**Comparative proteomic analysis of mustard lung as a complicated disease using systems biology approach**

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**Abstract**

During Iraq-Iran conflict, chemical weapons, particularly SM gas, were used numerous times, whose aftereffects are still present. This study aimed to compare serum proteome in the chronic ML (n=10) and HC (n=10). TMT labelbased quantitative proteomics was used to examine serums from two groups. Among total significant proteins, 14 proteins were upregulated (log2≥FC 0.5, p 0.05), and 6 proteins were downregulated (log2≤FC −0.5, p 0.05). By helping PPI network, and EA, 11 main pathways connected to significantly different protein expression levels were discovered, including inflammatory and cell adhesion signaling pathways. It may be deduced that the wounded organs of exposed individuals experience poor repair cycles of cell degeneration and regeneration because certain repair signals were elevated while other structural and adhesion molecules were downregulated. The systems biology approach can help enhance our basic knowledge of biological processes, and contribute to a deeper understanding of pathophysiological mechanisms, as well as the identification of potential biomarkers of disease.

**Keywords:** Mustard lung, Systems biology, Proteomics, Enrichment analysis