PROTEOMIC ANALYSIS OF SERUM PROTEINS AT THE ONSET OF ARDS IN PATIENTS
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PURPOSE: The purpose was to examine the changes in serum protein expression in patients with ARDS.

METHODS: 5 ARDS patients (Patient group) and 5 healthy individuals (Control group) were enclosed. 2 distinct pooled serum samples were used for immunodepletion of High-Abundance Plasma Proteins, then protein concentration was measured. The precipitated proteins were digested with sequence-grade modified trypsin. Peptides were labeled with the TMT for subsequent high pH reverse phase separation. LC-MS analysis were performed on an EASY-nLC 1000 system and Orbitrap Fusion mass spectrometer. Different expressed proteins were filtered if their fold change were over 2.0 fold and statistical p-value below 0.05.

The patterns of protein expression were analyzed using principal component analysis (PCA). Biological processes that were enriched in the serum proteins of Patient group were identified using Gene Ontology (GO) analysis. Protein networks that model the protein interactions were generated using Ingenuity Pathway Analysis.

RESULTS: there were 162 differentially expressed proteins from patients with ARDS and healthy volunteers, 128 were upregulated and 34 were downregulated in Patient group. Bioinformatics analysis showed most of the identified proteins was functionally related to specific cell processes, including apoptosis, oxidative stress, inflammation.

CONCLUSIONS: The proteomics analysis revealed the complex property of pathogenesis in ARDS. The results provide new insights about protein networks in ARDS, and identify novel mediators that are likely to be involved in the pathogenesis of ARDS.

CLINICAL IMPLICATIONS: Proteomic analysis of serum proteins is conducive to the discovery of potential pathogenesis, the biomarkers for predicting the clinical outcomes, and assessment on severity status as well.

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