



Microbiota and probiotics in canine and feline welfare



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ABSTRACT

Dogs and cats have been cohabiting with us for thousands of years. They are the major human companions. Today, dogs and cats live in urban areas. Cats and most dogs are on high carbohydrate diets and face similar life-style challenges as the human beings. The health and well-being of companion animals, just as their owners, depends on the gut microbes. Providing a proper care and nutritionally balanced diet to companion animals is recognised as a part of our responsibility to maintain the health and well being of our pet. However, as microbiota differences may facilitate exposure to pathogens and harmful environmental influences, it is prudent to search for novel tools to protect dogs and cats and at the same time the human owners from pathogens. Specific probiotic strains and/or their defined combinations may be useful in the canine and feline nutrition, therapy, and care. Probiotic supplementations have been successful in the prevention and treatment of acute gastroenteritis, treatment of IBD, and prevention of allergy in companion animals. New challenges for probiotic applications include maintenance of obesity and overweight, urogenital tract infections, *Helicobacter* gastritis and parasitic infections. The probiotics of human origin appear to be among the new promising tools for the maintenance of pets' health. However, the host-derived microorganisms might be the most appropriate probiotic source. Therefore, more controlled trials are needed to characterise new and safe probiotic preparations with an impact on general health and well being as well as health maintenance in dogs and cats.

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1. Introduction

Pet population is increasing especially in westernised countries, and dogs and cats are the major human companions. Both have been domesticated and are co-existing with humans for thousands of years. Most of pet owners consider the animals to be family members, and other consider their pet as companions [1]. Domestic dogs and cats still live in conjunction with humans benefiting from each other. Mutual interest has evolved into companion animals being a stable part of human life and therefore, the health and well being of pets have increasingly raised interest during last decades.

Dogs and cats are carnivores with a history of high protein diets [2,3]. Today, cats and most dogs are on high carbohydrate diets living in urban areas and thus face similar life-style challenges as the human beings. The health and well-being of companion animals, just as their owners, depends on the gut microbes. Microbiota

composition and activity have been associated with several diseases in both the animals and their owners [4–6]. This interrelationship would benefit from more exact knowledge on microbiota in pets and information on how the microbiota affects the health of the pets in the long-term.

A major part of the animal health derives from the intestine. The 'healthy gut' is known to be crucial for the physiology and well being of the host. The gastrointestinal tract (GIT) harbours a complex microbial community. This microbial ecosystem acts in several ways, affecting both absorption and metabolism of nutrients, trophic and protective functions of the host. Any disturbances within the gut microbiota may lead to the development of a multitude of diseases and disorders e.g. diarrhoea, allergies, obesity, and stress symptoms [5].

Knowledge on the canine and feline intestinal microbiota is still expanding. Most studies on microbial community in the dog and cat GIT implemented in traditional microbiological techniques, however several recent reports characterised microbiota using novel molecular methods such as qPCR, FISH or 16S rRNA sequencing [7,8]. To balance the disturbed microbiota and to

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combat infections, different therapeutic agents have been proposed, among them probiotics. However, published papers on probiotic applications in companion animals are greatly limited compared to data regarding humans. The aim of this review is to describe the current knowledge on the gut microbial community and advances in probiotic therapy in dogs and cats.

2. Canine and feline microbiota

All animals harbour a vast and complex community of microorganisms. Dogs and cats have high numbers of microorganisms in the GIT which in fact outnumber those living in human gut. However, both dogs and cats have distinct bacterial species that differ between each other and also vary in different dog and cat species, various gut niches and geographical areas. Microbial diversity and concentration increase along the length of the gastrointestinal tract. The predominant bacterial phyla in the colon and faeces of both dogs and cats are represented by *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and *Fusobacteria* as well as *Eubacterium* in cats. The microbial differences between dogs and cats are demonstrated in the microbial groups and species levels. Molecular fingerprinting has also revealed that every individual pet has a unique and stable microbial ecosystem [9].

Molecular analysis using 16S rRNA sequencing revealed that *Firmicutes*, *Fusobacteria*, *Bacteroidetes*, and *Proteobacteria* commonly inhabit the canine GIT [7,10]. Clostridia predominate in the duodenum and jejunum and are highly abundant in the ileum and colon [11], while *Fusobacteria* and *Bacteroides* bacteria are the most abundant in the ileum and colon [7,11]. Fungi, such as *Ascomycota*, *Basidiomycota*, *Glomeromycota*, and *Zygomycota* have been identified as well [10].

Lactobacilli inhabit commonly all parts of the dog intestine [11], ranging from 10^4 to 10^8 CFU/ml and among them *Lactobacillus acidophilus* is dominant [12]. *Lactobacillus fermentum*, *Lactobacillus rhamnosus*, and *Lactobacillus salivarius* are reported being a part of health canine intestine [13]. Other canine lactobacilli are represented by *Lactobacillus murinus* and *Lactobacillus reuteri* [12], *Lactobacillus animalis*, *Lactobacillus sanfranciscensis* and *Lactobacillus paraplantarum* [14].

Lactobacilli found in cats are typical intestinal lactobacilli, e.g. *L. acidophilus*, *L. salivarius*, *Lactobacillus johnsonii*, *L. reuteri* and *Lactobacillus sakei*, which can be seen in other animals, including human [15]. However, *Lactobacillus* distribution, similar to bifidobacteria, varies between individuals.

Bifidobacteria have been difficult to characterise using pyrosequencing due to methodological difficulties, although the microorganisms are well known to be beneficial in several animals and especially in human infants. Jia and collaborators reported that dogs contain over 10^8 cells/g of bifidobacteria in their faeces, as determined by fluorescence *in situ* hybridisation (FISH) [8]. This is consistent with the reports studied by culturing [16,17]. Both animal type (e.g. *Bifidobacterium pseudolongum* and *Bifidobacterium animalis*) and human type (e.g. *Bifidobacterium catenulatum* and *Bifidobacterium bifidum*) of bifidobacteria have been found in dog faeces [18–20]. Bifidobacteria were major proportions in healthy cats with cell number of 9.34 (log₁₀ cells/g faeces), as determined by FISH. Significantly lower numbers of bifidobacteria have been found in cats with IBD [21]. Ritchie and co-workers [15] found several human-type and animal-type bifidobacteria in cats using clone library combined with *Bifidobacterium* group-specific primer set. They have also found that individual cats contained several unique *Bifidobacterium* species.

A study on pet cat oral microbiota indicated *Proteobacteria* being dominating (75.2%) leaving amounts of *Bacteroides* (9.3%), *Firmicutes* (6.7%), unculturable (2.7%), *Spirochaetes* (1.8%), *Fusobacteria*

(1.3%), and *Actinobacteria* (0.6%) low [22].

Feline faeces have been found to contain high numbers of obligate anaerobes, and such quantities are considered abnormal in dogs and humans [23]. Based on the analysis of 16S rRNA, it was reported that the feline GIT is often represented by five phyla where *Firmicutes* dominate (68%), followed by *Proteobacteria* (14%), *Bacteroidetes* (10%), *Fusobacteria* (5%), and *Actinobacteria* (4%), [15]. However, a more recent study using the metagenomic approach revealed that the feline gut microbiota is predominated by *Bacteroidetes/Chlorobi* group bacterial phylum comprising around 68% of total classified diversity and followed by *Firmicutes* (~13%) and *Proteobacteria* (~6%) respectively, while known *Archaea*, fungi (*Ascomycota*), and viruses represent minor communities in the overall microbial diversity [10,24]. Minamoto and collaborators [25] summarised the studies on feline small and large intestine microbiota showing in detail microbiota to genus level. Most studies have been conducted in shorthair cats [8] which leaves much of the microbiota of other pet cats in different breeds to be studied more in detail. Thus, the composition appears to be distinctly different from both canine and human studies. Since different techniques may create bias from one report to another and the result, more studies are needed to uncover the details of variation within the canine and feline community and also between individual animals.

An increasing numbers of reports have changed the old dogma suggesting initiation of microbiota development at birth. These reports clearly demonstrate that humans and mice are colonised by microbiota already in utero and prior to birth [26,27]. There are no studies on canine and feline microbial colonisation prior to delivery, however similar possibilities cannot be excluded since both are mammals and share similar physiological and some anatomical patterns with humans.

The skin microbiota plays an important role in skin function, potentially enhancing the skin barrier and reducing the colonisation by potentially pathogenic microorganisms. One recent study using pyrosequencing demonstrated that canine skin is inhabited by rich and diverse microbial communities. Healthy dogs have high individual microbial variation between samples collected from different skin sites. Also higher species richness and microbial diversity are observed in the samples from haired skin when compared to mucosal surfaces or muco-cutaneous junctions. The most abundant phyla and families identified in the different regions of skin and mucosal surfaces are members of *Proteobacteria* and *Oxalobacteriaceae*. On the other hand, the skin of allergic dogs is characterised by lower species richness when compared to the healthy dogs, with lower proportions of the β -*Proteobacteria* *Ralstonia* [28].

The composition of canine and feline microbiota is shown in Fig. 1a, b.

3. Microbial interaction between pets and owners – is there a connection?

Gastrointestinal disorders are one of the main reasons owners bring their pets to the veterinarian for healthcare. In addition, specific bacterial canine enteropathogens such as *Salmonella* and *Campylobacter* are well-documented zoonoses [4,29] being a challenge for pet owners, veterinary and medical care. Dogs may harbour and shed cysts of protozoan parasite *Giardia lamblia* without showing clinical signs [30] and ascariasis. Both are common potentially zoonotic diseases leading to human infections [31]. The enteric zoonotic agents in domestic cats are also important. A study by Tun and collaborators [24] identified a range of potential enteric zoonotic pathogens (0.02–1.25%) and genes involved in antimicrobial resistance (0.02–0.7%) in feline excrements which

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