Introduction COPD is thought to result largely from neutrophilic inflammation. Relatively little focus has been given to the endothelium, through which neutrophils transmigrate to reach the lung, despite observation of abnormal amounts of endothelial tissue in COPD which behaves in a dysfunctional manner. We sought to determine if coding (mRNA) and non-coding (miRNA) alterations in pulmonary endothelium exist in COPD, and if so what their effect is on endothelial function.

Methods Patients with and without COPD undergoing thoracic surgery were recruited (n=52); power calculations indicated that 10 in each group were required to detect differences in miRNA between health and COPD. Human Pulmonary Endothelial Cells (HPAECs) were isolated from lung tissue by positive selection using Ulex europeus lectin-coated magnetic beads and extracted RNA used for miRNA and mRNA microarrays, as well as confirmatory qPCR. Significance Analysis of Microarrays (SAM) was used to perform differential miRNA or mRNA analysis; ingenuity pathway analysis (IPA) was also carried out to guide functional work. The miRNA which differed most between health and COPD was transfected into endothelial cells and a range of cellular functions were assessed, including matrigel and spheroid assays.

Results 2071 genes and 43 miRNAs were significantly upregulated in COPD. 6 miRNAs and 8 miRNAs were appropriate for further validation. 4 targets were validated by qPCR, of which miR-181b-3p exhibited the most significant differential expression and was chosen for functional validation. IPA suggested that cell growth/proliferation, eicosanoid signalling and TGFβ (transforming growth factor beta) driven pathways were affected most between health and COPD was transfected into HUVECs and assessed in a range of cellular functions were assessed, including matrigel and spheroid assays. Results 2071 genes and 43 miRNAs were significantly upregulated in COPD. 6 miRNAs and 8 miRNAs were appropriate for further validation. 4 targets were validated by qPCR, of which miR-181b-3p exhibited the most significant differential expression and was chosen for functional validation. IPA suggested that cell growth/proliferation, eicosanoid signalling and TGFβ driven pathways were among the most relevant for further study. There was significantly reduced tube formation (figure 1) and endothelial sprouting in Human umbilical vein endothelial cells (HUVECs) transfected with miR-181b-3p, consistent with an effect on angiogenesis.

Abstract S113 Figure 1. An example of image from a matrigel experiment. A: HUVECs transfected with miR-181b-3p mimic. B: HUVECs transfected with negative siRNA. There is reduced tube formation seen in HUVECs transfected with the mimic.

Conclusions Upregulation of miR-181b-3p reduces tube formation and sprouting by endothelial cells. This might be significant in the development of emphysema as lung vasculature is important in the structural maintenance of alveoli. Correcting miR-181b-3p expression levels could be a route for treating emphysema by promoting support of alveolar structure and regeneration.
potentially contributing to the observed differential protein release.

Conclusions Hypoxia augments NE release in a PI3K-dependent manner, further increased during COPD exacerbations, and hypoxic neutrophil supernatants injure endothelial cells in vitro. Unbiased characterisation of hypoxic neutrophil secretomes identified several upregulated proteins which may contribute to cellular/tissue damage. In addition to degranulation, NDMP release may underpin differential protein secretion under hypoxia. Hypoxia engenders a neutrophil phenotype with potential to cause local and distant tissue damage in COPD: novel targets in the hypoxic neutrophil secretome may identify new therapeutic opportunities.

S115 MECHANISMS TO REVERSE IMPAIRED MACROPHAGE EFFEROCYTOSIS IN COPD

COPD patients have defective innate immunity, characterised in part by macrophage dysfunction. In established disease, both monocyte derived macrophages (MDM) and alveolar macrophages (AM), have impaired phagocytosis of bacteria and apoptotic cells (effectorosis). Failure to adequately effectorose dying cells leads to further release of inflammatory mediators and ongoing recruitment of immune cells, culminating in inflammation that is both damaging and ineffective. The transcription factor, Nrf2 is the master regulator of the antioxidant-response-element. Previous work using the non specific Nrf2 agonist, Sulforaphane, has partially restored defective bacterial phagocytosis in COPD AMs, however the specificity and mechanism of action in this context remains unknown. The role of Nrf2 activation in restoring macrophage effectorosis in COPD has yet to be examined. We questioned if impaired macrophage phagocytosis and effectorosis in COPD share a common mechanism and consequently if the defect in macrophage effectorosis can be therapeutically manipulated using highly selective Nrf2 agonists. AMs and MDMs were isolated from patients with established COPD (GOLD stage 1–3). Macrophage effectorosis of apoptotic neutrophils from each donor was correlated with bacterial internalisation of Streptococcus pneumoniae. Effectorosis assays were carried out in the presence or absence of Sulforaphane and Compound 7, a highly specific Nrf2 agonist (supplied by GSK). Both COPD MDMs and AMs have significantly impaired phagocytosis of bacteria and apoptotic cells compared to Healthy Controls (p values all <0.05). Moreover, there was a correlation between donor macrophage phagocytosis of apoptotic cells and of bacteria (r = 0.71). In vitro studies using Sulforaphane enhanced effectorosis of apoptotic cells in both COPD MDMs and AMs (p < 0.01). This effect was replicated using Compound 7 in both MDMs (p < 0.05) and AMs. This was more pronounced in current smokers. In summary, we observe a correlation between impaired macrophage phagocytosis and effectorosis in COPD, suggesting a common mechanism. Furthermore, we describe partial rescue of defective COPD MDM and AM effectorosis by Sulforaphane and via specific activation of the Nrf2 pathway using Compound 7. Together, these data highlight the importance of the Nrf2 pathway in reversing macrophage dysfunction in COPD patients and provide key mechanistic insights into the underlying defect.

S116 CELL-DISASSOCIATED HAEMOPHILUS INFLUENZAE AND BACTERIA-ASSOCIATED INFLAMMATORY MEDIATORS IN THE AIRWAYS OF PATIENTS WITH CHRONIC OBSTRUCTIVE PULMONARY DISEASE

Background Patients with COPD have a susceptibility to respiratory tract infections associated with increased pulmonary inflammation. Bacteria can reside within the host as cell-associated (attached to host cells via adhesins, pili or biofilm formation) or cell-dissociated bacteria. It is unclear how bacteria-to-cell interactions affect pulmonary inflammation and whether