

The nucleotide and deduced amino acid sequences of insulin-like growth factor II cDNAs from adult bovine and fetal sheep liver

W.M.Brown, K.M.Dziegielewska, R.C.Foreman and N.R.Saunders
Department of Physiology and Pharmacology, The University of Southampton, Bassett Crescent East, Southampton SO9 3TU, UK

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Using immunological screening a partial insulin-like growth factor II cDNA clone was isolated from an adult bovine liver library in λgt11 (Clontech). The clone (EMBL accession number X53553) encodes most of the B chain, the whole of the C, D and E peptides and the A chain of prepro IGF-II (for nomenclature see 6).

The deduced (partial) amino acid sequence of mature IGF-II (i.e. without signal peptide or the E domain) is in complete agreement with the protein sequence reported in (2) and differs only by one substitution from that reported in (3) – we observe *ile* at position 35, not *ser*.

The bovine clone was used to screen a fetal sheep liver (pooled 40–60 day tissue) cDNA library in λgt10. A full length clone was isolated encoding the whole of prepro IGF-II. The sequence of both clones was determined by the dideoxynucleotide method (5).

The sheep clone (EMBL accession number X53554) is significantly longer than that reported in (4), the 3′-untranslated region (UTR) being some 70 bases longer and 5′-UTR over 200 bases longer and of a different sequence. The coding sequence is, however, identical.

The IGF-II gene has been extensively studied in recent years, and it is now clear that multiple transcripts arise from a single-copy gene, by use of three different promoters (1, 4, 6 and references therein). In the rat, there is a splice site six bases 5′- to the initiation codon, and alternative transcripts arise as a result of 3 different exons being spliced at this point to the first coding exon E4 (1). Our sequence deviates from that in (4) seven bases 5′ to the initiation codon. It, thus, seems likely that a similar splicing mechanism operates in sheep. By comparison with the rat sequences reported in (1), it appears that the 5′-UTR reported here corresponds to rat exon E2.

Both sequences are presented. Numbers to the right refer to nucleotides, to the left to the amino acid sequence of the mature IGF-II, the putative signal peptide having negative numbers. The extent of mature IGF-II is indicated by underlining. The E domain is enclosed by square brackets. The termination codon is indicated by an asterisk (*).

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