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.

RESULTS

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.

<table>
<thead>
<tr>
<th></th>
<th>Coverage</th>
<th>Richness</th>
<th>α-diversity (Simpson 1-D)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control Mean</td>
<td>454.33</td>
<td>50.167</td>
<td>0.834</td>
</tr>
<tr>
<td>Asthmatic Mean</td>
<td>3949.6</td>
<td>82.577</td>
<td>0.868</td>
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<tr>
<td>T-value</td>
<td>0.831</td>
<td>1.795</td>
<td>1.981</td>
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Figure 2. Lung Microbiota in Healthy vs Asthmatic

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.

ACKNOWLEDGEMENTS


REFERENCES