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Title: The effect of cigarette smoking on BAL protein profile

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Body: BACKGROUND: BAL proteomic analysis gives a panorama of the complex network of proteins of different origin and function and their modifications at alveolar level, simultaneously providing new information about events in the alveolar microenvironment and insights into lung physiology and pathology. In this study we applied the proteomic approach to the study of BAL in order to evaluate the effect of smoking exposure to BAL protein composition. AIM: Aim of this study was to investigate qualitative and quantitative differences in BAL protein profiles from cigarette smoker and no-smoker healthy subjects. METHODS: BAL samples were obtained by 10 healthy never-smoker and 8 asymptomatic smoker subjects. After centrifugation, dialysis and denaturation of samples, BAL samples were analyzed by two-dimensional electrophoresis and proteins differentially expressed were identified by mass spectrometry. RESULTS: 20 BAL proteins were differently expressed: 15 were up-regulated in smokers and 5 proteins were up-regulated in never-smokers. Among these proteins some were involved in immune-regulation, host defense (i.e.Pulmonary Surfactant-associated protein A2), apoptosis, inflammatory responses (i.e. α -1-antichymotrypsin) and oxidant/antioxidant balance (i.e. Glutathione S transferase P and Annexin A5). CONCLUSION: In healthy subjects smoking exposure modifies the expression of several BAL proteins implicated in the regulation of crucial biological activities (such as oxidant/antioxidant balance, inflammation and tissue matrix turnover) potentially involved in the pathogenesis of several smoke-induced lung diseases.