Patient Pathway: Improves efficiency of patient flow for biologic eligibility.

Patients referred for assessment at a specialist asthma service undergo early adherence monitoring and biomarker profiling – “pharmacist/nurse-led adherence clinic”

Abstract S88 Figure 1

assessing patient suitability for biologic asthma therapies and to support adherence in routine care.

REFERENCE

1. Heaney, et al. (RASP-UK) *Am J Respir Crit Care Med* 2019;**199**(4):454–464.

Please refer to page A190 for declarations of interest related to this abstract.

New insights into airways disease

S89

COMPARISON OF THE LUNG MICROBIOME IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE AND IN HEALTH: AN IN SILICO STUDY

¹B Short, ²C Delaney, ²MC Butcher, ¹G Litherland, ²C Williams, ³L Martin, ⁴K Thornbury, ¹WG Mackay, ²G Ramage. ¹University of the West of Scotland, Paisley, UK; ²University of Glasgow, Glasgow, UK; ³Queens University Belfast, Belfast, UK; ⁴Dundalk Institute of Technology, Dundalk, Ireland

10.1136/thorax-2021-BTSabstracts.95

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.

S90

COMPREHENSIVE MULTIOMICS ANALYSIS DEMONSTRATES SURFACTANT DYSREGULATION IN COPD

¹V Hristova, ^{2,3}A Watson, ¹M Glover, ¹J Wang, ⁴B Angermann, ⁵S Ashenden, ⁵A Bornot, ²H Burke, ²D Cellura, ¹R Chaerkady, ²A Freeman, ⁶A Mackay, ⁴D Muthas, ⁵S Novick, ⁴L Öberg, ⁴K Ostridge, ⁴A Platt, ²AD Postle, ²CM Spalluto, ⁵W Yu, ¹S Hess, ²KJ Staples, ²TMA Wilkinson. ¹Dynamic Omics, Antibody Discovery and Protein Engineering (ADPE), R&D, AstraZeneca, Gaithersburg, USA; ²Clinical and Experimental Sciences, Faculty of Medicine, University of Southampton, Southampton, UK; ³University of Birmingham, Birmingham, UK; ⁴Translational Science and Experimental Medicine, Research and Early Development, Respiratory & Immunology, BioPharmaceuticals R&D, AstraZeneca, Gothenburg, Sweden; ⁵Data Sciences and Quantitative Biology, Discovery Sciences, R&D, AstraZeneca, Gothenburg, Sweden; ⁶NHLI, Imperial College, London, UK

10.1136/thorax-2021-BTSabstracts.96

Introduction and Objectives Pulmonary surfactant homeostasis is critical to lung function as it coats the vast air-liquid