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411. Inflammation and remodelling in lung disease

PA3925

Serum metabolomic analysis of mustard airway diseases by nuclear magnetic resonance spectrometry: A pilot studyB. Fatemeh Nobakht M. Gh.¹, Rasoul Aliannejad², Salman Taheri³, Mostafa Rezaei-Tavirani¹, Fariba Fathi⁴, Afsaneh Arefi Oskouie⁵

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Introduction: Nuclear magnetic resonance (NMR) spectroscopy is an ideal platform for the metabolic analysis of biofluids. Sulfur mustard (SM) is a alkylating chemical warfare agent that cause lung injury and despite years of research there is no common consensus about the pathophysiological basis of mustard airway disease. **Aims and objectives:** we used ¹H NMR spectroscopy to explore the metabolic profile of sera from mustard airway disease patients. **Methods:** A total of twenty nine serum samples obtained from SM-injured patients (n=17) and healthy controls (n=12) were investigated. Random forest (RF) analysis was capable of distinguishing SM-exposed patients from controls. **Results:** A total of 18 metabolites differed significantly in intensity between the two groups. Serum samples from SM-injured patients were characterized by increased concentrations of amino acid metabolism (L-glutamine, L-glutamate, L-asparagine, L-lysine, L-glycine, L-proline, and 4-hydroxyproline), lipid metabolism, citrate, ketone bodies, organic acid (lactate and acetate), urea pathway (citrulline), and creatine, relative to control subjects. **Discussion:** Our study reveals the metabolic profile of sera from SM-injured patients and indicates that NMR-based methods can distinguish these patients from healthy controls. Also, serum Metabolomic profile of COPD patients differ with mustard airway disease by increased levels of methylhistidine (a muscle protein) and reduced levels of branched-chain amino acids as well as 4-hydroxyproline and proline. It suggests that Metabolomic-based diagnostics not only can distinguish mustard airway disease with healthy controls, but also can diagnose from COPD.