European Respiratory Society
Annual Congress 2013

Abstract Number: 3519
Publication Number: P4403

Abstract Group: 10.1. Respiratory Infections
Keyword 1: Sepsis **Keyword 2:** Biomarkers **Keyword 3:** Proteomics

Title: Preliminary proteomics analysis for sepsis biomarkers with iTRAQ labeling and LC-MS/MS

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Body: Introduction Sepsis is a leading cause of mortality in ICU, which need to be diagnosed and treated as quickly as possible. However, there remains no effective biomarkers satisfied in clinical practice. Objectives To screen potential sepsis biomarkers for diagnosis making, severity assessment, and outcome prediction. Methods Serum potential biomarkers were identified using iTRAQ coupled with LC-MS/MS. The database search against the International Protein Index was performed with Mascot software. Bioinformatics analyses were dissected by ANOVA analysis, protein expression profiles, principal component analysis, proteins network construction. Results This study involved 27 healthy control, 17 SIRS without infection, 18 diagnosed with sepsis, and 17 as severe sepsis, and 30 sepsis patients within 48 h before death. A total of 214 proteins were identified through three replicates and fold change>1.2. 52 proteins had significant tendency in expression profiles ($P<0.05$). Among these, 12 proteins were selected for further investigation based on spectra number≥3 and peptide number≥2. The data from PCA revealed that they can differentiate sepsis, severe sepsis, and bad outcome. Protein network analysis demonstrate that three, hemopexin(HPX), vimentin(VIM), and Isoform 2 of heat shock protein 90-alpha(HSP90Aa1), localized in the core of the network. When patients suffering from sepsis, the serum concentration of these three proteins rapidly elevated, and would become increasingly higher as the severity of the disease worsen, or even death. Conclusion Three identified proteins, HPX, VIM, and HSP90Aa1, provide new insight into the study of sepsis biomarker, which maybe potential markers in the future.