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Diagnosis of lung diseases based on proteomic analysis of exhaled breath condensate

COPD - diagnosis, Pneumonia, Proteomics

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Objective: a comparative study of the protein spectrum of exhaled breath condensate (EBC) in healthy volunteers and patients with COPD, pneumonia and NSCLC, as well as to assess the possibility of using proteomic analysis of EBC for the diagnosis and differential diagnosis of these diseases.

Materials and methods: We examined 18 patients with COPD, 13 - with community-acquired pneumonia, 26 - with NSCLC and 24 healthy non-smoking volunteers. EBC was collected using ECoScreen. EBC-samples lyophilized, hydrolyzed and analyzed by HPLC and tandem mass spectrometry.

Results: Proteomic analysis of EBC four groups of donors identified more than 300 different proteins, most of them were cytoskeletal keratins (CK) type I and II. The content of CKs (5, 6, 14) in the EBC samples of NSCLC patients was significantly higher than in healthy volunteers. Dermcidin, cytoplasmic actin, immunoglobulin- α -kininogen, serum albumin, Zn- α 2-glycoprotein were identified in EBC healthy volunteers and patients with COPD and pneumonia. The high concentration of peroxiredoxin in EBC of COPD refers to a pronounced oxidative stress. The high levels of acute phase proteins of inflammation and hypoxia (annexins A1 and A2, HSP90B, cystatins M and B, collagen and histones fragments) were detected in EBC samples of patients with pneumonia. Also α - и β -subunit of hemoglobin, NUCKS, POTEE, high mobility group protein (HMG-I/HMG-Y) and lactoferrin were identified in EBC of patients with NSCLC.

Conclusions: We found that samples of EBC groups of healthy nonsmokers, patients with COPD, pneumonia and NSCLC have a characteristic protein spectrum. Most of the identified proteins could be offered as a panel for the diagnosis of these diseases.