Documenting Respiratory Dysbiosis in Spontaneous Feline Asthma

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INTRODUCTION

Previously the lung was considered sterile and the presence of microbial populations indicated disease. Through using new microbial identification techniques like 16S rRNA sequencing, the lung was shown to have rich and diverse microbial populations. The richness and diversity of commensal microbial populations in the lung can be affected in a diseased state; this is known as "dysbiosis". Asthma is an important and common disease of cats; it is a type 1 hypersensitivity reaction to aeroallergens causing airway inflammation and airflow limitation.

HYPOTHESIS

We hypothesized that there would be significant differences in microbial communities between healthy and asthmatic pet cats suggestive of respiratory dysbiosis in the latter population.

MATERIALS AND METHODS

Cats were chosen from clinical cases at the University of Missouri Veterinary Health Center from 2015-2019 based on meeting asthmatic criteria (clinical signs, thoracic imaging, and >7% eosinophils in bronchoalveolar lavage fluid (BALF)). Twenty-six cats met the asthmatic criteria and their BALF samples were used to investigate the microbial communities using analysis of 16s rRNA sequencing (**Figure 1**). Historical data from healthy cats served as a control population.

Figure 1. 16S rRNA Sequencing

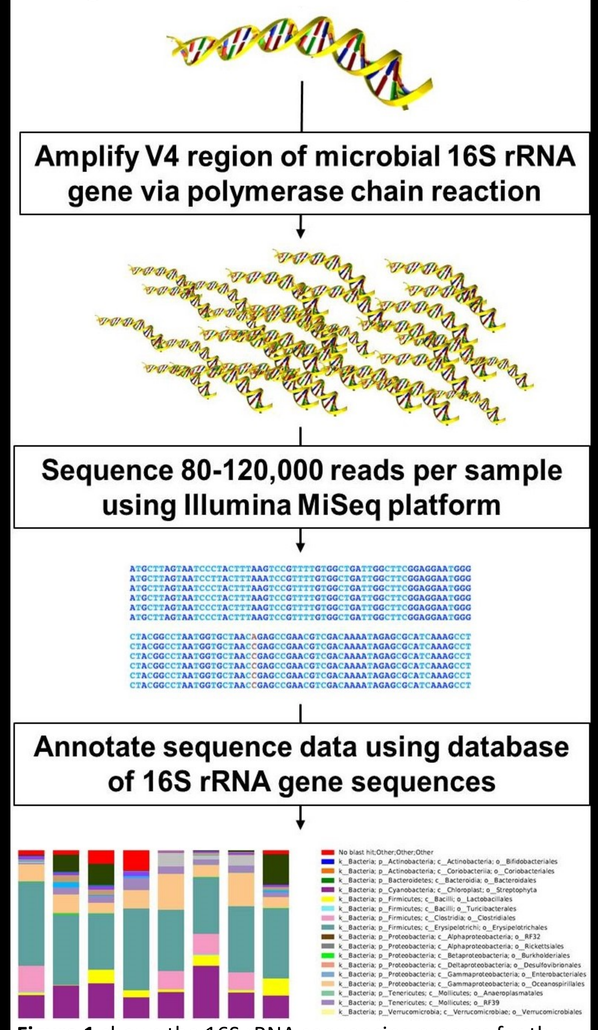

Figure 1 shows the 16S rRNA sequencing process for the samples after undergoing DNA Extraction.

RESULTS

	Coverage	Richness	α-diversity (Simpson 1-D)
Control Mean	454.33	50.167	0.834
Asthmatic Mean	3949.6	82.577	0.686
T-value	0.831	1.795	1.381

Table 1 shows the coverage (number of sequences read), richness (number of distinct OTUs), and α-diversity (combined value showing richness and distribution) were compared between the two groups by a two sample t-test with Past software. The critical t value (p=0.05) for each was 2.042 based off of 32 total samples.

Figure 2. Lung Microbiota in Healthy vs Asthmatic

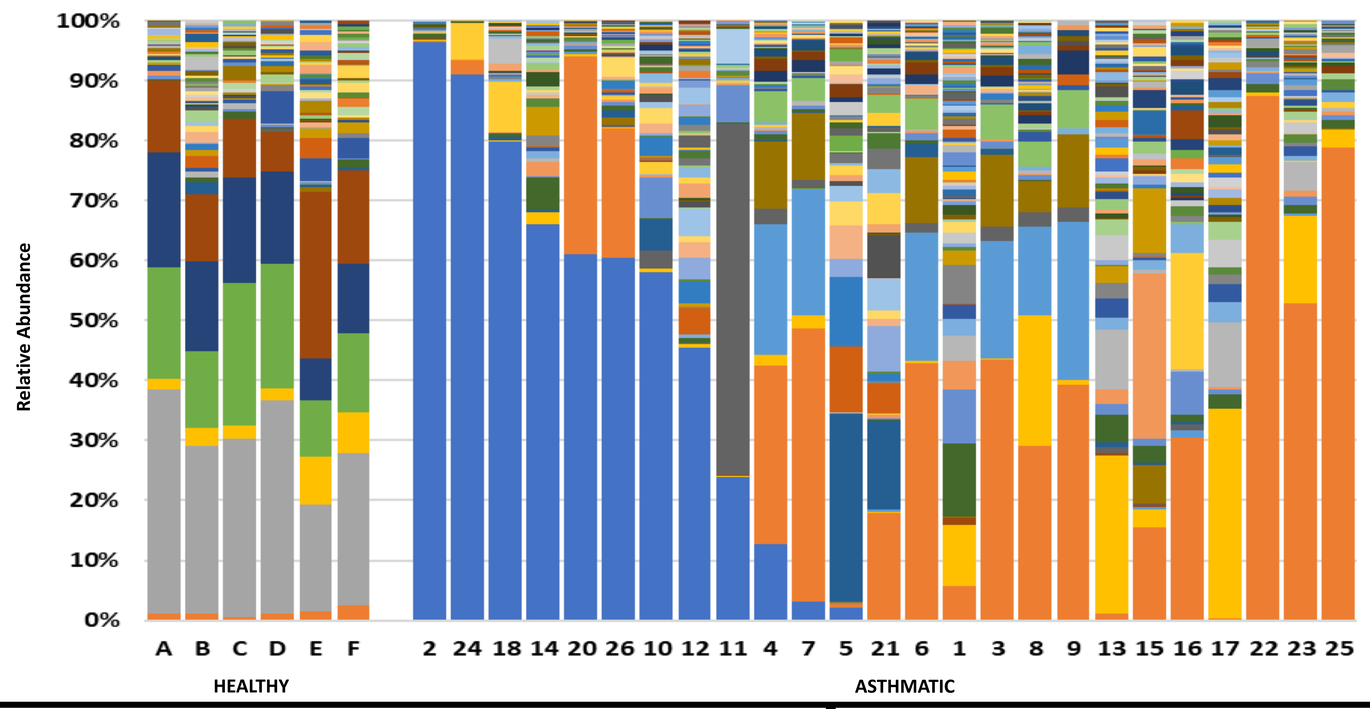

Figure 2. Relative abundance of each OTU (operational taxonomic unit) in the BALF samples of healthy control (letters) and asthmatic cats (numbers). An OTU is defined as a group of sequences that share 97% of their nucleotides, which in this study is the V4 region of 16S rRNA.

Figure 3. Bray-Curtis PCoA Plot

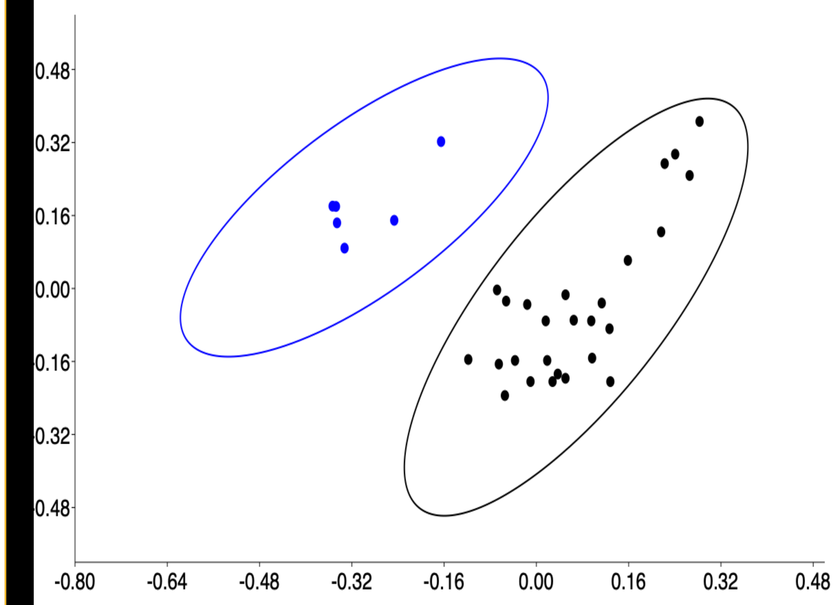

Figure 3 represents the Bray-Curtis Principal Coordinates Analysis showing lower airway microbial DNA in healthy control cats (blue) and asthmatic cats (black) in BALF. The analysis was performed by Past software.

Figure 4. Bray-Curtis Dendrogram

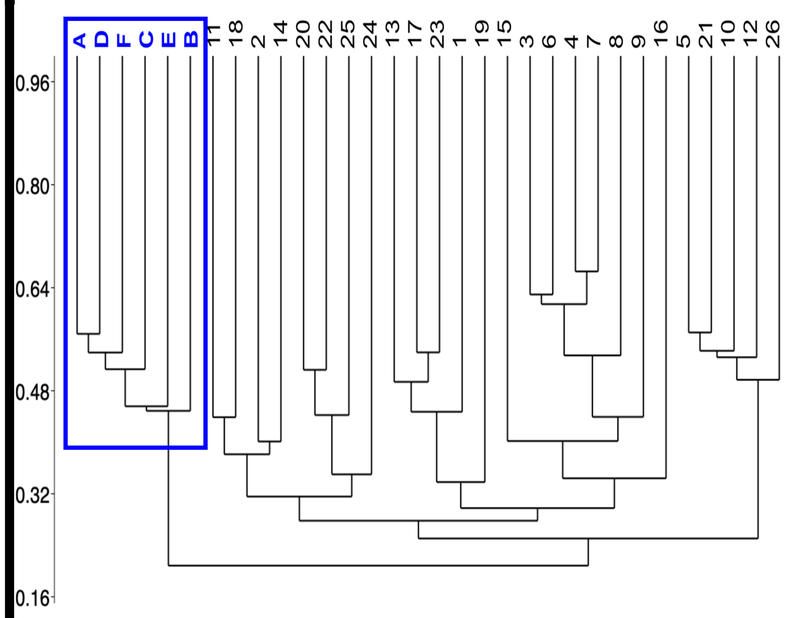

Figure 4 shows a dendrogram representation of the relationship between the lower airway microbial DNA in the BALF samples of healthy (blue, lettered) and asthmatic (black, numbered) cats.

DISCUSSION

This study shows that there are significantly different microbial communities within the lower airways between healthy and asthmatic cats supporting the concept of dysbiosis in asthma. Further studies should be done to determine how different factors (eg. diet, antibiotics, environment, etc.) could impact microbial communities in asthmatic cats. **This study represents the first step towards investigating if novel treatments restoring healthy microbial communities have a beneficial impact on the asthmatic phenotype.**

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1. Vientós-Plotts, A. I., Ericsson, A. C., Rindt, H., Grobman, M. E., Graham, A., Bishop, K., Cohn, L.A., Reinero, C. R. (2017). Dynamic changes of the respiratory microbiota and its relationship to fecal and blood microbiota in healthy young cats. PloS one, 12(3), e0173818. doi:10.1371/journal.pone.0173818