

Identification of Proteins Differentially Express in Patients with Renal Cell Carcinoma by Proteomics Technology

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Renal tumors represent 3% of the adult malignancy and it is one of the most lethal urologic cancers. Renal Cell Carcinomas (RCC) account 85% of the renal cancer. Therefore understanding RCC pathogenesis using proteomic techniques is relevant to create target specific drugs and new methods for early diagnose and/or follow-up of the disease. These techniques have been used to identify proteins or changes in protein pattern. Our objective was to identify proteins differentially expressed in the urine and kidney tumoral tissue of patients with RCC compared to the control group. For that purpose twenty five patients were separated in groups of good and bad prognosis, in accordance with the histological type and Fuhrman degree. Their urine and tissue were collected during the chirurgical procedure to remove the kidney. Proteins from urine (patients and health donors) and tissues (tumoral and surrounding non-cancerous kidney) were extracted and pooled, separated by 2DE and identified by MALDI-TOF-TOF using Mascot Program. 407 and 412 proteins from urines and tissues were identified, respectively, from which 10 and 16 proteins were differentially expressed. For instance, psoriasin showed to be increased in urine of patients and HSP27 was over expressed in the tumor tissue. The validation of these results should provide a helpful resource for the investigation of specific markers for RCC, related to its early diagnosis and prognosis, and/or to the development of new therapies.

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