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

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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.

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COMPREHENSIVE MULTIOMICS ANALYSIS DEMONSTRATES SURFACTANT DYSREGULATION IN COPD

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

interface, reducing surface tension and preventing alveolar collapse. surfactant proteins (SP)-A and D play essential anti-pathogenic defence and immunoregulation roles to maintain lung homeostasis. SP-D is reduced in COPD. We hypothesised lipid and protein surfactant dysregulation could contribute to pathological COPD mechanisms, this requires detailed characterisation.

Methods We conducted mass spectrometry-based multiomic (proteomic, lipidomic and metabolomic) analysis of bronchoalveolar lavage to comprehensively characterize surfactant dysregulation in a well-characterised ex-smoking mild/moderate COPD cohort (n=31), with median (IQR) age of 70 (9.5) and FEV1% predicted 73 (21), compared with healthy ex-smoking volunteers (n=20), with age 67.5 (6.75) and FEV1% predicted 100.5 (11.75). To identify the multiomic signatures of COPD, we fitted linear mixed-effects models to the data, accounting for the effects of confounding variables, such as age, gender and individual differences simultaneously. We further characterised purified alveolar macrophage gene expression differences.

Results SP-A, SP-B, and SP-D levels were lower in COPD vs control with log2fold changes (FC) of -0.7 ($p=1.1 \times 10^{-6}$), -0.6 ($p=4.8 \times 10^{-6}$) and -0.6 ($p=3.0 \times 10^{-5}$), and showed positive correlations of 0.65 ($p=1.5 \times 10^{-12}$), 0.62 ($p=7.7 \times 10^{-11}$) and 0.43 ($p=2.3 \times 10^{-4}$) with lung function (FEV1/FVC), respectively. SP-C was below detection limit. NAPS and CTSH, responsible for SP-B synthesis, were lower in COPD, log2FC of -0.1 ($p=2.8 \times 10^{-6}$) and -0.4 ($p=4.3 \times 10^{-4}$), respectively. Fatty acid binding protein 4 (FABP4) and CD44, involved in surfactant regulation, were decreased in COPD, log2FC of -0.4 ($p=8.0 \times 10^{-3}$) and -0.7 ($p=1.1 \times 10^{-5}$), respectively. Histamine and hypoxanthine metabolites were increased in COPD, log2FC of 0.8 ($p=2.5 \times 10^{-2}$) and 1.0 ($p=4.0 \times 10^{-2}$), respectively, which could indicate immune-dysregulation and inflammation. Surfactant lipid levels were decreased in COPD, specifically, PC, PG, and PI, log2FC of -2.1 ($p=2.6 \times 10^{-7}$), -2.4 ($p=5.3 \times 10^{-8}$) and -1.5 ($p=9.0 \times 10^{-6}$), respectively.

Conclusions We used a multiomics approach to comprehensively describe surfactant dysregulation in a well-characterised COPD cohort, with an aim to generate novel insights into key aspects of this biology within the COPD lung. Further mechanistic studies could help to understand the role this plays in pathological mechanisms and allow novel therapeutic target identification.

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

S91

GATEWAY TO THE HIDDEN ZONE: USING PCLE TO STUDY RELATIONSHIPS BETWEEN ELASTIN REMODELLING AND SMALL AIRWAYS DISEASE IN THE COPD LUNG

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Introduction Small airways disease (SAD) is a hallmark of COPD and often precedes the development of airflow obstruction and clinically evident emphysema. SAD requires study

Healthy

Mild COPD

Abstract S91 Figure 1 Examples of the analysis output, with detected elastin fibres in green

however, this has been complicated by the absence of direct sampling and imaging techniques and is beyond the resolution of CT. Probe-based confocal laser endomicroscopy (pCLE) produces fluorescence images of tissue obtained in vivo during endoscopy. pCLE can image extra-cellular matrix (ECM) remodelling in the submucosa of airway walls. We developed imaging and analysis techniques and used these to describe the ECM remodelling and relationships to features of SAD and early COPD.

Methods We performed pCLE-bronchoscopy to directly visualise the airways in 8 never smokers (mean [$\pm$ SD] age, 48 $\pm$ 8), 8 smokers with normal spirometry (mean [$\pm$ SD] age, 55 $\pm$ 5) and 12 patients with COPD (mean [$\pm$ SD] age, 61 $\pm$ 4, mean [$\pm$ SD] FEV1%, 83.5% $\pm$ 13.5). Alveolar opening dimensions were measured, and the structural disorder caused by the remodelling process was objectively quantified and expressed as an elastin linearity score (ELS) using novel quantitative image analysis software.

Results COPD was associated with larger mean alveolar opening diameter (350.1 μ m $\pm$ 15.1 vs 289.8 μ m $\pm$ 21.6, p = 0.000) and greater cross-sectional area.

There was greater disorder of airway elastin fibre alignment, even in mild COPD (mean [$\pm$ SD] ELS, 54.9 $\pm$ 6 vs 44.7 $\pm$ 9, p = 0.002). ELS was inversely correlated with several lung function and CT imaging parameters including FEV1% (r = -0.477, p = 0.016) FEV1/FVC% (r = -0.640, p = 0.001) MEF_{25-75%} (r = -0.649, p = 0.001), and mean expiratory to inspiratory ratio of the mean lung density (E/I MLD) (r = 0.438, p = 0.032).

Conclusions This is the first pCLE study to describe airway microscopic changes related to lung function and CT indices of small airways disease in COPD. These results suggest this novel imaging analysis technique may help uncover the earliest signs of airway remodelling in COPD offering new insights into key mechanisms of disease and potential novel endpoints for development of novel disease modifying treatments for this important disease.

S92

FENO NON-SUPPRESSION IDENTIFIES CORTICOSTEROID-RESISTANT TYPE-2 SIGNALING IN SEVERE ASTHMA

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Rationale Patients with severe asthma, raised fractional exhaled nitric oxide (FeNO) and high blood eosinophil (Eos) counts are at increased risk of asthma attacks.