Comparison of the lung microbiome in chronic obstructive pulmonary disease and in health

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A number of clinical studies have defined the lung microbiome of chronic obstructive pulmonary disease (COPD) patients. However, these studies are limited by several factors such as cohort size, lack of standardised processing and analysis methods as well as being confined to a single geographic location. Herein, a meta-analysis of publically available COPD microbiome data was performed. Search criteria to select for next generation sequencing (NGS) studies were formed to select for publications studying the microbiome in COPD and in health. This returned 686 studies, which was narrowed down to 60 relevant studies. Relevant studies were subjected to scoring criteria to determine data quality. Eighteen studies from across Europe, North America and Asia were identified as high-quality studies and sequencing data was retrieved and analysed using standardised methods. Quality control, read trimming and processing was performed using Qiime2 and imported to R for manipulation and visualisation. Geographical location of the study and 16S target region were found to have the largest influence on the lung microbiome. Interestingly, bacterial diversity was found to be markedly increased in COPD samples when compared to healthy subjects, which was associated with an overgrowth of pathogens, such as Haemophilus, and a decrease in commensal organisms. The abundance of several genera such as Moraxella and Veillonella were also found to be significantly increased in COPD patients, proposing potential markers for COPD diagnosis. The level of abundance of these genera have potential to be used as defining criteria in the diagnosis of COPD. In conclusion, this meta-analysis provides detailed insight into the composition of the lung microbiome in COPD, highlighting the importance and benefits of utilising publically available data to build upon our current understanding of COPD and disease biology.