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

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Canine idiopathic pulmonary fibrosis (CIPF) is a parenchymal lung disease affecting mainly old West Highland white terriers (WHWTs). CIPF shares 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. The objectives of the present work were to identify and characterize the microbiota present in the lung of healthy beagles and healthy WHWTs compared with the microbiota of WHWTs affected with CIPF. For this purpose, BALF samples were obtained from young and adult healthy research beagles, and client-owned healthy and CIPF WHWTs. Metagenetic analysis were performed on V1-V3 hypervariable region of 16S rDNA after total bacterial DNA extraction 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. 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. When comparing specifically CIPF WHWTs with healthy WHWTs, *Pasteurella*, *Conchiformibius* and *Bergeyella* spp. were found more abundant in CIPF dogs. 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.