

## **Differential Proteome Analyses of Serum from Patients with Hodgkin's Lymphoma According to Epstein-Bar Virus Status**

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Hodgkin's Lymphoma (HL) is a malignant lymphoid tumor with cure rates close to 90%. Such neoplasia has been extensively investigated regarding a causal infection character. The Epstein-Barr Virus (EBV), a lymphotropic herpesvirus, came out as likely etiologic agent. EBV is widespread in about 90% of human population and it is associated with 50% of HL cases. Scientific investigations attempt to clarify the influence of EBV and bystanders through the pathophysiology of HL, notwithstanding, which mechanisms might be involved in pathogenesis of EBV-negative HL remains to be elucidated. With this aim, the present study was carried out to identify the differences in the serum protein from patients with HL and from health individuals according to EBV status using two-dimensional gel electrophoresis analysis and mass spectrometric identification. Proteins with different amount among groups of study were excised for identification. Those proteins were CFB, ITIH4, HP, HPX, A1BG, SERPINA3, plasminogen, alpha-1B glycoprotein, alpha-1 antichymotrypsin, serum fibrinogen beta and gamma chains. Most of them are related to inflammatory response and its pattern among the groups shows remarkable qualitative differences. As far as we know, no proteomic approach yet published has correlated the EBV-positive and EBV-negative forms of HL with respect to their protein pattern. Such comparative results may be disease elucidative and, furthermore, contributive to better understanding of the association of EBV to the HL pathogenesis.

**Key Words:** Epstein-Barr virus, Hodgkin's Lymphoma, Mass Spectrometry, Proteome, Serum.

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