[794] **UPREGULATION OF PEROXIDEROXIN-6 IN HUMAN RENAL ADENOCARCINOMA CELLS 786-0, AFTER IONIZING RADIATION**

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Introduction: Renal cell carcinoma (RCC) accounts for 3% of human malignancies and approximately 90% of renal malignancies and among urological tumors. RCC is quite resistant to conventional radiotherapy. This technique allows the dose of radiation, in a single fraction, to be precisely applied to the tumor and the tissues adjacent to it, most of the time, are spared. Proteomics has allowed large-scale studies of protein expression in different tissues and body fluids, under different conditions and / or times. Mass spectrometry allows the identification and quantification of thousands of proteins and peptides in a biological fluid or lysed cells, and is analyzed on a platform to identify differences in the expression of proteins associated with cancer cell proliferation and to establish potential biomarkers predictive of the response therapy. The peroxideroxin- 6 (PRDX 6) protein encoded by this gene is a member of the antioxidant protein family. The PRDX family contains six members that function in detoxifying ROS and providing cytoprotection from internal and It may play a role in the regulation of phospholipid turnover as well as in protection against oxidative injury.

Aim: To analyze the expression of PRDX6 in 786-0 cells, after radiation.

Methods: A cell culture of the 786-0 cells was performed and to evaluate the mitotic potential, the clonogenic assay was performed with doses of 2 to 10 Gy irradiated in GammaCell (CTR, IPEN) and incubated for 10 days in normoxia conditions. After 10 days, the colonies of the respective doses were stained with methanol 20% and crystal violet 0,5% and counted, and the multiple comparisons was analized by One-way ANOVA followed by Bonferroni´s test and at the defined dose the cells were irradiated and the cytoplasmic proteins were extracted by the PE kit Subcellular proteome extraction (Merck, USA), dosed by the Lowry method and stored at -20º. For the qualitative analysis of proteins, SDS-PAGE was performed with 50ug of protein and the protein band obtained was digested and analyzed by nanoUPLC tandem nanoESI-MSE mass spectrometry in the LNBio laboratory in Campinas-SP. The generated result was analyzed by MASCOT server for peptides searchs and quantitatively analized by scaffoldTM 4.6 software.

Results: After the clonogenic assay was performed, 8 Gy was defined as the dose for cell irradiation, an average protein yield of 786-0 non-irradiated 2,59± 0,07 mg/mL and 786-0 irradiated with 3,13± 0,67 mg/mL was obtained. Mass spectrometry revealed the presence of the PRDX6 protein with a 95% coverage and a fold-change of 3.1 compared to the non-irradiated group.

Conclusion: The overexpression of PRDX6 after radiation, suggests a potential role for PRDX6 in protection against oxidative stress and a radioresistance to renal cells,

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Palavras-chave: Prdx6; ionizing radiation; 786-0