THE FECAL MICROBIOME OF DOGS WITH EXOCRINE PANCREATIC INSUFFICIENCY

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Abstract

Exocrine pancreatic insufficiency (EPI) is a syndrome of inadequate synthesis and secretion of pancreatic enzymes, which leads to delayed onset of maldigestion. Previous reports show that small intestinal bacterial dysbiosis occurs in dogs with EPI and is reversed with pancreatic enzyme therapy. However, there are no studies examining the fecal microbiome of dogs with EPI. The objective of this study was to compare the fecal microbiome of healthy dogs (n=18), untreated (n=7) dogs with EPI, and dogs with EPI treated with enzyme replacement therapy (n=19).

Materials and methods

Sample analysis

- Extracted DNA from fecal samples was used for Illumina sequencing of the bacterial 16S rRNA gene and analyzed using Quantitative Insights into Microbial Ecology (QIME).
- The analysis of similarities (ANOSIM) function in the statistical software package PRIMER E (PRIMER-E Ltd., Luton, UK) was used to calculate the unweighted UniFrac distance matrix to determine similarity of samples from different bacterial communities. There was a significant difference in fecal microbial communities when healthy dogs were treated to EPI (p=0.001) and untreated (p=0.001) dogs with EPI. There was a significant decrease in diversity when compared to healthy dogs (n=18), treated dogs with EPI when compared to healthy dogs. (n=18).

Results

- There was a significant difference in fecal microbial communities when healthy dogs were treated to EPI (p=0.001) and untreated (p=0.001) dogs with EPI. There was a significant decrease in untreated and treated EPI dogs compared to the healthy dogs (p=0.001).
- The families Bifidobacteriaceae (p=0.006), Enterococcaceae (p=0.035), and Lactobacillaceae (p=0.001) were significantly increased in the untreated and treated dogs with EPI when compared to healthy dogs. (n=18).
- In contrast, Lachnospiraceae (p=0.001), and Blautia (p=0.001) were significantly decreased in dogs with EPI.

Discussion and Conclusion

- This study suggests that the fecal microbiome of dogs with EPI (both treated and untreated) is different from that of healthy dogs.
- Further studies are necessary to elucidate the mechanisms that are responsible.

References


Disclosure

The authors disclose no conflicts of interest.

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Figure 1: A) β diversity: (A) principal coordinates analysis (PCOA) of unweighted UniFrac distances of 16S rRNA genes. (B) Alpha rarefaction curve showing number of observed species at a depth of 2200 sequences/sample, error bars show standard deviation. (C) Comparisons of α diversity. Red lines represent the median for each measure. *p < 0.05; **p < 0.01

Figure 2: Taxonomic cladogram obtained using Linear discriminant analysis (LDA) effect size (LEfSe) based on 16S rRNA gene sequences and identifies the most differentially abundant taxa in treated and untreated dogs with EPI and healthy dogs.