Comparative analysis of the respiratory microbiota of healthy dogs and dogs with canine idiopathic pulmonary fibrosis

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Canine idiopathic pulmonary fibrosis (CIPF) is a progressive parenchymal lung disease of unknown origin affecting mainly old West Highland white terriers (WHWTs). CIPF shares several clinical and pathologic features with human IPF. The use of next generation sequencing technologies recently allowed to identify differences in the composition and diversity of the respiratory microbiota in human IPF. Increased bacterial burden in bronchoalveolar lavage fluid (BALF) of IPF patients was proved to predict decline in lung function and mortality, with *Heamophilus*, *Streptococcus*, *Neisseria*, and *Veillonella* spp. being more abundant in IPF cases. The objectives of the present work were to identify and characterize the microbiota present in the lower respiratory tract of healthy beagle dogs and healthy WHWTs compared with the microbiota of WHWTs affected with CIPF. For this purpose, BALF samples were obtained from 4 groups of dogs: young healthy research beagles (n=6, median age 7.6 months), adult healthy research beagles (n=6, 8.8 years), healthy client-owned old WHWTs (n=5, 11.2 years) and client-owned WHWTs affected with CIPF (n=7, 11.6 years). Metagenetic analysis were performed on V1-V3 hypervariable region of 16S rDNA after total bacterial DNA extraction from BAL specimens and sequencing on a MiSeq Illumina sequencer. Taxonomical assignation and microbiota community analysis were done with MOTHUR V1.35 with an OTU clustering distance of 0.03. Data analyses demonstrated that the same phyla predominated in all groups of dogs with *Proteobacteria*, *Firmicutes*, *Actinobacteria*, and *Bacteroidetes* being the most abundant in a descending order. Bacterial species richness was significantly higher and evenness significantly lower in WHWTs, either healthy or affected with CIPF, in comparison with beagles, while there was no difference between groups for bacterial diversity. Beyond the effect of the breed, impact of the living environment (house-holding vs. experimental kennel) might serve as an explanation for those differences observed between beagles and WHWTs. When comparing specifically CIPF WHWTs with healthy WHWTs, *Pasteurella*, *Conchiformibius* and *Bergeyella* spp. were found more abundant in CIPF dogs. Whether those alterations in the respiratory microbiota of CIPF dogs are a cause of a consequence of the disease remain to be elucidated. In conclusion, results of the present study demonstrate the existence of a core airways microbiota in dogs that might be influenced by the breed, the environment or the disease status. Further studies are needed to better understand whether alteration in the microbiota may take part in the pathogenesis or in the predisposition for CIPF.