Airway Microbiota in Healthy and Bronchitic Dogs

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Introduction

• Chronic bronchitis (CB) is a common and irreversible inflammatory disorder of the lower airways of dogs, usually of unknown cause. The typical syndrome, defined by a cough >2 months duration with airway inflammation, is associated with non-degenerate neutrophils. Another poorly characterized syndrome is chronic eosinophilic bronchitis, which has similar clinicopathologic features and was also included in this study.

• Based on culturing methods, the lower airways have been considered to be sterile in disease-free states.

• Dysbiosis of the canine airway may similarly contribute to respiratory disease like CB, making the airway microbiota a potential new target for treatment.

• The objective of this study is to compare the upper and lower airway microbiota in healthy versus bronchitic dogs and determine if bacterial richness and diversity, or overall community structure, differs in bronchitic airways.

Methods

Animals

• Healthy research dogs (n=16) and client-owned dogs diagnosed with CB at the University of Missouri Veterinary Medical Teaching Hospital (MU VMTH) (n=14) were studied.

• Research dogs had unremarkable physical exams and nasals, oropharyngeal, and bronchoalveolar lavage fluid (BALF) samples were collected.

• Clinicopathologic features of bronchitic dogs were gathered from the medical record system of the MU VMTH. BALF was collected as part of the diagnostic work-up of pet dogs with CB and prospectively banked for the study.

Next-generation Sequencing

• Next-generation sequencing demonstrated the existence of a core airway microbiota, similar among dogs in the operational taxonomic units (OTU) present and the abundance of shared OTUs.

Study Participants

• Signalment of research dogs – All healthy research dogs were intact female beagles. The group mean age was 3.8 years (range: 2 to 8 years) and group mean body weight ± SD was 11 ± 1.4 kg.

• Signalment of pet dogs with CB – Eleven different purebreeds were represented. Seven dogs were males (4 neutered, 3 intact) and seven were females (all spayed). The group mean age was 7.7 years (range: 1 to 13 years) and group mean body weight ± SD was 18.1 ± 16.3 kg.

• Clinicopathologic features of pet dogs with CB – Clinical signs included chronic cough (n=14), exercise intolerance (4), and increased respiratory effort (3). Thoracic radiographs taken in seven dogs all showed a diffuse bronchial or bronchointerstitial pattern. Bronchoscopy performed in ten dogs revealed hyperemia of the airways (n=7), narrowing or collapse of bronchi and bronchioles (7), bronchiectasis (4), and mucus accumulation (3). Bacterial culture showed aerobic growth in five of twelve dogs, and Mycoplasma PCR was positive for one of three dogs.

Results

Conclusions

• Next-generation sequencing demonstrated the existence of a core airway microbiota, similar among dogs in the operational taxonomic units (OTU) present and the abundance of shared OTUs. Actinobacteria, Bacteroidales, Cyanobacteria, Firmicutes, and Proteobacteria were the most abundant phyla present.

• No significant difference was found in richness, or the number of distinct OTUs, between healthy and bronchitic dogs (P=0.126, t-test). Lack of clustering on the PCA suggests that the microbial communities are dissimilar among healthy and bronchitic dogs.

• Compared to healthy dogs, bronchitic dogs showed a significant increase in the abundance of phyla Bacteroidetes and Fusobacteria and a significant decrease in the abundance of Actinobacteria and Cyanobacteria. Significant differences were not seen in the more prominent microbial families (e.g. Moraxellaceae, Pseudomonadaceae), but in other well-represented families. In bronchitic dogs, there was an increase in the abundance of fecal microbial families and a decrease in the abundance of environmental microbial families that are a part of the core airway microbiota.

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