

NONCODING INTRONIC RNAS AND THE COMPLEXITY OF GENE EXPRESSION IN EUKARYOTES

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RNAs transcribed from intronic regions of genes are involved in a number of processes related to post-transcriptional control of gene expression. A recent analysis of sequence databases conducted by our group indicates that the majority of human genes (74% of RefSeq) harbour transcriptional units located within introns. Guided by this information, we designed an oligoarray platform containing sense and antisense probes for 7,135 randomly-selected totally intronic transcripts plus the corresponding protein-coding genes. Using this platform we identified exonic and intronic tissue-specific expression signatures for different human tissues (liver, prostate and kidney). A subset of intronic and protein-coding signatures transcribed from the same genomic *loci* has correlated expression patterns, suggesting that intronic RNAs regulate the abundance or the pattern of exon usage in protein-coding messages. Notably, the most highly expressed intronic RNAs were transcribed from introns of protein-coding genes involved in Regulation of transcription. We anticipate that a gene-oriented approach such as described here, using a combined intron-exon oligoarray should permit further comparative analysis of intronic transcription under various physiological and pathological conditions, thus advancing current knowledge about the biological functions of noncoding RNAs in eukaryotes.