Fecal microbiota are altered and concentration of volatile fatty acids decreased in dogs with inflammatory bowel disease

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Introduction: Microbial dysbiosis has been implicated in the pathogenesis of canine inflammatory bowel disease (IBD) (*1*). The aim of the present study was to characterize the composition (mainly focused on butyrate producing bacteria) and functionality of gut microbiota of dogs with IBD.

Animals, material and methods: Twenty-three dogs diagnosed with IBD (0.8-12.3 years) and 11 healthy control dogs (0.5-8.0 years) were included in the present study. Dogs with IBD were given a clinical score using the canine chronic enteropathy clinical activity index (CCECAI) (*2*). Fecal samples (n: IBD: 15; control: 11) were used for DNA extraction, denaturing gradient gel electrophoresis (DGGE), real-time PCR and volatile fatty acid (VFA) analyses. Differences between IBD and control dogs were analyzed using the T-test after data has been confirmed to be normally distributed. Within the IBD group, Pearson's correlation coefficients were calculated between CCECAI and abundance of different bacterial groups.

Results and discussion: IBD and control dogs did not show distinct fecal microbial communities based on DGGE profile cluster analysis; most probably due to the large variations in age and breed. Similarly, real-time PCR revealed no significant differences in the abundance of total Bacteria, Firmicutes, Bacteroidetes, *Enterobacteriaceae*, *Clostridium* clusters I, IV and XIVa and gene expression of butyryl-CoA: acetate-CoA transferase in IBD vs. control group, except for lower abundance of *Lactobacillus* in dogs with IBD (P=0.029). A reduction in the abundance of *Lactobacillus* was also found in humans with Crohn's disease and ulcerative colitis (*3*). Simultaneously, fecal concentrations of total VFA (P=0.085), acetate (P=0.043) and isobutyrate (P=0.045) were lower in IBD vs. control dogs, whereas no difference was observed in butyrate between IBD and control dogs. However, negative correlations were found between CCECAI and *Clostridium* cluster IV, (r = -0.51, P = 0.050), XIVa (r = -0.60, P = 0.017), and butyryl-CoA: acetate-CoA transferase gene (r = -0.62, P = 0.014), suggesting lower numbers or lower activity of butyrate-producing bacteria in dogs with severe IBD vs. dogs with mild IBD indexes. These results indicate microbial dysbiosis might be more noteworthy in severe canine IBD.

Conclusions: Canine IBD was associated with a declined fecal abundance of *Lactobacillus* and butyrate-producing bacteria were decreased in severe cases of IBD. Altered gut micriobiota in dogs with IBD was accompanied with less pronounced VFA production.

References:

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