
Intron-exon structure of the human transforming growth factor- β precursor gene

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Two genomic DNA libraries, one derived from a normal fetal liver (1) and one from the Calu-1 tumor cell line (2), were screened by hybridization to human transforming growth factor- β (TGF- β) cDNA (3) restriction fragments. Restriction fragment mapping of the hybridizing genomic DNA fragments and DNA sequence analysis (4,5) revealed that the coding sequence of the TGF- β precursor gene is divided in seven distinct exons with six introns as shown below. No differences in the sequence or in the gene organization were observed between the gene fragments from both libraries. The exon sequences were in general agreement with the reported human TGF- β precursor cDNA sequence (3). However, the gene encodes a Leu residue at amino acid position 10 of the precursor in contrast to the reported Pro based on cDNA analysis, and an Arg at position 25 instead of the Pro in the cDNA. Also, the derived precursor sequence is 390 amino acids long in contrast to the reported length of 391 amino acids. This is due to the absence in the gene of the Arg at the previously assigned position 159. The differences between the sequences of the gene and the cDNA are likely due to errors in the enzymatic synthesis of the double stranded cDNA and to one mistake in the reading of a cDNA sequencing gel. The genomic sequence should therefore be regarded as the correct one. We have now also established the sequence which precedes by 1140 bp the 5' most residue (asterisk) of the TGF- β precursor cDNA. The putative polyadenylation sequence is indicated with an arrow and is closely followed by a sequence which resembles an Alu-repetitive element. The flanking intron sequences are shown in lowercase letter type. The introns are very large and were therefore not further characterized.

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