Proteomic Analysis of Murine Plasma Proteome on Schistosoma mansoni Infection

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Plasma proteins are a fine source of information towards understanding disease processes. During schistosomiasis worms regurgitate by-products of their digestion, hence releasing proteins into the bloodstream. Proteomic approaches can contribute to the understanding of how parasites modify or induce alterations in the host plasma proteome. These approaches might also be useful in the search of novel biomarkers. The objective of this project was the comparative compositional analysis of the plasma proteome from control and S. mansoni-infected mice. Plasma samples from non-infected and infected Balb/c mice were collected at 7 weeks post-infection. Protein samples were separated using 1D and 2D SDS PAGE. In parallel, a shotgun spectrometric-based approach was used to assess the compositional analysis and label-free quantification of the investigated samples. The 1D SDS PAGE profile revealed dominance of protein bands in both groups. The 2D profiles revealed spots uniquely present in the infected sample. The compositional analysis performed using shotgun mass spectrometric approach revealed the identification of 359 proteins. Of these, only three plasma constituents (albumin, serotransferrin and pregnancy zone protein) corresponded to 85% of the protein content present in the analyzed proteomes. In all, 95 constituents were differentially expressed, of which 81 were upregulated in infected animals. The latter were mostly related to immune functions such as immunoglobulins, complement factors and acute-phase related proteins. The presence of parasites living in the host bloodstream modify the composition and abundance of plasma constituents. However, the inherent dominance of a few plasma proteins poses a challenge for the identification of lower abundant ones. Further studies are under way for depletion of major serum components and they should potentially increase the repertoire of molecules associated with S. mansoni infection. Financial Support: Fapemig/UFOP.