Volume 17 Number 6 1989 Nucleic Acids Research

Nucleotide sequence of rat liver glutamate dehydrogenase cDNA

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Submitted February 13, 1989 EMBL accession no. X14044

Using a bacteriophage Lambda vector (Lambda ZAP), a rat liver cDNA library was constructed. From this library cDNAs corresponding to glutamate dehydrogenase mRNAs (GDH; EC 1.4.1.3) were isolated by screening with a human GDH cDNA (1). The most complete cDNA (sequence shown) contains a 5'untranslated region of 60 bp, a protein coding region of 1674 bp, a 3'untranslated region of 1129 bp and a 11 base poly(A) tract. Comparison of this sequence with human liver and fibroblast homologues (2,3,4) shows that the coding regions have the same length (precursor protein of 558 amino acids) and a high sequence homology (91 percent). At the deduced amino acid level, a homology of 97 percent is found. The 3'untranslated regions also show a high sequence homology (71 percent). Within this sequence, five putative polyadenylation recognition sites are present. A cDNA containing a poly(A) tract starting at position 2260, but otherwise identical, was isolated. This indicates in vivo usage of the polyadenylation recognition site at position 2237. Therefore, both mRNAs present in rat liver are probably derived from the same gene.

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   1 GTCCAGGCCTGCAAGCTCTG ATCTTCTGTGCTCCCGCCGC TCTCGCCTCAGCCCGCCGCC ATGTACCGCCGTCTGGGCGA AGTGCTGCTACTGTCCCGCG
 101 CCGGGCCCGCTGCCCTGGGC TCTGCGGCTGCAGACTCAGC CGCACTGCTGGGCTGGGCTC GCGGACAACCCTCTGCTGTC CCGCAACCCGGGCTCACGCC
 201 GGTCGCCAGGCGCCACTACA GCGAAGCGGCCACCGACCGC GAAGACGACCCCAACTTCTT CAAGATGGTGGAGGGCTTCT TCGACCGCGGCGCCAGCATC
 301 GTGGAGGACAAGCTGGTGGA AGACCTGAAGACCCGGGAGA ACGAGGAGCAGAAGCGGAAC CGAGTGCGCGGCATCCTGCG GATCATCAAGCCTTGCAACC
 401 ATGTGTTGAGCCTCTCCTTC CCCATCCGGCGCGACGACGG CTCCTGGGAGGTCATCGAAG GCTACCGGGCCCAGCACAGC CAGCACCGCACGCCCTGCAA
 501 GGGAGGTATCCGGTACAGCA CTGACGTGAGTGTGGATGAG GTGAAGGCGCTGGCGTCCCT AATGACCTACAAGTGTGCAG TGGTTGATGTGCCATTTGGA
 601 GGTGCTAAAGCAGGCGTTAA GATCAATCCCAAGAACTATA CAGATAATGAATTAGAAAAG ATTACACGAAGATTCACCAT GGAGCTGGCAAAGAAGGGTT
 701 TTATTGGTCCTGGCATTGAT GTGCCTGCCCCAGACATGAG CACGGGCGAGCGGGAGATGT CCTGGATCGCTGACACCTAT GCCAGCACCATAGGGCACTA
 801 TGATATCAATGCACACGCCT GTGTCACTGGTAAACCCATC AGCCAAGGAGGCATCCACGG ACGCATCTCCGCTACTGGCC GGGGTGTTTTTCATGGGATT
 901 GAGAACTTCATCAATGAAGC TTCCTACATGAGCATCTTAG GGATGACCCCGGGGCTTGGC GATAAGACGTTTGTTGTTCA GGGATTTGGTAATGTGGGCC
1001 TGCACTCTATGAGATATTTA CATCGTTTTGGTGCTAAGTG TGTTGGTGTTGGAGAATCTG ATGGGAGTATATGGAATCCA GATGGTATTGACCCAAAAGA
1101 ACTGGAAGATTTCAAGTTGC AACATGGATCAATTCTGGGC TTCCCCAAAGCCAAGGTCTA TGAAGGAAGCATCTTGGAGG CTGACTGCGACATTTTAATT
1201 CCTGCAGCCAGCGAGAAGCA GTTGACCAAATCCAATGCAC CCAGAGTCAAAGCCAAGATC ATTGCTGAAGGAGCCAATGG CCCAACCACTCCAGAGGCCG
1301 ATAAGATTTTCCTAGAAAGA AACATCATGGTTATTCCAGA TCTCTACCTGAATGCTGGAG GAGTGACAGTATCTTACTTT GAGTGGCTAAAGAATCTAAA
1401 TCACGTCAGCTATGGCCGAT TGACCTTCAAATATGAAAGG GACTCGAACTACCACTTGCT CATGTCCGTTCAAGAGAGTT TAGAGAGAAAGTTTGGAAAG
1501 CACGGCGGGACTATCCCTGT GGTCCCCACAGCAGAGTTCC AGGACAGAATATCGGGTGCA TCTGAGAAAGACATCGTGCA CTCTGGCTTGGCCTACACAA
1601 TGGAGCGATCTGCCAGGCAA ATTATGCGCACAGCCATGAA GTATAACCTGGGATTGGACC TGAGAACAGCTGCCTACGTC AATGCCATTGAGAAAGTCTT
1701 CAAGGTGTACAATGAGGCTG GCGTGACCTTCACATAGACA GGTCACAGCTGACTTCTTTA CCACCCTCTTCACCTATAAT TTCTGCAGACCTGTCACAAG
1801 TTTACATGTAACCACAGAAA TCTGTTCTTGTGACTCATTA GTTAATGGACACTGTTCTCA ACAAGTCAGTTGGAATCAGC CCCTTAAGAGAAAGATTAAG
1901 TTAGCGGATCATGTACCAGC TGATGGTGTAAAGGTAGGAA TCACGTGTATCCTGCCAGTT AGGTGTTTCGCTTTTAAGTA AAGTTTCTGCTCCTGGCCAT
2001 GCTGCCTTGCTCTGGACTCT TCCCAACAGGGTTAGTGCTG TTGCCAGGGAAGGCAGTCAA GAGTCAGTCACTTCCTGACA AGTCTGGGTACTTGAGCACA
2101 TAAGAAGTAGGCGTGTGGCA TTTGCAAAGGTGGCATGGTC TTCGAGTGAGTTATTGCTGC TTTACATCAGCAAAATAACT CAGTCTCTAAGTCGCAAACA
2201 AATAAAAGCTATTTCTCATG TATTTTATTCTTTCAGAATA AACCAGTTCATGCTGCTGTA ATAAAATTGCCTTCAACCAC TTAAGCCTAACCTTTACTCA
2301 AGCAGTGAACGCCTAAAATA TAGGAAATGGAAGAAGCTAG TTTTTATAACATAAAACAGT ATAATTTAGCTTATCGGCCC TGCAGCATAGTCCAGCAGAA
2401 ATAAAGTAGCACCTGGGGGC AGGCGTACCTGCAAGTGACA CGGGAGGGACACTTGGGAAC TTGTTATGCAGTCCAGAGAG TGAAGTAACCACTTTACCAA
2501 TTTGGAGATCTATTATGTTG AGTAATTGAACCATACTTCA AATAGAGTGTCCCAGAAGAA AAGACTGGCTCCCTGTTTGG AGGCTGGCAGACTTCAGACT
2601 CAGCCTGTGTGTCCCTTCTC CAAGGCTTTGCCGTCTACAC AGCACCTCGCTATCCACAGG CTGGAGACTGCCTGGGGTTG ACTTCTGTTTGGGGAGTTAC
2701 TGGCCAGGGCTTTTGAACAG GAGTGTTCCACAGAAGTACC AGACATTATTTATATAAGAA TGAGCGCTTCTTTTTAACAG TACCCTTTCAGAAATTTCTA
2801 ACTACTTTGTAACTGCATGA TTAACTTGGTGATAAAAGCA GTTATTAAAAGTCTACCTTT TCCAAAAAAAAAAA
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Acknowledgements: We would like to thank Dr C.Banner and Dr J.L.Mandel for making their GDH (c)DNAs available to us (1,5).

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