

Results CRTH2 cell counts were reasonably repeatable within patients (ICC 0.84; $n = 9$). Mean \pm SD CRTH2+ cell counts were 168 ± 81 , 322 ± 191 , 710 ± 322 and $290 \pm 179 \times 10^6$ cells/L in normal controls ($n = 12$), patients with mild to moderate asthma ($n = 12$), patients with severe asthma at BTS step 4 ($n = 10$), and patients with severe asthma at BTS step 5 ($n = 11$) respectively (Figure 1). Most CRTH2 + cells were eosinophils (Figure 1).

Conclusion Blood CRTH2+ cells are increased in subjects with severe eosinophilic asthma, mainly because of increased CRTH2 + eosinophils. Eosinophils and basophils numbers are significantly increased in severe eosinophilic asthma at step 4 but not step 5. Th2 and Tc2 cell numbers are less clearly associated with severe asthma. CRTH2+ cell numbers are lower in patients treated with prednisolone.

S96 FREE-LIVING HAEMOPHILUS INFLUENZAE IS ASSOCIATED WITH INCREASED PULMONARY INFLAMMATION

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10.1136/thoraxjnl-2015-207770.102

Introduction The most common pathogen in the lower airway of patients with COPD is *Haemophilus influenzae*. *H. influenzae* has been shown to be linked to inflammation and increased inflammation. Emerging evidence shows that pathogens can exist as either cell-associated or free-living (non-cell associated). We investigated whether detectable free-living *H. influenzae* correlates with pulmonary inflammation.

Methods Cell-free sputum supernatants samples from 29 COPD patients (24 men), with a mean (range) age of 71 (45 to 88) years were analysed. All samples were collected at stable state and bacterial DNA was extracted, using a commercial assay and then quantified using real time-PCR utilising taqman hydrolysis probes. The omp P6 gene from *H. influenzae* was inserted into a positive cloning vector and transformed to generate plasmids. These plasmids were used as standards within the qPCR, allowing the accurate detection of very small levels of *H. influenzae* within the samples. Cytokines were measured using the meso-scale multi-array platform within the same sample set.

Results Free Living *H. influenzae* was detected in 15/29 (52%) of cell-free samples, with a bacterial load of (geometric mean (95% CI)) of 1.23×10^6 gene copies/ml (2.63×10^5 to 5.75×10^6). Correlations were seen between free-living *H. influenzae* and Interleukin-1 Beta (IL1- β) ($r = 0.47$, $p = 0.01$), MMP8 ($p = 0.04$, $r = 0.38$), CCL3 ($p = 0.002$, $r = 0.57$), CCL13 ($p = 0.02$, $r = 0.54$), CCL26 ($p = 0.03$, $r = -0.31$), CCL4 ($p = 0.04$, $r = 0.38$). No significant correlations were seen between free-living *H. influenzae* and IL8 ($p = 0.11$, $r = -0.30$), IL10 ($p = 0.10$, $r = -0.36$) or TNF-alpha ($p = 0.61$, $r = -0.12$).

Conclusion Free-living *H. influenzae* is associated with increased pro-inflammatory mediators in the airway. Whether this is

related to the pathogenesis of COPD needs to be further investigated.

S97 SEVERITY OF LUNG BUT NOT LIVER DISEASE IMPACTS CARDIOVASCULAR RISK IN ALPHA-1 ANTITRYPSIN DEFICIENCY

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10.1136/thoraxjnl-2015-207770.103

Introduction Alpha-1 antitrypsin deficiency (AATD) is a genetic condition associated with COPD; patients homozygous for the mutant 'Z' allele (PiZZ) are predisposed to severe, early-onset emphysema of the lung, and also progressive fibrosis and cirrhosis of the liver. There is a well-known association between COPD and cardiovascular disease, with around 1 in 3 COPD deaths attributed to a cardiac cause.¹ We hypothesised that cardiovascular risk in AATD may be independently modified by the severity of lung and liver disease, through common or related pathophysiological processes.

Methods Cardiovascular risk was ascertained in 43 patients with PiZZ AATD using QRISK2 score and aortic pulse wave velocity (aPWV). These values were correlated with indicators of lung (FEV₁, D_{LCO}, K_{CO}, RV) and structural liver disease (transient elastography and liver ultrasound).

Results The severity of airflow obstruction (FEV₁), emphysema (gas transfer) and gas trapping (RV) all related to cardiovascular risk as assessed by aPWV and QRISK2, Table 1. In contrast, there was no significant association between the presence or increased severity of structural liver disease, as assessed by ultrasound and transient elastography respectively, and either indicator of cardiovascular risk ($p < 0.05$).

Abstract S97 Table 1

	FEV ₁ (l)		D _{LCO} (mmol/min/kPa)		K _{CO} (mmol/min/kPa/l)		RV (l)	
	r/rho	p	r/rho	p	r/rho	p	r/rho	p
aPWV (m/s)	-0.459	0.002	-0.516	<0.001	-0.454	0.002	0.485	0.002
QRISK2 (% risk)	-0.335	0.043	-0.462	0.004	-0.336	0.042	0.388	0.026

Conclusions These findings demonstrate that the severities of emphysema and airflow obstruction are associated with increased cardiovascular risk in AATD. In contrast, there was no association between the severity of structural liver disease and cardiovascular risk. Therefore, in conclusion, cardiovascular risk varies in PiZZ A1AD patients according to disease phenotype.

REFERENCE

¹ McGarvey LP, et al. *Thorax* 2007;**62**(5):411–15