PROFILING INTRONIC NONCODING RNA EXPRESSION IN RENAL CELL CARCINOMA WITH A COMBINED INTRON/EXON 44K OLIGOARRAY

Fachel, A.A.[1], Nakaya, H.I.[1], Campos, F.S.[2], Reis, E.M.[1] and Verjovski-Almeida, S.[1]

[1] Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, SP, Brasil; [2] Instituto Nacional de Cancer, RJ, Brasil.

Noncoding RNAs (ncRNAs) appear to comprise a complex network of signals that control various levels of gene expression in Eukaryotes. Our group has found that 74% of all spliced human genes contain transcriptionally active intronic regions, of which we selected a set to build a 44,000-element combined intron/exon oligoarray platform which was custom-printed. The array was used to investigate a possible correlation between intronic ncRNA expression levels and malignant transformation in Renal Cell Carcinoma (RCC), the most lethal cancer of the urinary system. We compared expression profiles from four pools of adjacent non-tumor kidney tissue versus four pools of tumor kidney tissue prepared from 17 paired RCC patient samples. Expression data was filtered, quantile normalized and submitted to statistical analysis: Significance Analysis of Microarray (FDR = 10%) plus Signal to Noise Ratio with bootstrap ($p = 0.05$). We identified 1677 exonic and 207 intronic differentially expressed messages which perfectly segregate non-tumor from RCC samples. Cross-referencing of intronic and exonic expression signatures identified 58 wholly/partially intronic transcripts potentially involved in the modulation of the corresponding protein-coding exonic transcript. These transcripts are candidate biomarkers for RCC. These findings contribute to advance current knowledge about the involvement of noncoding RNAs in cancer.

Supported by FAPESP and CNPq.