# ROLE OF DNA METHYLATION ON THE TRANSCRIPTIONAL CONTROL OF INTRONIC NONCODING RNAs

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Our group has recently characterized a new class of noncoding RNAs (ncRNAs), which are long intronic transcripts expressed both in sense and antisense orientation relative to the corresponding protein-coding mRNA. Expression levels of intronic ncRNAs where shown to correlate with the degree of prostate tumor differentiation, and to the abundance or to the pattern of exon-usage of the corresponding protein-coding transcript. While possible functions of intronic transcripts begin to emerge, the mechanisms governing their biogenesis are largely unknown. DNA methylation is a mechanism of epigenetic control of gene expression that is involved in normal and pathogenic biological processes, such as in cancer. In this work we investigated the role of DNA methylation in the transcriptional control of intronic ncRNAs. Using a spotted cDNA microarray enriched with intronic sequences, we found 37 intronic transcripts differentially expressed ($p$= 0.001) in a prostate cancer cell line (DU-145) treated with a DNA demethylating agent (5-Aza-deoxicytidine) compared to untreated control cells. 11 out of 37 intronic transcripts were upregulated in 5-Aza-deoxicytidine- treated cells and at least 6 of these contain CpG islands in putative 5' promoter regions as determined by bioinformatics analysis (MethPrimer). This result suggests a possible role of DNA methylation in the transcriptional regulation control of intronic noncoding RNAs.

**Supported by** FAPESP and CNPq