European Respiratory Society
Annual Congress 2012

Abstract Number: 7180

Publication Number: 345

Abstract Group: 5.2. Monitoring Airway Disease

Keyword 1: Asthma - management **Keyword 2:** Proteomics **Keyword 3:** Exacerbation

Title: Urinary proteomics in asthma: Search for a biomarker

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Body: Background: The use of inflammatory indices such as sputum eosinophilia to guide anti-inflammatory treatment in asthma has been shown to reduce the frequency and severity of exacerbations. Aims: Sputum induction can be unpleasant for patients and analysis is costly and labour intensive necessitating alternative methods to differentiate inflammatory phenotypes, guide anti-inflammatory treatment and predict exacerbation risk. Method: Performing Surface Enhanced Laser Desorption/Ionisation Time of Flight Mass Spectrometry utilising 6 different “chips” we analysed spectra from 3 groups, the first (exacerbation vs recovery (n=16), second (prospective patient samples thrice weekly, before, during and after an exacerbation (n=3), and third (patients with different inflammatory phenotypes (eosinophilic, neutrophilic, mixed granulocytic and paucigranular) (n=10) Results: Differential protein signatures were found between inflammatory phenotypes (p=<0.05) and between exacerbation and recovery states (p=<0.05). The IMAC Cu chip identified a signature which delineated onset, exacerbation and recovery states. Protein signatures were able to distinguish patients in each comparative group (P=<0.05)

Conclusion: Further work is warranted with a larger sample size to corroborate our findings and identify the proteins these signatures represent. This may ultimately identify a urinary marker indicating pre-exacerbation states in asthma enabling early intervention.