TRANSCRIPTION ANALYSIS OF ALTERNATIVELY SPLICED FORMS OF *TLE* GENES

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TLE proteins are transcriptional co-repressors of a wide variety of transcription repressors and play multiple roles in developmental and tumorigenic pathways. By specifically searching the public mRNA and EST databases, we found evidence for all four members of the *TLE* gene family of alternatively spliced mRNAs, with additional exons or retained introns, containing a premature stop codon that could encode a shortened protein. These putative truncated proteins encoded by the alternatively spliced gene isoforms may negatively regulate normal TLE proteins, perhaps by sequestering them into non-productive complexes. Here we present a custom oligoarray platform that was used for detection of these alternatively spliced isoforms in 3 different human tissues, namely normal liver and kidney and prostate tumor. We also identified by orientation-specific RT-PCR an antisense partially intronic non-coding RNA that overlaps a novel exon of the *TLE3* gene, raising the possibility of regulation of alternative splicing by this non-coding transcript. Finally, using quantitative Real-Time RT-PCR, we show that the alternatively spliced isoform of *TLE3* gene is up-regulated in prostate tumors in comparison to normal adjacent tissue of the same patient. These results demonstrate that different isoforms of *TLE* genes are commonly transcribed in human tissues and suggest that they could be involved in cancer development.
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