Comparison of the lung microbiome in chronic obstructive pulmonary disease and in health
Short, B.; Delaney, C.; Butcher, M. C.; Litherland, G.; Williams, C.; Martin, L.; Thornbury, K.; Mackay, W. G.; Ramage, G.

Published in:
THORAX

DOI:
10.1136/thorax-2021-BTSabstracts.95

Published: 08/11/2021

Document Version
Peer reviewed version

Link to publication on the UWS Academic Portal

Citation for published version (APA):

General rights
Copyright and moral rights for the publications made accessible in the UWS Academic Portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
If you believe that this document breaches copyright please contact pure@uws.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Comparison of the lung microbiome in chronic obstructive pulmonary disease and in health: an *in silico* study

Bryn Short¹,², Christopher Delaney³, Mark C. Butcher², Gary Litherland¹, Craig Williams², Lorraine Martin³, Keith Thornbury⁴, William G. Mackay¹ and Gordon Ramage²

¹University of the West of Scotland; ²University of Glasgow; ³Queens University Belfast; ⁴Dundalk Institute of Technology

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.