

Importance of gut microbiota for pets

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Introduction

The gut microbiota is composed of a diverse microbial community which includes bacteria, archaea, viruses, fungi and protozoa. As bacteria are the more predominant microbes in the gut and as less is known about the other domains of prokaryotic life, this review will focus on bacteria. The gut microbiota is increasingly considered as a symbiotic partner for the maintenance of health in humans and animals. Further, the intestinal tract of humans and animals is among the most densely populated microbial habitats on record, with estimates of densities in the colon up to 10^{12} cells/ml. Gut microbes play a crucial role in the regulation of host health, by stimulating the immune system and development of gut structure, aiding in the defense against invading pathogens and providing nutritional benefit to the host (ie, production of short chain fatty acids (SCFA) and vitamins B9 and B12). In contrast a microbial dysbiosis has been identified in dogs and cats with gastro-intestinal (GI) diseases. The review aims 1) to summarize current information about the roles of the intestinal microbial ecosystem in dogs and cats and 2) to present the effects of nutritional intervention on gut microbiota in the dog and the cat.

Gut, microbiota and health

As carnivores tend to have a short, relatively simple GI tract, the studies of the fermentation products were scarce until the end of the nineties. In the dog, Banta & al. (1979) reported that the highest concentrations of volatile fatty acids were found in the cecum and the colon and were not significantly affected by the diet (a cereal based dry food *versus* a all meat canned food). Further, it was concluded that the nutritional significance of organic acid production in the GI tract of the dog was probably marginal. As a consequence, it was considered that organic acids were of minor significance in meeting the energy needs of the animal but the authors suggested a possible “physiological” function in the dog.

Substrates for fermentation are undigested protein or protein by-products -found to be the sources of deleterious substances as bio-amines-, undigested carbohydrates as resistant starch and dietary fiber, epithelia cells and endogenous mucus produced by epithelia.

The major fermentation end-products are SCFA, phenolic and indolic compounds, ammonia, amines, and gases. Many different microbial genera and species are contributing to the metabolite formation; however our knowledge of the relationship between the specific bacteria and their metabolic compound is currently limited. Generally, SCFA are the main products from carbohydrate fermentation. The pathways of acetate and propionate are known but the butyrate pathway is still investigated in the dog. Butyrate is known to provide a large energy supply for colonic epithelium *in vitro*. Butyrate also exerts anti-inflammatory and anti-apoptotic properties that may be important for the prevention of inflammatory bowel disease (IBD) and colorectal cancers in humans. Furthermore, SCFA play an important role in determining the gut environment, influencing pH, and gut transit time. Anaerobic degradation of peptides and proteins in the colon by the resident microbiota, a process called putrefaction, also produce SCFA (including branched chain fatty acids – BCFA), but in the mean time, generates other substances like ammonia, amines, phenols and indols. In humans, many of these metabolites are considered to be potentially toxic.

In the nineties, dietary fiber –especially soluble and/or fermentable fiber- was considered as important to prevent constipation, to decrease the energy concentration of diets in sedentary pets and even in a general way to promote “gut health”. Most of the studies were made using 1) experimental dogs or 2) *in vitro* models of fermentation with inoculum of feces. As a consequence, the effects of many dietary fibers on dog’s or cat’s metabolism or feces quality or their fermentation products were published (Swanson & al., 2002) but the mechanisms were unknown since the more recent studies of the effects of the diet on the microbiota are quite recent.

Knowledge on the canine and feline intestinal microbiota is still expanding (Rochus & al., 2014, Grzeskowiak & al., 2015). Several recent reports characterized microbiota using novel molecular methods such as qPCR or 16S rRNA sequencing. 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 GI tract (Rochus & al., 2014, Grzeskowiak & al., 2015). The predominant bacterial phyla in the colon and feces of both dogs and cats are represented by *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and *Fusobacteria* as well as *Eubacterium* in cats. However, the proportions of the different phyla vary between studies and between diets (Middelbos & al., 2010). The microbial differences between dogs and cats are demonstrated in the microbial groups and species levels. The microbial ecosystem acts in several ways, affecting both absorption and metabolism of nutrients, trophic and protective (barrier) function of the host.

Nutritional factors affecting gut microbiota

Diet has a strong impact on health and well-being in humans and animals. This could be due to its effects on modulating the composition of gut microbiota. Among other factors that may influence gut microbiota, diet is the easiest to modify and therefore presents the simplest route for therapeutic intervention of gut microbiota associated diseases. It has been shown in humans that long-term diets were strongly associated with enterotypes (ie the *Bacteroides* enterotype is strongly correlated with dietary animal protein and *Prevotella* is correlated with dietary carbohydrates) (David et al, 2014). However, the knowledge of the existence of enterotypes, in similarity to humans, is not well understood/known in dogs.

In the pets, the best-known examples of dietary changes influencing the gut microbiota are the use of dietary fiber, non-digestible carbohydrates (Rochus & al., 2014) and prebiotics (Deng & Svenson, 2014). Lactate-producing bacteria (such as *Lactobacillus* and *Bifidobacterium*) are considered beneficial members of the colonic microbiota. By contrast, *Clostridium spp.* and *E.coli* are considered to be potential pathogens (Swanson & Fahey, 2006). About ten studies have been published in the dog about the effect of dietary fiber inclusion on microbiota; about 50 % demonstrated increased faecal bifidobacteria and/or decreased faecal clostridia concentrations in dogs consuming fibers (Patra, 2010). It is been shown in the dog that a relatively small amount of dietary fiber (7.5 % beet pulp vs. a control diet) changed the structure of the gut microbiota detectably. Feeding dietary fiber decreased *Fusobacteria* and increased *Firmicutes*, but these changes were not equally apparent in all dogs. These changes may be of importance because of the emerging evidence that distinct differences exist between “healthy” and “diseased” gut microbial communities (Middelbos & al., 2010).

Feeding probiotics and prebiotics can modulate the intestinal microbiota. Unlike the situation with probiotic in which allochthonous microorganisms are introduced to the gut, and need to compete against established colonic microbial communities, an advantage of using prebiotics to modify gut function is that the target bacteria are already commensal to the large intestine. Consequently, in a preventive way, prebiotics are perhaps a more practical and efficient way to manipulate the gut microbiota than probiotics.

Addition of prebiotics to feline diet may positively affect gut microbial populations. Cats fed diet supplemented with FOS (4% of diet) had increased bifidobacteria concentrations while counts of *E.coli* decreased (Barry & al., 2010). Fructan supplementation may benefit senior cats as it modulates stool odor-forming compounds and decreases some protein catabolites and pathogenic gut microbiota (*E. coli*) concentrations without affecting N retention (Barry & al., 2014). Typically, concentrations of bifidobacteria increase with fructan supplementation in cats and dogs (Middelbos et al., 2007; Barry et al., 2010).

It has also been shown that a common practice as *ad libitum* feeding, increased significantly the order *Clostridiales* in research dogs (Handl & al., 2013).

Gut microbiota and diseases

Any disturbances within the gut microbiota may lead to the development of a multitude of diseases and disorders e.g. diarrhea, allergies, obesity, and stress or pain symptoms.

Data characterizing the intestinal microbiota in diseased states are currently poorly available in companion animals. Clinical studies suggest the presence of a dysbiosis in IBD (Inness & al., 2007). Comparing the microbiota of lean and obese dogs, it has been shown that the phylum *Actinobacteria* and the genus *Roseburia* were more abundant in the obese pet dogs (Handl & al., 2013).

In the cats, the rectal microbiota differed between animals with FIV infection and uninfected controls. Some of the changes that were noted have been associated with « dysbiosis » and proinflammatory states in other species, so it is possible that subclinical alteration in the intestinal microbiota could influence the health of FIV-infected cats (Weese & al., 2015).

Further studies are required to increase our understanding of the role of gut microbiota in diseases such obesity and diabetes in companion animals.

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