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Proteomic analysis reveals the enhancement of human serum apolipoprotein A-1(APO A-1) in individuals infected with multiple dengue virus serotypes

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Abstract

Objectives: Human serum protein profiling of the individual infected with multiple dengue virus serotypes for identifying the potential biomarkers and to investigate the cause for the severity of dengue virus infection.

Methods: Dengue virus NS1-positive serum samples were pooled into two groups (S2 and S3) based on the molecular serotyping and number of heterotypic infections. The pooled serum samples were subjected to two-dimensional gel electrophoresis (2DGE) to identify the differentially expressed proteins. The peptide masses of upregulated protein were detected by matrix-assisted laser desorption-ionisation time-of-flight MALDI-TOF mass spectrometry and analysed by MASCOT search engine. The results were compared with the control group (S1). The commonly upregulated protein was validated by quantitative ELISA and compared with control as well as single serotypic infected samples.

Results: Based on 2DGE, total thirteen proteins were differentially upregulated in S2 and S3 groups as compared to control. Some of the upregulated proteins were involved in mediating the complement activation of immune response. The apolipoprotein A-1 (APO A-1) was upregulated in S2 and S3 groups. Upon validation, APO A-1 levels were increased in line with the number of heterotypic infection of dengue viruses.

Conclusion: Heterotypic infection of dengue viruses upregulate the serum proteins involved in the complement pathway in the early phase of infection. There was a significant increase in the level of APO A-1 in three different serotypic infections of dengue virus as compared to control. Further, the role of APO-A1 can be explored in elucidating the mechanism of dengue pathogenesis.

Keywords: MALDI; 2DGE; APO A-1; dengue; electroforesis bidimensional; multiple; múltiple; serum; suero; sérum.