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The gut microbiome and health of companion animals: Insights into physiology, dysbiosis and disease association

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Abstract
Gut health is vital for pets. It is a complex system that constantly interacts with ingesta, environmental pathogens, and pollutants, while maintaining symbiosis with the local microbiome. This system is supported by other physiological systems, such as the hepatobiliary tract. It is necessary to understand how this system fundamentally operates, the importance of quality gut, how various disease processes and other factors affect it. The aim of this review article is to provide insights into gut health and its microbiome, highlight recent studies and scientific contributions, present updates provided by various professionals and to explore in detail about complex interactions with a specific focus on their implications for the health of domestic pets particularly cats and dogs by integrating insights from both veterinary science and relevant human data.

Keywords: Microbiome, Dysbiosis, gut, immunity, health, relevant human data, veterinary science

1. Introduction
The gastrointestinal system, commonly referred to as the gut, serves as the primary organ responsible for acquiring nutrients and essential compounds required to sustain the host's physiological functions. Health of animals is highly influenced by the multidirectional interaction between the gut microbiome and various organ systems (Rindels JE and Loman BR., 2024) [1]. Maintaining a healthy gut is fundamental to the proper functioning of the body on a daily basis. This system does not rely exclusively on the host's digestive enzymes; rather, it depends significantly on activity of the microbiota to digest and metabolize compounds that host alone cannot efficiently process.
This symbiotic relationship plays a critical role in maintaining intestinal health, which in turn has a profound impact on the overall well-being of the host. Despite its importance, the host-microbe interaction is frequently underestimated and insufficiently addressed, especially in pets.

"A healthy gut reflects a healthy pet".

2. Physiology of gut microbiome
The term gut microbiome refers to the collection of microbes that reside in the gastrointestinal tract. It includes bacteria, viruses, bacteriophages, protozoa, and fungi and forms an integral part of host metabolism (Belkaid Y and Hand TW, 2014) [2]. These gut microbes maintain a positive and balanced (symbiotic) relationship with host's gut. However, microbial composition and abundance were influenced by various factors such as age, nutritional status, type of feed, management practices, concurrent diseases, hormonal changes, medications, and stress, all of which can alter their population.
Due to these varying factors, there is a considerable variation in gut microbiota not only between species but also among individual animals.

Each animal possesses a unique gut microbiome profile. According to Li Q *et al*., 2017 [3], canine models fed high-protein, low-carbohydrate (HP-LC) diets had lower *Bacteroidetes/Firmicutes* ratios and higher *Bacteroides/Prevotella* ratios compared to those fed low-protein, high-carbohydrate (HC) diets. Additionally, the abundances of *Clostridium hiranonis*, *Ruminococcus gnavus*, and *Clostridium perfringens* were increased. This study demonstrates that even dietary variations can significantly influence the composition of the gut flora in pets.

In neonates, microbial population is usually low. However, as the animal ages, the diversity and complexity of the microbial community increase. Exposure to environmental microbes facilitates the development of immunity, often indirectly. These microbes also act as a protective barrier by colonizing the gut and preventing the attachment and replication of pathogenic organisms. Function and composition of gut is shaped by competition and interactions among microbes (Machado D *et al*., 2021) [4]. Additionally, gut microbes secrete antimicrobial peptides that inhibit the growth of harmful organisms.

Common antimicrobial peptides secreted in the gut include defensins, cryptdin-related peptides, and cathelicidins. Among these, defensins are most prominent (Marlon H. Cardoso *et al*., 2022) [5]. The breakdown of nutrients by gut microbes surpasses the capability of host's digestive enzymes. Moreover, these microbes contribute to the synthesis of several essential compounds, including vitamins and neurotransmitters (such as Serotonin). The majority of gut microbes colonize the gastrointestinal tract through ingesta; hence, nutrition has a vital role to play in shaping gut. Gut influenes metabolism and overall growth, both directly and indirectly. Directly it supports nutrient digestion and absorption, indirectly it modulates microbial products such as short-chain fatty acids (SCFAs), and influences gut–endocrine signalling via ghrelin- or leptin-mediated pathways, which in turn regulate growth hormone secretion. Loss of these commensal microbiota is associated with decreased SCFA and bile acids. Compounds like tryptophan from the gut play a significant role in daily metabolism, including inflammation, immune modulation, and the synthesis of serotonin.

3. Microbiome Population

Various species of bacteria (most predominant), archaea, fungi, protozoa, and viruses inhabits the gastrointestinal tract (GI) of cats and dogs (Suchodolski JS., 2011) [7]. According to Pilla R and Suchodolski JS., 2020 [8], majority of bacterial population of canine gut comprises of *Firmicutes*, *Fusobacteria*, *Bacteroidetes*, *Proteobacteria* and *Actinobacteria*. These inhabitants of intestinal tract usually trillions in number may interact with one another and with the host through direct or indirect mechanisms (Wang S *et al*., 2023). A- and β-diversity metrics are used to study gut microbial diversity, in which alpha denotes the diversity of microbes within a single sample or group, whereas beta compares the microbial composition between different groups or samples.

The Bacterium count in ileum is approximately 10^{7} CFU/g or ml and in colon of dogs and cats, it ranges between 10^{9} and 10^{11} CFU/g or ml of intestinal content. The bacterial groups that are predominantly cultured from intestines of dogs and cats are *Bacteroides*, *Clostridium*, *Lactobacillus*, *Bifidobacterium spp* and *Enterobacteriaceae* (Suchodolski JS., 2011) [7]. 16s rRNA sequencing can be used to identify the microorganisms and its divergence is measured in β-diversity.

According to a study by Foster ML *et al*., 2013, they identified a total of 5 phyla of fungus *spp.* from naturally defecated stools. Among these, more than half of dogs were found with *Ascomycota* and *Basidiomycota* (in both groups of diseased and healthy). The remaining phyla that are identified were *Chytridiomycota*, *Neocallimastigomycota* and *Microsporidia*. Shi Y *et al*., 2021 [12] in their meta-analysis, concluded that dogs have a gut viral population comprising a total of 31 DNA and 32 RNA virus families. It includes population homologous to the animal viruses of family Astroviridae, Coronaviridae, phages of the family Microviridae, Siphoviridae and unclassified phages etc. These two studies reflect the high variability present in the gut microbiome.

4. Role of the Gut in Immunity

In the development of the host immune system, gut has an important role to play (Belkaid Y and Hand TW, 2014) [2]. Various pathogens through the ingesta enters the body, which in turn primes the host's adaptive immunity (T and B cells). The gut microbiome can enhance the host's non-specific immunity by maintaining and strengthening the intestinal barrier function. Mucus production is also pivotal for host defense, as it forms a physical barrier that separates bacteria from the host and avoids breach of the intestinal barrier (Takiishi T *et al*., 2017) [14]. Mucoprotein (MUC2) is the most abundant mucin in the gut and is found in the outer mucus layer. It competes with pathogenic bacteria to bind to the surface receptor, thereby inhibiting pathogen colonization. Antigens encountered at the gut epithelium help stimulate both local and systemic immune responses, particularly through the activation of enteric immune mechanisms. The development, growth and immune system activity is influenced and regulated by complex interaction between intestinal cell lining, residing microbiota and its metabolites (Soderholm AT and Pedicord VA, 2019) [15].

The host's response to both foreign and symbiotic microbes is essential for maintaining homeostasis, with Toll-like receptors (TLRs) playing a key role. Various metabolites that are metabolized by the microbiota are capable of communicating between immune cells and the gut epithelium (Ullah H *et al*., 2024) [16]. Lipopolysaccharides of bacterial cell wall mainly gram negative, is recognised by Toll-like receptor 4 (TLR4), which in turn activates the downstream antibacterial signalling pathways (Meghali Nighot *et al*., 2019) [17]. In neonates, establishment of intestinal immune defence, its maturation and homeostasis is influenced by early microbiota colonization (Takiishi T *et al*., 2017) [14]. Gut metabolites such as short-chain fatty acids (has anti-inflammatory activity), lysozymes, secondary bile acids, and antimicrobial peptides, can kill pathogenic bacteria. Additionally, for maintaining immune tolerance to commensal bacteria in alimentary tract intestinal lymphoid tissue termed as Gut-associated lymphoid tissue (GALT), plays a critical role (Ullah H *et al*., 2024) [16].

5. Gut–Brain Axis

The two-way communication between central nervous system and microbiome of gut occurs via a network called gut–brain axis (GBA), this complex signalling pathway (nervous, immune, endocrine and metabolite(s)-mediated) regulates behaviour and cognition of host (E. Salvo-Romero *et al*., 2020), hence enteric nervous system is often termed as second

brain of body (Kiełbik and Piłaszewicz *et al*., 2024) [19]. Vagal tone is highly affected by stress; as a potential stress stimulus can disrupts the tone of vagus nerve (part of cholinergic anti-inflammatory system) and have negative impact on health of the intestine and its microbial composition (Bonaz B *et al*., 2018 and Sacoor C *et al*., 2024) [20, 21]. The level of neurotransmitters such as norepinephrine, serotonin, GABA and dopamine is regulated by microbiome which in turn effect the neuronal operations and impacts the mental health (Gonçalves S *et al*., 2022 and Sacoor C *et al*., 2024) [22, 21]. Mood, sleep, behaviours such as anxiety, interactions is chiefly regulated by Serotonin (Berger M *et al*., 2009; Kiełbik and Piłaszewicz *et al*., 2024) [23, 19]. In humans, major part of dopamine synthesized in intestine and microbiota greatly influence its synthesis (Eisenhofer G *et al*., 1997; Kiełbik and Piłaszewicz *et al*., 2024) [24, 19]. In animals, dopamine is involved in behaviour and learning, and also plays important roles in attention, cognition, and executive functions (Volkow N.D. *et al*., 2009; G Martínez *et al*., 2024) [25, 26].

6. Microbial dysbiosis

Immunoglobulin A (local secretory Ig), stomach acid (HCL), bile and other intestinal secretions, along with the continuous movement of gut (peristalsis), valves (illeo-caecal) are part of an inbuilt defence system that regulates and prevents microbial overgrowth in the gut (Sorathia SJ *et al*., 2025) [27]. When these mechanisms fail, dysbiosis can occur. Dysbiosis refers to significant disturbances in the population, composition, and functional activity of the gut microbiome. It is generally categorized into 3 types: (a) decreased beneficial microbes, (b) increased pathogenic organisms, and (c) a lack of diversity in microbial species (MM Roshan *et al*., 2022) [28]. A wide range of factors may contribute to dysbiosis, including age, enteral or extra-enteral infections, and secondary dysbiosis associated with primary dysfunction of organs such as the pancreas. Additional contributing factors include nutritional profile (particularly the type and quality of nutrients), exposure to acute or chronic toxins and chemicals, drug administration (especially antibiotics), hygiene practices, and environmental conditions. The disruption of the gut microbiota ecosystem can have far-reaching consequences. These effects can be broadly divided into: (1) Gut barrier disruption and (2) host immune and metabolic systems imbalances (Llorente C and Schnabl B., 2015; Hrncir T., 2022) [29, 30].

Dysbiosis can both result from and contribute to intestinal inflammation. It has been associated with a greater risk of several conditions, including cancer, obesity, and inflammatory bowel diseases (IBD), especially due to cytokine imbalance (both pro-inflammatory and anti-inflammatory cytokines) in humans. It occurs due to changes in normal population and colonization of disease promoting organisms (Ronald Tyszkowski and Raman Mehrzad, 2023) [31]. Although dysbiosis can occur due to a range of underlying causes, it is notably observed in certain diseases, such as exocrine pancreatic insufficiency. Disruption of the gut microbiome adversely affects intestinal function, compromises mucosal barrier integrity, and disturbs gut homeostasis, with potential systemic implications. Silvestrino M *et al*., 2025 [32] reported that dysbiosis has been linked to neuro-inflammatory and neuro-degenerative conditions, including epilepsy in dogs. This microbial imbalance can also lead to inflammation and altered expression of IFN-γ, TNF-α etc., which has been well studied in humans. In some cases, the disturbance is characterized not by a change in the overall microbial population but by alterations in microbial community composition such as the replacement of commensal anaerobes with facultative anaerobes and opportunistic pathogens like *Clostridium difficile*, which can markedly intensify dysbiosis.

7. Impact of Antimicrobials

It is essential to discuss antimicrobials whenever the gut microbiome is being discussed. Antimicrobials are double-edged swords; they have a significant effect in controlling infections, but when used unregulated, they can have severe and deleterious effects on the body. Prolonged oral use of antimicrobials especially causes serious damage to the gut microbiome. These drugs are non-selective; they kill both symbiotic and pathogenic organisms, leading to gut dysbiosis. Rebuilding the damaged gut flora can take years, and in some cases, it may never fully return to its original state. The effects are particularly harmful in neonates and young animals, where the gut microbiome is still developing and maturing. Early disruption may result in persistent dysbiosis, even into adulthood. Moreover, antimicrobial abuse promotes antimicrobial resistance, allowing resistant organisms to colonize and potentially spread to other hosts, further disturbing their microbiomes. Therefore, the choice of antimicrobials including their type, dose, and duration should be carefully considered before prescribing.

8. Dysbiosis Index

The Dysbiosis Index (DI) is a validated quantitative qPCR assay and also assessable via metagenomic sequencing for fresh faecal samples (<12 hours) that quantifies the abundance of seven key bacterial taxa and summarizes the results as one single value, accurately predicting global shifts in the microbiome (Suchodolski JS., 2022; Sung CH *et al*., 2023) [33, 34]. Al Shawaqfeh MK., 2017 reported a sensitivity of 74% and specificity of 95% for differentiating healthy dogs from those with chronic inflammatory enteropathies using the Dysbiosis Index. Suchodolski JS., 2022 [33] also noted that the DI can be used to assess the microbiome in clinical patients over time and in response to therapy (e.g., fecal microbiota transplantation). In cats, a panel of quantitative PCR (qPCR) assays was used by Sung CH *et al*., 2022 to measure the fecal abundance of total bacteria and seven bacterial taxa: *Bacteroides, Bifidobacterium, Clostridium hiranonis, Escherichia coli, Faecalibacterium, Streptococcus,* and *Turicibacter*. In contrast, Al Shawaqfeh MK *et al*., 2017 used a qPCR panel consisting of eight bacterial groups: total bacteria, *Faecalibacterium, Turicibacter, Escherichia coli, Streptococcus, Blautia, Fusobacterium,* and *Clostridium hiranonis.*

9. Diseases and Gut microbiome

9.1 Skin diseases

The gut is a strong immune regulator and when any changes occur, it affects various systems such as skin. In fact, their association is understudied, and only a few manifestations have been reported in various pathological conditions (O'Neill CA *et al*., 2016) [44]. A study on the skin and gut microbiota in canine atopic dermatitis conducted by Thomsen M *et al*., 2023 [45] concluded that in parallel with skin dysbiosis, there was also clear dysbiosis in the gut of atopic dogs and a decrease in the beneficial bacteria. In canids, high faecal concentrations of butyrate and propionate are positively correlated with the faecal abundance of *Fusobacterium* (Minamoto Y *et al*., 2019) [46] and it is also reported that in

humans, significantly higher levels of butyrate and propionate showed decreased risk of atopy.

9.2 Enteric disorders

Inflammatory responses are often stimulated due to an increase in permeability to lipopolysaccharide, leading to chronic inflammation, which is the primary cause of overgrowth of microbes in human gut (Banaszak M *et al*., 2023) [47]. However, such reports are not yet well established in companion animals. There are only a few reports regarding changes in gut population associated with enteric disorders of dog and cat. Park JS *et al*., 2019 [48] reported that a decreased species richness of alpha diversity metrics was observed in dogs with canine parvoviral enteritis compared to healthy dogs. Nagahara T *et al*., 2023 [49], conducted research on dogs with intestinal lymphangiectasia and healthy dogs. Their study revealed a decrease in intestinal bacterial diversity and butyrate-producing bacteria in affected dogs.

9.3 Chronic Kidney Disease (CKD)

In chronic kidney disease, severe changes in gut microbial composition are due to an increase in the luminal pH. Higher concentrations of ammonia, a microbial product of urea metabolism are found in intestinal lumen of affected patients either by diffusion, as a consequence of impairment to intestinal lining or through entero-hepatic cycle (Bourke E *et al*., 1966, ND Vaziri *et al*., 2012, Summers S and Quimby J., 2024) [50-52]. Ammonia (uremic toxin) accumulation, leads to disrupted profiles of essential compounds such as fatty acids and amino acids due to microbial dysmetabolism. This in turn promotes systemic inflammation and further impairs renal function (Summers S and Quimby J., 2024) [52]. Kim KR *et al*., 2023 [53], from their study, concluded that the gut microbial population and composition may vary based on stage of CKD, observing a decrease in saccharolytic bacteria and an increase in proteolytic bacteria. These findings highlights the necessity of giving attention to gut health in management of CKD in dogs.

9.4 Exocrine Pancreatic Insufficiency (EPI)

In EPI, due to changes in pH, more available undigested nutrients in the gut, and a lack of pancreatic antimicrobial peptides (in pancreatic juice), there is severe faecal microbiota dysbiosis (restricted to the intestinal lumen [Anitha Isaiah *et al*., 2017]) [54] and SIBO, causing diarrhoea, toxin build-up in the gut, and also elevated serum folate levels (Vikram Chandu V *et al*., 2024) [55].

9.5 Cardiac Disorders

There is limited data available regarding the correlation between cardiac disorders and gut dysbiosis. However, Li Q *et al*., 2021, studied the association between myxomatous mitral valve disease (MMVD) and gut-derived metabolites. They concluded that, there was an inverse association between *Clostridium hiranonis* (a gut bacteria important in converting bile acid) and MMVD. They also mentioned that the gut dysbiosis index increased in proportion to the severity of disease. In contrast, Seo J *et al*., 2020 [57], reported that there was no significant change in microbiome diversity and richness in dogs with congestive heart failure. However, they did observe an increase in the abundance of *Proteobacteria* in the congestive heart failure study group.

9.6 Hepatobiliary disorders

The hepatobiliary system is a key part of the alimentary tract. A vast number of disorders affect it, which reflects the changes in gut homeostasis. Kummen M and Hov JR., 2019 [58], reported that gut microbial dysbiosis was present in biliary biliary disorders such as primary biliary cholangitis and primary sclerosing cholangitis. These modifications may result from several mechanisms during chronic hepatobiliary disease (CHD); however, deeper alterations are due to cholestasis (Habermaass V *et al*., 2023) [59]. In cats, suspected of having hepatobiliary disease, bile sample do not contain a core microbiota and uncultured bacteria may contribute to the pathogenesis of the disease with bile *E. coli* bile infection.

9.7 Nervous disorders

A study by Silvestrino, M *et al*., 2025 [32], concluded that epileptic dogs had reduced gut bacterial richness and uneven α-diversity compared to healthy controls, with no variations in β-diversity. Furthermore, their study observed a decrease in SCFA-producing bacteria, namely *Faecalibacterium*, *Prevotella*, and *Blautia*, and an increase in *Escherichia coli*, *Clostridium perfringens*, and *Bacteroides* in epileptic dogs. Although many studies have addressed the microbiota and its influence on anxiety disorders in humans and rodent models, there is a lack of insightful information on canine anxiety disorders (Sacoor C *et al*., 2024) [21].

9.8 Gut Health and Cancer

The relationship between gut health and cancer development, while supported by limited data, is a growing area of research. The gut microbiome plays an important role in tumour initiation and progression, either by promoting inflammation, by altering microenvironment of tumour or by regulating the anti-cancer immune response. According to Breczko WJ *et al*., 2024 [62], disruptions to this delicate balance can lead to chronic inflammation and a disturbed immune system. When these disruptions are combined with environmental and genetic factors, they may contribute to the development and progression of cancers, particularly of lymphatic system.

10. Conclusion

Studies on gut health in pets have expanded in recent years, leading to new discoveries, the development of novel treatment modalities, and support for maintaining optimal gut health in companion animals. However, while these mechanisms are well-documented in humans, data on similar interactions in dogs and cats remain limited. Although cross-species insights offer a valuable theoretical framework, targeted research in canine and feline models is essential to deepen our understanding and improve clinical outcomes.

Conflict of Interest
Not available

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Not available

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