

European Respiratory Society Annual Congress 2013

Abstract Number: 5033

Publication Number: P624

Abstract Group: 3.2. Airway Cell Biology and Immunopathology

Keyword 1: Proteomics **Keyword 2:** Cell biology **Keyword 3:** COPD - mechanism

Title: Proteomic profiling of alveolar epithelial cells exposed to cigarette smoke extract

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Body: Cigarette smoke (CS) is the most relevant risk factor in the development of lung cancer and chronic obstructive pulmonary disease. CS contains more than 4000 chemicals, many of which are known to be strongly oxidizing and carcinogenic. These compounds can easily interact with proteins of the first environmental barrier of the lung, the epithelial cells, thereby inducing post-translational modifications and alterations of structure and abundance of proteins. The aim of this study is to use label-free quantitative mass spectrometry (i.e. LC-MSMS) to globally assess changes in the proteomic profile of different cellular compartments of alveolar epithelial A549 cells after exposure to cigarette smoke extract (CSE). We successfully enriched plasma membrane, cytosolic, nuclear and secreted proteins in different fractions that were subsequently analyzed by LC-MSMS. The performed fractionation workflow proved to be highly reproducible for the A549 cells and resulted in the identification of altogether more than 2000 proteins. Using a comparative approach, we are currently investigating cell fractions from epithelial cells exposed to CSE. This will allow for the identification of altered protein profiles at plasma membranes, in the cytoplasm and nucleus as well as the analysis of differentially secreted proteins. Moreover, we aim for the identification of post-translational modifications of these affected proteins. Ultimately, the results of this study may lead to the identification of affected cellular pathways, therefore improving our understanding of the effect of CS on the alveolar epithelial cells and consequently in the context of lung diseases.