Differences between the gut microbial composition of dogs with enteropathies and healthy animals

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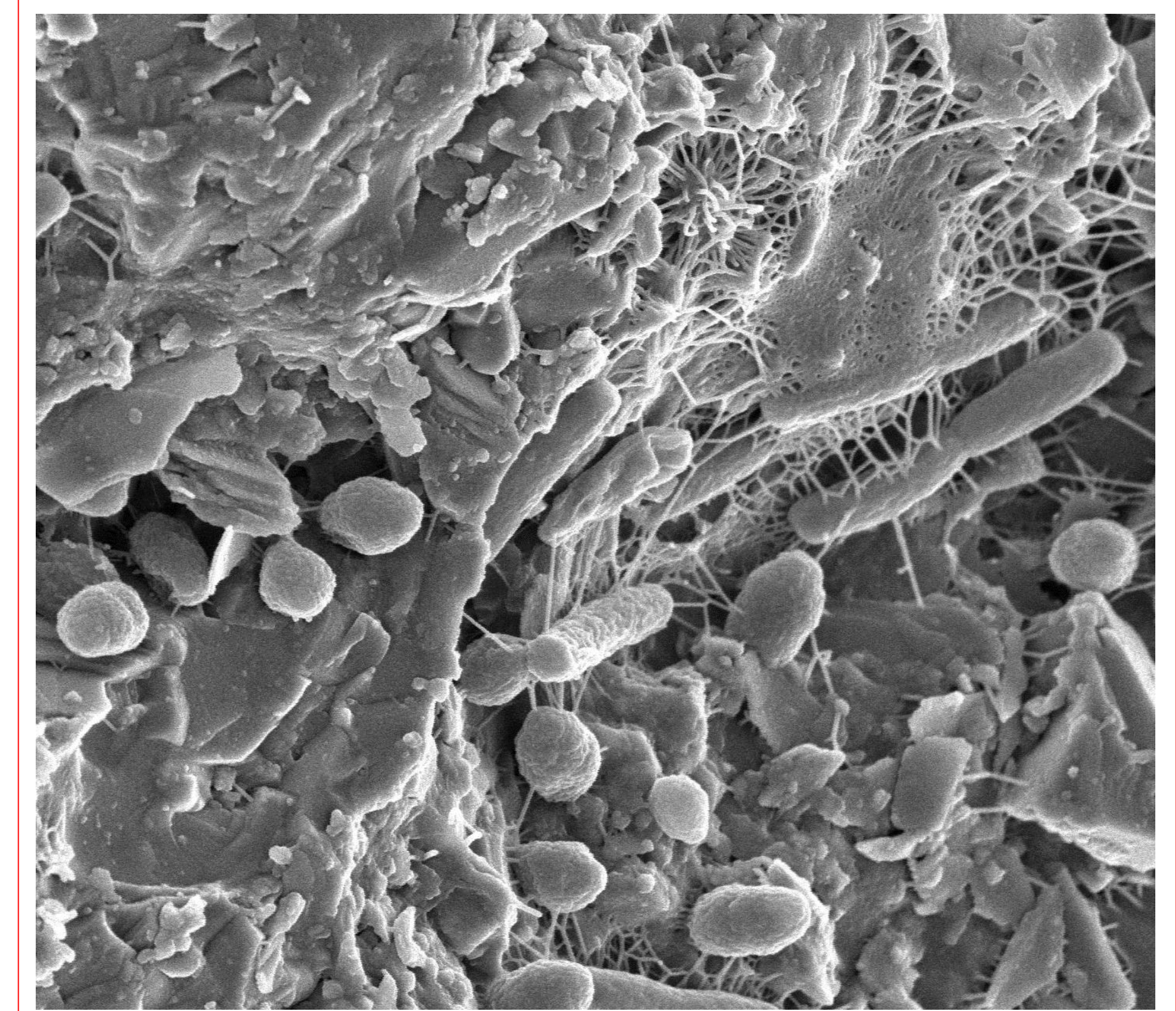
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Introduction

Imbalances in the microbial composition of the intestinal microbiome are associated to various gastrointestinal diseases like chronic inflammatory enteropathy or inflammatory bowel disease. Recent studies have identified distinct bacterial groups that are significantly altered in dogs with chronic or acute gastrointestinal symptoms in comparison to healthy individuals and therefore may be used as biomarkers for dysbiosis. Aim of the study was to establish a method suitable for routine diagnostic screening and evaluation of the intestinal microbiome for dysbiotic changes in dogs.

Material and Methods

DNA from fecal samples of dogs that showed signs of diarrhea (n=30), dyspepsia (n=30), intestinal inflammation (n=25) and healthy controls (n=30) was extracted during veterinary routine diagnostics. Subsequently quantitative PCR assays targeting 16S rRNA genes of seven phylogenetic bacterial groups (total bacteria, *Escherichia coli, Faecalibacterium prausnitzii, Fusobacterium spp., Blautia spp., Turicibacter spp. and Clostridium hiranonis*) were performed. Fecal concentrations of canine calprotectin, bile acids and canine pancreatic elastase levels were analyzed to evaluate intestinal inflammatory activity, mucosal integrity and digestion efficiency. Exclusion criteria were as follows: endoparasitosis, presence of obligate enteropathogens and viral diseases.
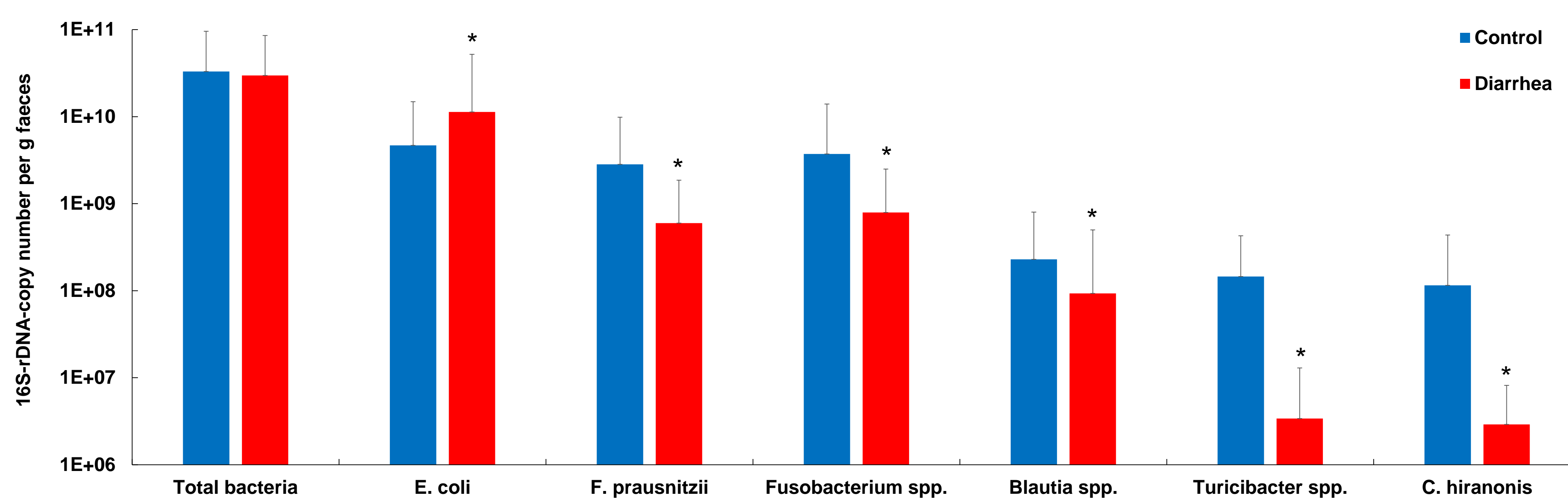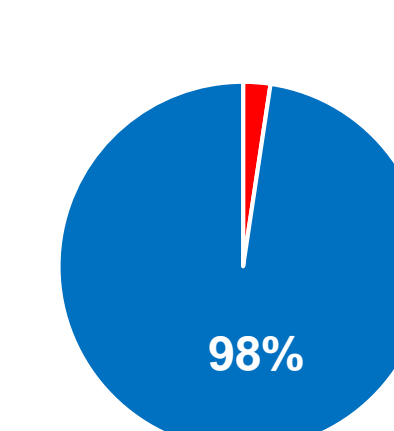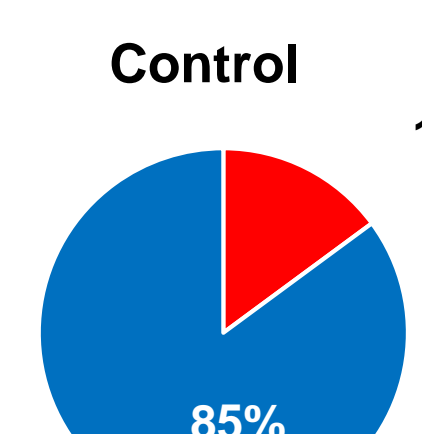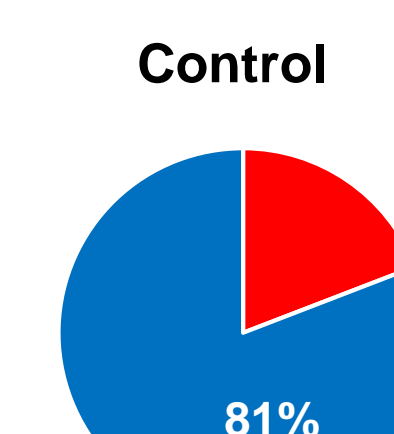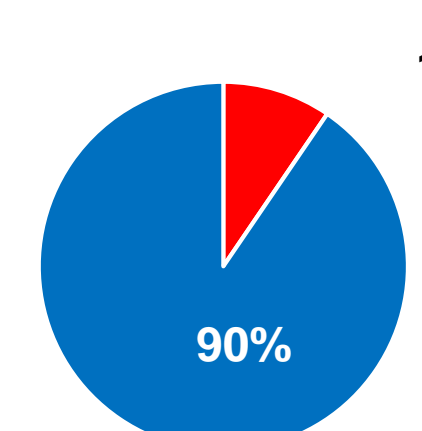

Bacterial biofilm on mucosal surface. Image courtesy of the Lewis Lab at Northeastern University. Image created by Anthony D'Onofrio, William H. Fowle and Kim Lewis.

Dysbiosis and mucosal integrity

A significant underrepresentation of mucosa-protective microbes like *Faecalibacterium prausnitzii*, *Blautia spp.* and *Turicibacter spp.* hints at intestinal dysbiosis. Concurrently, prevalence rates of colonic inflammation and disturbances in the enterohepatic bile acid circulation are significantly higher when compared to healthy animals. Asterisks indicate significant differences (p<0.05, Wilcoxon-Mann-Whitney-Test) between groups.
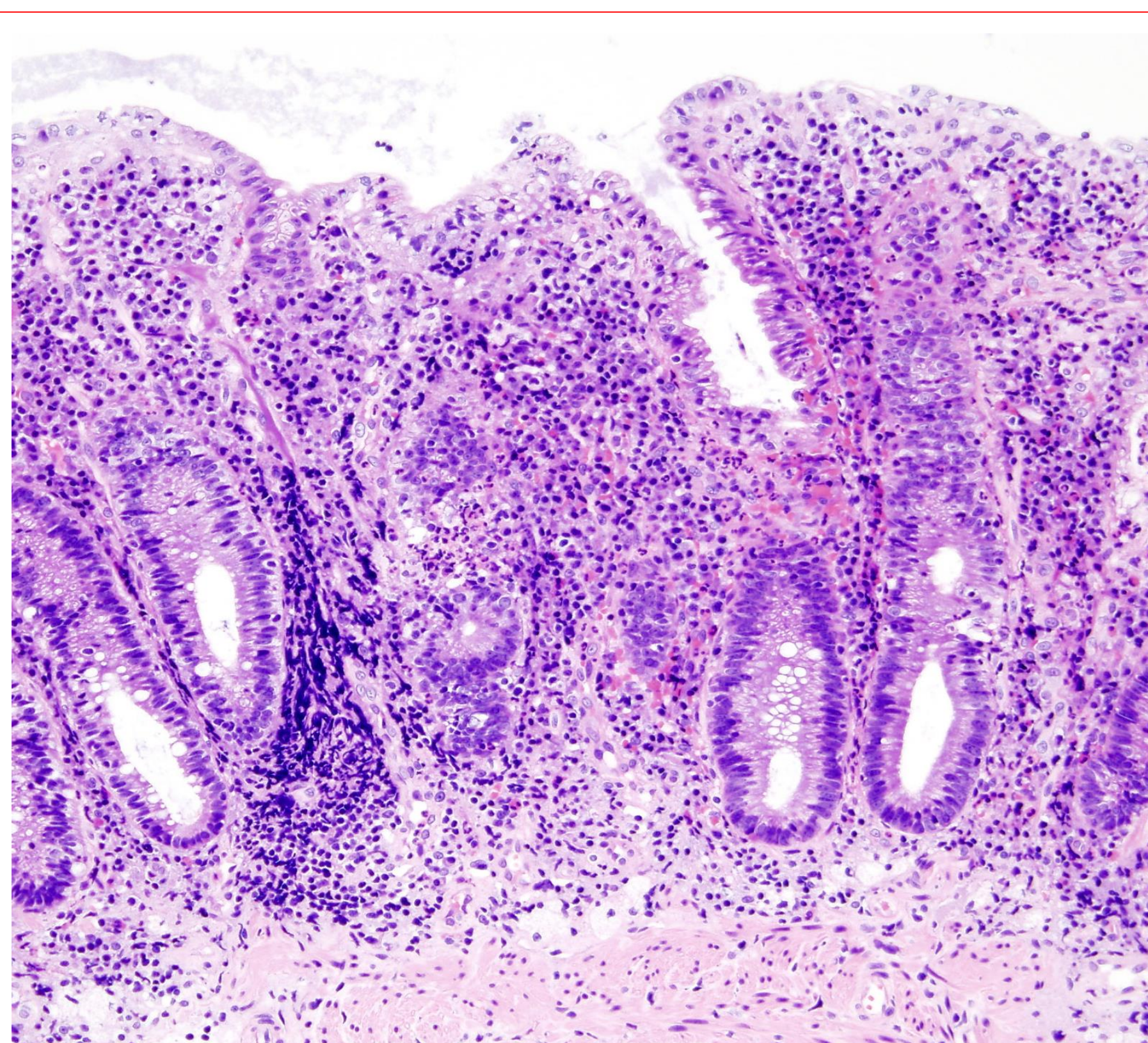
Histopathological image of the active stage of ulcerative colitis. Endoscopic biopsy. Hematoxylin & eosin stain. Source: Wikimedia Commons.

Dysbiosis and intestinal inflammation
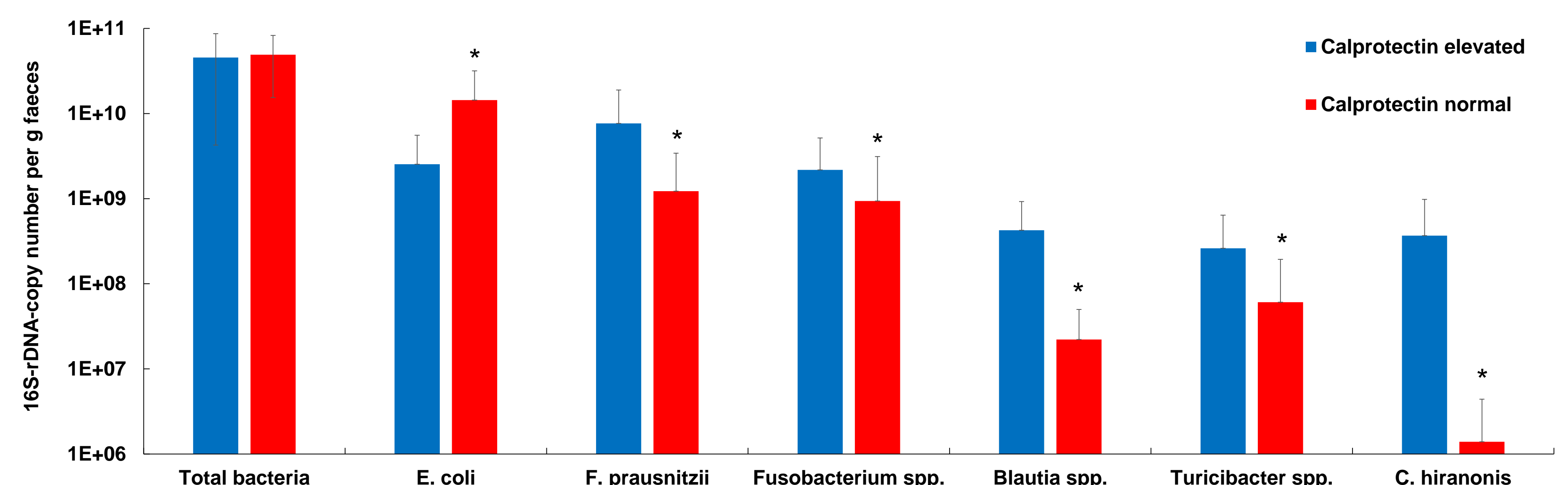
Significant differences in the intestinal bacterial distribution could be observed in dogs with increased fecal calprotectin levels in comparison to control animals. Fecal calprotectin has been shown to be an indicator for gastrointestal inflammatory activity as well as overall gastrointestinal health. Asterisks indicate significant differences (p<0.05, Wilcoxon-Mann-Whitney-Test) between groups.
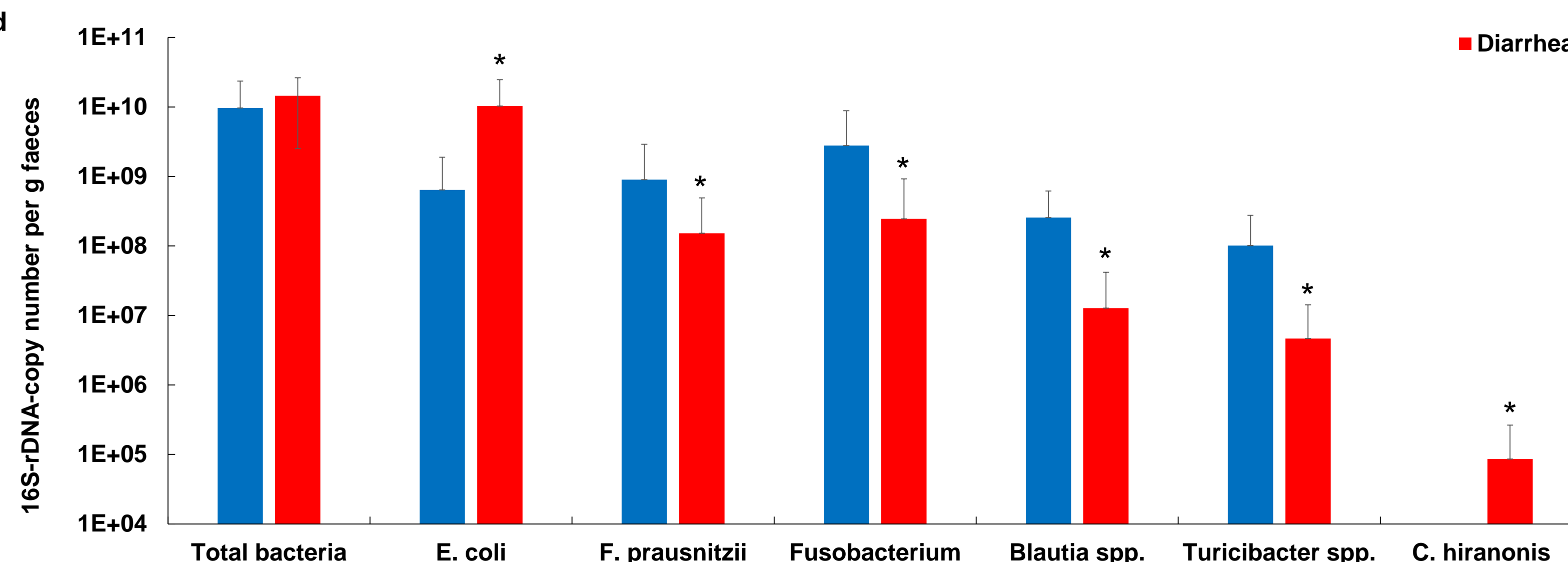
Dysbiosis and indigestion
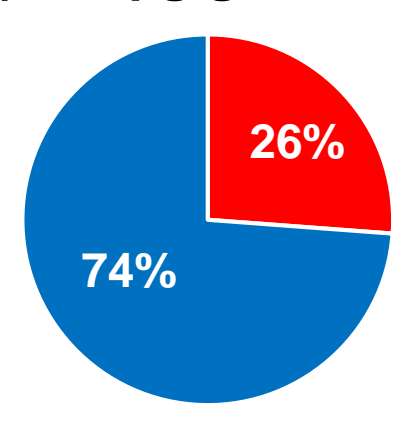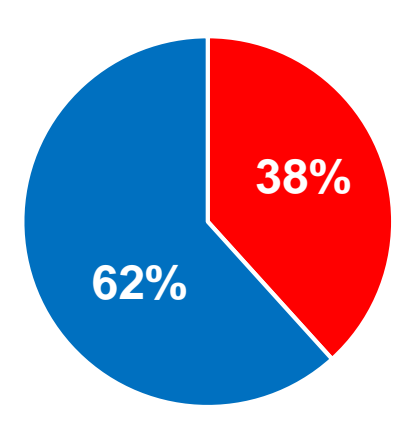
Exocrine pancreatic insufficiency can be associated with dysbiotic compositional changes in the intenstinal microbiota. This may result from an increased availability of highly digestible carbohydrates, proteins and fats in the small intestine and colon. Asterisks indicate significant differences (p<0.05, Wilcoxon-Mann-Whitney-Test) between groups.

Results

Dysbiotic changes in the fecal microbiome correlate significantly with enteropathies like acute diarrhea and intestinal inflammation. Particularly bacterial species with mucosa-protective properties on the integrity of the intestinal mucosal barrier were decreased. However, the contribution from the gut microflora to the pathogenesis of multifactorial diseases like Chronic Inflammatory Bowel Disease has yet to be determined.

Nevertheless, the presented quantitative fecal microbiome analysis can already be useful for differential diagnostic purposes of idiopathic gastrointestinal diseases or to check for microbiota changes in response to clinical treatment.

References

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Heilmann RM, Berghoff N, Mansell J, et al. Association of fecal calprotectin concentrations with disease severity, response to treatment, and other biomarkers in dogs with chronic inflammatory enteropathies. J Vet Intern Med. 2018;32(2)