The use of proteomics for the study of infectious and chronic diseases

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Proteomic analysis have been used in order to study infectious and chronic diseases using a variety of approaches and with different objectives in order to better understand the development of the disease or to find specific biomarkers for diagnosis. In our laboratory Dengue virus infection and cancer are currently under investigation. Dengue virus is a Flavivirus and is transmitted to humans via Aedes aegypti that causes dengue fever. At present 2,5 billion people live in areas of risk. The aim of this work was to identify the presence of proteins and peptides that could be associated with dengue infection. For that, proteins secreted by HepG2 cells (human hepatoma cell lineage) infected or not with Dengue virus type 2 were analyzed using chromatography and mass spectrometry. The data analysis resulted in the identification of 119 proteins from which 25 were exclusively found in infected cells. We also conducted studies on Renal tumors that represent 3% of the adults malignancy in humans and it is one of the most lethal urologic cancer. Renal Cell Carcinomas (RCC) account for 85% of the renal cancer in adults. Our main objective is the identification of the proteins differentially expressed in the urine of patients with RCC, compared to the control group. Pools of proteins from urine of patients with clear cell renal carcinoma and healthy donors have already been analyzed by 2-DE. In the urine pools, 22 differentially expressed proteins have been analyzed by MALDI-TOF. We analyzed proteins that were present in patients, but not in the control group, as well as the ones that were present in the control group and not in the patients group. After validation, these proteins could be used as specific markers of this tumor type, related with the prognostic of the illness, the early diagnosis or in the development of new therapies.

Financial support: Finep-GENOPROT, FAPERJ, Programa de Oncobiologia, CNPq, CAPES