DIFFERENTIAL EXPRESSION OF INTRONIC NONCODING RNAs IN RENAL CELL CARCINOMA USING QUANTITATIVE RT-PCR

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Noncoding RNAs (ncRNAs) are abundantly transcribed in complex organisms. The potential importance of ncRNAs in gene regulation is suggested by the observation that the complexity of an organism is poorly correlated with its number of protein-coding genes, yet highly correlated with its number of ncRNA genes. We have demonstrated that ncRNAs totally mapping inside of introns of known genes and transcribed in the opposite direction of the protein-coding transcript are correlated to the degree of tumor differentiation in prostate cancer (Reis et al., Oncogene 23: 6684-6692, 2004). We have now extended the study by investigating the levels of intronic ncRNAs in renal cell carcinoma (RCC) compared to non-tumor adjacent renal tissue, using custom-designed 4K-element cDNA microarrays. The present work validates through an independent approach – strand-specific reverse transcriptase assay followed by quantitative real-time PCR – the findings obtained with cDNA microarrays. We have identified 6 intronic transcripts that seem to be strongly correlated to malignancy by microarray analysis ($p<0.0001$). Significant differential expression of 3 of these intronic transcripts was confirmed by strand-specific RT-qPCR in at least 3 different patients using tumor or non-tumor tissues samples. This validation is an important step to identify differentially expressed intronic noncoding RNAs, an innovative and powerful approach in characterizing cancer molecular markers.

Supported by FAPESP and CNPq.