NUCLEAR LOCALIZATION OF INTRONIC *RASSF1* TRANSCRIPTS IN HUMAN TISSUES USING *IN SITU* HYBRIDIZATION

Oliveira, A. C. A., Verjovski-Almeida S., Reis, E. M.

Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo.

A new class of long intronic noncoding RNAs (ncRNAs) transcribed in the human genome with sense and/or antisense orientation relative to the corresponding protein-coding gene was recently identified. These intronic ncRNAs are postulated to be involved in processes related to post-transcriptional control of gene expression in normal and diseased tissues. Among them, intronic antisense transcripts (GenBank accession AY545527 and AY545528) originated in the *RASSF1* locus, a tumor suppressor gene, were shown to have levels correlated to tumor malignancy in prostate cancer. In this work we investigated the expression pattern and sub-cellular localization of *RASSF1* intronic transcripts using RNA *in situ* hybridization. We detected the presence of both sense and antisense intronic *RASSF1* transcripts in histological sections of kidney tumor and non-tumor tissue adjacent to surgically removed prostate tumor. The sense transcript *RASSF1* was more abundant than its corresponding antisense transcript, as previously observed in quantitative PCR experiments performed by our group. Interestingly, intronic *RASSF1* transcripts seem to predominantly localize at the cell nucleus. These results support a mechanism where intronic *RASSF1* transcripts exert their function by acting in *cis* through base-pairing with unprocessed sense *RASSF1* pre-mRNA in the nucleus, thus affecting the levels of Rassf1 protein.

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