Expression Changes of STAT3 and Phosphorylated STAT3 in the Clear Cell Renal Cell Carcinoma

Introduction and Objective: Transcription factor STAT3 has an important role in oncogenesis and proliferation of human tumors. STAT3 influences the expression of target genes including those involved in apoptosis, cell cycle regulation, and induction of growth (Bcl-2, cyclin D1). We observed the changes of expression of total STAT3 and phosphorylated STAT3 (pySTAT3) in clear cell renal cell carcinoma (ccRCC) and correlate their expression with prognostic indices of the disease progression.
Material and Methods: Tumor samples and adjacent healthy kidney tissue were obtained after radical nephrectomy from patients with ccRCC. The expression of STAT3 and pySTAT3 were determined by immunoblotting analysis.
Results: STAT3 was detected in all samples, but changes in the expression of STAT3 were not observed. We found a high level of phosphorylation of STAT3 (control $100\pm22.78\%$ and tumor $230.54\pm78.82\%$, $P< 0.05$). Additionally we studied the ratio of total STAT3 and pySTAT3 in regards to TNM classification and Fuhrman's nuclear grading. The ratio was significantly higher in all stages of TNM classification (control 100 ± 22.78; T1-T2 $157.64\pm37.14\%$; T3-T4 $296.81\pm136.96\%$; $P<0.05$) and all grades of Fuhrman's nuclear grading (control 100 ± 22.78; G1-G2 $165.66\pm34.52\%$; G3-G4 $301.90\pm151.31\%$; $P<0.05$) when compared to controls.
Conclusion: In this study we observed the expression of total STAT3 and pySTAT3 in ccRCC. STAT3 could be a new therapeutic target for the treatment of ccRCC.