COMPARATIVE PROTEOME PROFILING REVEALED DIFFERENTIAL REGULATION BETWEEN SURVIVAL AND NON-SURVIVAL SEPSIS PATIENT


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Introduction
Sepsis is a syndrome resulted from imbalance of inflammatory and anti-inflammatory processes after infection. Complications of this infection with multiple organ failure lead to more lethal conditions, such as severe sepsis and septic shock. There are several sources of infection reported such as lung, abdomen and urinary tract infection. Typically 50% of all sepsis cases start as lung infection and commonly known as pneumonia. In the last decade, progress has been made in the early detection and treatment of sepsis. Despite these improvements it still remains with high mortality and with several caveats in the understanding of mechanism.

Objectives
Identification of differentially expressed proteins between survival and non-survival septic patients

Materials and Methods
In the present study, we compared proteome profiling of septic patient’s blood plasma from pneumonia as primary infection using quantitative proteomics approach. In brief, control (healthy volunteer; N = 23), survival (N = 20) and non-survival (N = 13) patient samples were depleted for high abundant proteins, trypsin digested and labelled with iTRAQ. Total 40 fractions were collected using SCX chromatography and analyzed with LC-MS. After this, raw data was processed and submitted to mascot search engine with selected to swiss-prot data base and 1% FDR.

Result and Discussion
Preliminary data screening shown differential proteome expression profile between septic survival and non-survival patients when compared against healthy volunteers. We also identified 42 differentially expressed proteins between survival and non-survival group, whereas 31 proteins were up-regulated and 11 proteins were down-regulated in non-survival. These proteins are key molecules for various signaling and biological processes.

Conclusion
Further validation of these results is under progress. This study may provide new insight of disease progression, mechanism and novel therapeutic targets for sepsis.