diet, genetics, the environment, and some drugs influence the composition and functional capacity of the intestinal microbiota. Given this, it is concluded that each individual's microbial profile is unique. (Suchodolski, 2011a, b). However, conservation of microbial genetic content is observed, which suggests a central microbiome, resulting in comparable microbial function among individuals (Guard & Suchodolski, 2016; Huang et al., 2020).

Different physiological mechanisms regulate microbial colonization of the GIT. Gastric acid, bile, and pancreatic enzymes have antimicrobial activity that prevents the invasion of most ingested microbes. Furthermore, peristalsis is an event that hinders the adhesion of microorganisms to the SI mucosa, propelling them to the LI, whose motility is lower. Finally, the ileocolic valve acts as an obstacle that prevents the retrograde migration of bacteria from the LI to the SI (Suchodolski, 2020).

Different bacterial populations colonize different regions of the canine GIT. This is due to physiological differences between segments of that tract, which favor developing and maintaining unique microbial ecosystems. These differences include transit time, availability of substrate, host secretions, pH, and oxygen tension. This is physiologically important, as these niches perform specialized functions closely related to host homeostasis. As a result, in quantitative and qualitative terms, bacterial communities are distinct in each anatomical segment of the GIT (Barko et al., 2018; Garcia-Mazcorro & Minamoto, 2013; Pilla & Suchodolski, 2020, 2021; Schmitz & Suchodolski, 2016; Suchodolski, 2011a, 2011b; Wernimont et al., 2020).

The canine stomach harbors a few bacteria that can survive in an acidic environment (Suchodolski, 2022). In the intestine, bacterial concentrations increase in the aboral direction. The ileum harbors about 10^7 colony-forming units (CFU) per gram (g) or milliliters (mL) of intestinal contents. While in the colon, it varies between 10^9 to 10^{11} CFU/g or mL of intestinal content (Suchodolski, 2011b). In addition, aerobic and facultative aerobic bacteria are predominant in the small intestine (SI), while in the large intestine (LI) most are strictly anaerobic, which corresponds to the decreasing oxygen gradient along the GIT. *Bacteroides*, *Clostridium*, *Lactobacillus*, *Bifidobacterium* spp, and *Enterobacteriaceae*, are the predominant bacterial groups in dogs isolated in cultures (Honneffer et al., 2017; Pilla & Suchodolski, 2020; Suchodolski, 2011b).

Molecular studies have allowed for a better characterization of the composition of the intestinal microbiome of dogs, as they have enabled the evaluation of bacteria that were not detected by culturing (Costa & Weese, 2019; Suchodolski, 2011b; Suchodolski & Simpson., 2013). The DNA or RNA of these microorganisms is extracted from intestinal samples (stool, luminal content, or tissue) and subjected to testing. For molecular or phylogenetic identification, a specific gene is amplified with universal primers, whose targets are the conserved regions of the gene. These locations flank the variable sites that allow for identification when sequenced. The 16S RNA gene is the most used for bacteria (Suchodolski, 2011b). Molecular studies using high-throughput sequencing are now the standard for microbiota characterization (Suchodolski, 2020).

The intestine is estimated to contain several hundred bacterial phylotypes (Suchodolski, 2020). Under normal conditions, in dogs, there is a predominance of phyla: Firmicutes, Fusobacteria, Bacteroidetes, Proteobacteria, and Actinobacteria (Honneffer et al., 2017). Others (less than 1%) include Spirochaetes, Tenericutes, and Verrucomicrobia (Suchodolski, 2020). The composition of each niche depends on the production and consumption of different metabolites. Obtaining samples (mucosal or intestinal) from higher regions of the tract is more challenging. Therefore, most clinical studies assess the fecal microbiota of dogs (Pilla & Suchodolski, 2021; Schmitz & Suchodolski, 2016).

In the fecal microbiome of healthy dogs, there is a co-dominance of three phyla: Fusobacterium, Bacteroidetes, and Firmicutes. The relevant bacterial taxa are listed in Table 1. The phyla Proteobacteria and Actinobacteria can also be identified, despite primarily colonizing the small intestine. As stated a priori, the proportion between the phyla can vary between individuals due to breed, diet,

Table 1 – The relevant bacterial taxa in the intestinal microbiome of dogs (extracted from Pilla & Suchodolski, 2020)

Phylum	Class	Family	Genus/Species
Actinobacteria	Coriobacteriia	Coriobacteriaceae	<i>Collinsella</i>
Bacteroidetes	Bacteroidetes	Prevotellaceae	<i>Prevotella</i>
		Bacteroidaceae	<i>Bacteroides</i>
Firmicutes	Clostridia	Clostridiaceae	<i>Clostridium</i>
		Ruminococcaceae	<i>Faecalibacterium prausnitzii</i>
	Bacilli	Peptostreptococcaceae	<i>Peptostreptococcus</i>
		Lachnospiraceae	<i>Blautia</i>
		Veillonellaceae	<i>Megamonas</i>
		Streptococcaceae	<i>Streptococcus</i>
		Lactobacillaceae	<i>Lactobacillus</i>
		Turicibacteraceae	<i>Turicibacter</i>
Fusobacteria	Fusobacteriia	Fusobacteriaceae	<i>Fusobacterium</i>
Proteobacteria	Betaproteobacteria	Alcaligenaceae	<i>Sutterella</i>
	Gammaproteobacteria	Enterobacteriaceae	<i>Escherichia coli</i>

age, environment, as well as the methods of analysis (Garcia-Mazcorro et al., 2012; Hand et al., 2013; Handl et al., 2011; Jarett et al., 2021; Jha et al., 2020; Middelbos et al., 2010; Pilla & Suchodolski, 2020). You and Kim (2021) developed a study comparing healthy dogs' intestinal microbiota. Fresh fecal samples from 96 dogs were analyzed by sequencing the V3-V4 region of the 16S rRNA gene. The major microbial phyla were Firmicutes (44.8%), Bacteroidetes (27.7%), Fusobacteria (14.2%), Proteobacteria (8.8%), and Actinobacteria (3.4% of the total average abundance).

According to Rigottier-Gois (2013), oxygen may be responsible for changes in the microbiome's composition. An increase in oxygen concentration allows for the uncontrolled growth of facultative anaerobic bacteria, such as species of the phylum Proteobacteria of the Enterobacteriaceae family, in addition to causing a reduction in strict anaerobic populations (Zeng et al., 2017).

Interactions Between the Intestinal Microbiota and the Healthy Host

As stated, intestinal microbiota consists of bacteria, archaea, viruses, and eukaryotic organisms (Pilla & Suchodolski, 2020). These microorganisms can interact with the host in a symbiotic way, for example, as nutritional support. Some bacteria present in the intestine produce short-chain fatty acids (SCFA) that help nourish the intestinal epithelium. In contrast, the mucus secreted by the intestinal epithelium can feed some beneficial bacteria (Vernia et al., 2003; Ma et al., 2021). SCFAs have immunomodulatory properties and modulate colonic and intracellular pH. Changes in pH influence inflammatory diseases of the intestinal tract and indirectly alter the composition of intestinal microorganisms, for example, reducing the growth and activity of potential pathogens (Vernia et al., 2003).

The phyla Firmicutes, Bacteroidetes, and Actinobacteria comprise some bacterial groups that produce metabolites that directly impact the host's health (Suchodolski, 2020). Bacteria present in SI and LI contribute differently to gastrointestinal health. Those present in the colon are the ones that most benefit the dog (Suchodolski et al., 2012). They act as a natural and physical barrier against exogenous transient pathogens, as they act as competitors for nutrients and binding sites in the intestinal epithelium and produce antimicrobial substances such as lactic acid and bacteriocins. They contribute to the formation of tight cell junctions called "tight junctions," which prevent the translocation of pathogens, toxins, and dietary allergens. They also help to break down nutrients and obtain energy from the diet, provide nutritional metabolites for enterocytes, and play an essential and fundamental role in regulating the host's immune system (Jergens, 2017; Suchodolski, 2013; Pilla et al., 2020). Other functions, such as synthesizing vitamins (K and B complex), the biotransformation of bile acids, and xenobiotic metabolism, have also been described (Mondo et al., 2019).

These complex interactions between microbiome, environment, and host are related to physiological and metabolic events. In addition to those already mentioned, the microorganisms participate in the natural defense mechanism against invading pathogens through competition for nutrients, control of oxygen concentrations, pH, and production of antimicrobial substances (National Research Council, 2006; Swanson et al., 2011). They can also control the proliferation, differentiation, and renewal of the intestinal epithelium, synthesis of vitamins, degradation and fermentation of amino acids, and modulation of intestinal permeability (Suchodolski & Simpson, 2013).

The primary metabolic function of the colon's intestinal microbiota is the fermentation of non-digestible nutrients (especially complex carbohydrates: starch, cellulose, pectin, and inulin) into short-chain fatty acids, e.g., acetate, propionate, and butyrate, which provide energy for bacterial metabolism and colonocytes, promote the growth and differentiation of intestinal epithelial cells, and regulate motility, in addition to detaining local and systemic anti-inflammatory action, as they induce immunoregulation of regulatory T lymphocytes (Tregs) (Barko et al., 2018; Machiels et al., 2014; Middelbos et al., 2007; Pilla et al., 2020; Teshima, 2003). It is noteworthy that bacterial enzymes can convert some primary host metabolites into secondary metabolites, such as indole (tryptophan degradation by-product), which improves intestinal permeability and increases mucin production, and secondary bile acids (deoxycholic, lithocholic) essential for fat absorption (Jergens, 2017; Suchodolski, 2020).

The activities performed by intestinal bacteria are specific to each bacterium and the products generated. *Clostridium* spp., *Peptostreptococcus* spp., and *Peptococcus* spp. are responsible for ammonia production from the decarboxylation and deamination of amino acids. *Clostridium hiranonis*, *Lactobacillus* spp., *Enterococcus* spp., *Pseudomonas* spp., *Sphingomonas* spp., and *Lactobacillus* spp. synthesize secondary bile acids, vitamin K, B12, biotin, and folic acid through deconjugation, dehydroxylation, and vitamin synthesis. *Clostridium cluster*, *Prevotella* spp., *Faecalibacterium* spp., and *Bifidobacterium* spp. produce lactic, propionic, acetic, and butyric acid through carbohydrate fermentation. From the fermentation of amino acids sulfate-reducing bacteria, *Desulfovibrio* spp., *Clostridium* spp., and *Peptostreptococcus* spp. produce hydrogen, methane, amines, phenols, ammonia, organic acids, and hydrogen sulfite. With the degradation of oxalate, the synthesis of methanoate and carbon dioxide occurs by *Oxalobacter formigenes*. *Bifidobacterium* spp. produces lactic acid from the breakdown of inulin and starch. Methane bacteria produce methane and carbon dioxide through the metabolism of hydrogen, alcohol, and acetic acid (Suchodolski, 2011a).

Despite the differences in the rates of microorganisms found in the segments of the GI tract, most clinical studies focus on the analysis of the fecal microbiota due to the ease of obtaining samples, which contrasts with the other niches (Pilla & Suchodolski, 2020). There are few studies on the small intestinal function of the microbiome in dogs (Suchodolski, 2020). Tiny intestinal bacteria have a more delicate relationship with the host. As a result of increased intestinal motility, they are adherent to the mucosa. These organisms are essential to mucosal immunity

(Suchodolski, 2013). Studies in healthy dogs have observed significant differences between the microbiome of the small and large intestines, including greater representation of Proteobacteria in the duodenum and increased *Lachnospiraceae* and *Ruminococcaceae* in the large intestine (Honneffer et al., 2017; Suchodolski et al., 2008). Honneffer et al. (2017) observed a high pyruvate concentration in dogs' small intestines in the metabolomic analysis. However, there is a need for more robust data to determine the function of the microbiota in this intestinal segment in that species (Suchodolski, 2022; Wernimont et al., 2020). It has been proposed in humans that the small intestinal microbiota is oriented around using simple, diet-derived carbohydrates (El Aidy et al., 2015).

It is essential to emphasize the relevance of, and the need for, several species that make up the microbiome and their respective purposes. If only one species performed the functions and activities, any aggression to the microbiome, such as using an antibiotic, would deprive the host of the beneficial function of a given organism. Therefore, the microbiome comprises several species to ensure resilience and maintain its functions, in addition to indicative of a healthy microbiome (Lozupone et al., 2012).

The Immune System in the Intestine

The immune system comprises cells, tissues, and organs that, together with hundreds of elements, act in the body's defense. Among the immunological components, those of the GIT stand out for their complex and dynamic lymphoid activity. Starting at the birth of animals, the physio-immunological modulation of this vital organ is constantly influenced by several factors, such as diet and gastrointestinal microbiome (Gomes, 2013; Teixeira & Abranches, 2015).

Exogenous factors, such as ingested food and exposure to microbiological agents (non-commensal), also determine the composition of the local microbiome. This, in turn, influences the mechanisms of the immune system, promoting the migration of B and T cells, in addition to the production of microbial peptides and pro-inflammatory cytokines (Teixeira & Abranches, 2015). Therefore, the general health status of animals is closely related to the metabolic activity of the gastrointestinal microbiome and its power to favor imbalances and immunological regulations (Gonçalves et al., 2016; Suchodolski, 2013).

From studies, it is known that the intestinal morphology of animals raised in microorganism-free environments presents structural tissue modifications at the level of epithelial and goblet cells, which impair the formation of crypts, villi, and mucus layer (Gomes, 2013; Gonçalves et al., 2016).

Daniel et al. (2021) reported the importance of the microbiome/host interaction for the health of the intestinal mucosa, which among many functions, participates in the maturation of the immune system and homeostatic control of the animal. Mediation of the immune system in the intestinal environment is believed to occur through the recognition of molecular patterns associated with pathogens by cellular pattern recognition receptors (PRRs) through interactions of microbial metabolites and molecular surfaces. This cell recognition activates factors that produce pro-inflammatory cytokines and chemokines (Gonçalves et al., 2016; Suchodolski, 2013).

Intestinal immunity has a highly active lymphoid tissue that acts on innate and adaptive immune responses. Faced with a challenge, the first to be effective is innate immunity, with epithelial cells and the immune system located in the lamina propria. When there is a disorder in the epithelial barrier due to the entry of bacteria, cellular and humoral responses develop through the activation of PRRs (Suchodolski, 2013; Teixeira & Abranches, 2015). The adaptive immune system is based on T and B lymphocytes and antigen-specific memory cells. The type of response induced by commensal and pathogenic agents influences the immune modulation in the intestinal environment (Gonçalves et al., 2016). The resident intestinal microbiome also participates in immunomodulatory functions, as it competes for mucosal adhesion sites and nutrients, leading to a physiologically restrictive environment for non-resident species. Furthermore, it regulates the production of local antibodies and establishes protection against endotoxins (Pilla & Suchodolski, 2020; Suchodolski, 2013). When captured in the intestine, most of these invasive bacteria are seized by dendritic cells, killed by macrophages, and presented to B lymphocytes (Tizard & Jones, 2018).

The secretion of IgA from the B lymphocytes and specific bacterial destruction occurs in the intestinal lumen. The microbiota composition affects the immune system and signals the activation of Treg cells, which in turn activate the T helper cells (Tizard & Jones, 2018). These cells control the response to microbial antigens triggering or inhibiting inflammation (Gonçalves et al., 2016; Tizard & Jones, 2018).

Dysbiosis of the resident microbiota in the intestine can lead to the translocation of invading bacteria to the mesenteric lymph nodes, together with an intense immune response against pathogens. The literature reports that many systemic and localized diseases can affect or be affected by the intestinal microbiome and, consequently, by dysbiosis (Pilla & Suchodolski, 2020). Suchodolski (2013) mentioned that several gastrointestinal disturbances in dogs result from dysbiosis.

The authors also noted consequences in extra-intestinal organs, such as the skin and genitourinary tract.

As mentioned previously, the diversity of the microbial population in the intestine is related to inflammatory and anti-inflammatory interactions, and thus not only intestinal homeostasis. Although there are grounds for the microbiome's participation in gastrointestinal and other diseases, there is still room for clarification on the exact mechanisms involved (Pilla & Suchodolski, 2020; Gonçalves et al., 2016).

Dysbiosis

Intestinal dysbiosis is broadly defined as a compositional and functional alteration in the microbiome, which is caused by a set of environmental and host-related factors. This alteration destabilizes the microbial ecosystem beyond its resistance and resilience capabilities (Levy et al., 2017). It may have one or more of three characteristics that may co-occur. These include loss of commensals, expansion of pathobionts, and loss of overall microbial diversity (Levy et al., 2017; Petersen & Round, 2014). Vangay et al. (2015) also include a fourth characteristic: the change in functional capability. It can be characterized by significant changes in the microbiome's composition due to decreased species diversity and changes in the proportion between symbiotic and pathogenic microorganisms (Kamada et al., 2013). According to Zeng et al. (2017), these changes in the microbiome's composition lead to functional changes in the microbial transcriptome, proteome, or metabolome.

In addition to the decrease in the diversity of microorganism species, intestinal and systemic inflammatory environment changes are due to bacterial translocation and endotoxin production (Barko et al., 2018; Suchodolski & Simpson, 2013). Although studies show that dysbiosis is responsible for the onset of the inflammatory process, it can be considered a consequence of inflammation of the intestinal mucosa (Alshawaqfeh et al., 2017). Barko et al. (2018) mention that there can also be an alteration in the metabolic relationships between the microorganism and the host.

In addition to the pathogenic microorganisms competing with the host for the nutrients coming from the ingestion that could be absorbed by the animal, in these situations where there is a decrease in the populations of commensal microorganisms and proliferation of undesirable bacteria, the nutritional needs of the host are impaired by the increase in the renewal speed of the enterocytes and by the decrease in the height of the villi. Consequently, there is an increase in the thickness of the mucosa and the depth of the intestinal crypts, an increase in the speed of intestinal transit, and an impairment of nutrient absorption (Wenk, 2006).

Walker & Lawley (2013) mention that in humans and laboratory animals, there is a decrease in the proportion of mandatory anaerobic bacteria and an increase in facultative anaerobes, including *E. coli* and genera such as *Salmonella*, *Proteus*, *Klebsiella*, and *Shigella*, even though the cause of dysbiosis varies between individuals and the pathological condition involved. A study carried out in dogs shows an increase in the relative proportions of bacteria from the Proteobacteria phylum in animals with idiopathic inflammatory bowel disease compared to healthy dogs. A decrease in the relative proportions of bacterial groups of the phyla Fusobacteria, Bacteroidetes, and species of the phylum Firmicutes can also be observed (Suchodolski et al., 2012).

According to Suchodolski (2016), these changes in the composition or the variety of species of microorganisms present in the intestinal microbiome can occur due to different factors. They may be related to different disorders and diseases, acute or chronic, not only in the gastrointestinal tract but also in organs or systems. Intestinal dysbiosis may be related to chronic enteropathies (responsive to food and antibiotics); idiopathic inflammatory bowel disease; acute hemorrhagic diarrhea syndrome, and acute diarrhea due to other causes (infectious and non-infectious); situations that cause intestinal stasis, such as anatomical abnormalities, congenital blind loops, neoplasms, foreign bodies, chronic intussusception and diverticula, strictures or adhesions of the small intestine; motility disorders due to hypothyroidism, diabetic autonomic neuropathy, and scleroderma; decreased gastric acid production in cases of atrophic gastritis and administration of acid-suppressing drugs such as H2 blockers and omeprazole; use of antimicrobials; pancreatic insufficiency exocrine, which results in decreased production of pancreatic antimicrobial factors.

Conclusions

Interactions between the intestinal microbiome and the dog are intense, active, and necessary for homeostasis. Its effects on the host are so relevant that some have recognized it as a metabolic and immune organ. In health, the intestinal microbiome performs several functions, such as natural defense against invading pathogens, control of proliferation, differentiation, renewal of the intestinal epithelium, synthesis of vitamins, degradation, and fermentation of amino acids, and modulation of intestinal permeability. However, in sickness, only some studies aim to understand canine intestinal dysbiosis. The imbalance in host-microbiome interactions is associated with different disorders and diseases in the gastrointestinal tract and other organs and tissue.

Thus, the characterization of this condition can be a challenge. Therefore, it is understood that the maintenance and recovery of the intestinal microbiome are essential tools in preventing dysbiosis since different factors may be related to changes in the composition or variety of species of microorganisms.

Conflict of Interest

None of the authors of this paper has a financial or personal relationship with other people or organizations that could inappropriately influence or bias the paper's content.

Ethics Statement

The study did not require ethical approval.

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Financial Support: None.