

A glutamate dehydrogenase gene sequence

J. Mark Cock⁺ and Robert R. Schmidt*

Department of Microbiology and Cell Science, University of Florida, Gainesville, FL 32611, USA

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A *Chlorella sorokiniana* genomic DNA library was screened with a NADP-specific glutamate dehydrogenase (GDH) cDNA. Two putative GDH sequences were isolated. One sequence is typically eukaryotic in that its coding region is interrupted by many introns (1). Southern blots showed that *C. sorokiniana* DNA contains the eukaryotic GDH gene but the second sequence could not be detected. The second sequence has characteristics of a prokaryotic GDH gene. The gene was expressed in *E. coli* CLR207recA (*gdhA*; 2) from a multicopy plasmid, giving GDH activity 54-fold higher than basal level in untransformed cells. The cloned gene is not positioned near a plasmid promoter, suggesting expression occurred from its own promoter. The proposed coding region is highly homologous to other cloned bacterial GDH genes, i.e., 81% identical (amino acid level) to the *E. coli* *gdhA* gene (3,4) but only 51% identical to the *Neurospora crassa* *am* gene (5). Codon usage (6) and the promoter sequences are those typical of a highly expressed bacterial gene (7). Nucleotides underlined in the sequence correspond, from 5' to 3', to putative -35 and -10 boxes, a consensus Shine-Dalgarno sequence, and initiation/termination codons, respectively. The positions of initiation/termination codons correspond exactly with those of the *E. coli* *gdhA* gene. Both strands were sequenced completely by the method of Sanger *et al.* (8).

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GGCCATCCGCGCAGCCCGCGAAGCTCGCTGAGGGGCACTGGAGCATCGGTACGCCTCGCCAAAACCGGCGCGAATCCCTGGGAATACCTGACCGACGACGGC
CATACGCAACCGCTCGAAGTGAACCGAGCCGGGTGGTGAACACGCGCAAGAGCTATATCGCCTGCTGCCGCGCGGGCTGGGGCTGATGCAAAATCCCGGCTACGA
CGTGCACACCTCGTACGACCGCGGTGAGTGGTGAAGTCTGCGCCGTTACCGCGCCGCTCCATGCGGATCGCCCTGATCATCCCATCGCCGCGAGCGATCGCG
CCGCTGGCGGTTTCATGAGTGGTTGAAGGCTGCTGCGAGCCGATCTGGAGCGCTGATTGCACATTTAGCGCTATACTTTGTAATAACGCTTAATAATCAAG
CGGTGACAGCGTTAAAGCCCGATAACCCATAGGCTTTTACGCCGCGCGGGGTACAAACGAAAAGATATCGGCGCGGAGAGATTTTCGATGCGCGCGAGTGTGATCGCCC
CAACATATCATTGCGTTATCCGAATGACTACTGGAACCAAAAGGCCAGGCGGGTAAACGGAACGCTGCTCAACCTTTTAAATCGGCATGTTTGAAGAGGAT
TCTTATGGCTTCAAAACACATACTGATCCGCGTGGACCTATCCCGGAAAGCAAGATCTGGTAGAAAAGCGCTCGATGCGCGGCGGACGACGCTAAAGTTTC
TCTGATCCAGCTCGATGACATACCGACCTACTACTGCGCTGATCGAGCTCAATCTGGCGACATGCAAAAACGCTCTCTGAGGAAACCCATCAGGCGCTGAT
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TCGAGGCCAACCGGCTATCGCGAACAGCGCGCTGTTGAGCGCTGTTGGAGCGGCGGAGCGTATCATTCAAGTTCCGCGTCAAGTGGGTGGACGATCGCGGCCAGGTG
AGGTCATTCGCGCTTCCGCGTGCAGTCAACTGCGCCATCGGCCCTATAAGGGCGGCAATGCGCTCCACCCATCGGTAACACTCGATCTCGAAGTTCCTCGGCT
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GCCAGGCGCTGATACCGAGCTGTACCCGCTATGGGCGGCAACCGAGCTGCGCGGCGGACATCGGCGAGCGGCGGCTGGAAGTCCGCTTTATGGCCGGCATGA
TGAAGAACTGTCCAACACCCGCTGCGTATTACCGGCAAAAGGCTCTCTCTGCGGCGGACGCTGATCCGCGGAGGCGACCGCTACGCGCTGTGTACTTTA
CCGACGCCATGCTGCAGCGCAACGCGCTGGGCTTTGAGGGCATCGGGTGGCGGTGTCGCGCTCCGGCAAGCTGGCGGATACACCATGAAAAGGCGCTGGAGCTGG
ACGCGCGGCTGATCCGCTATCGGATCCGCGGCGCACCTGGTGGAGCAAGAGCGGCTTCACTACCGAGAAGCTGGCACACCTGGCGGAGATCAAAAACAGCGTTACG
GCGGGTGGCGGACTACGCGCGCAACCGCGCTGACCTATCTGGCGGCGGACGCGGCTGGAACGTGCGGTTGATATCGCCCTCCGCTGCGCCACCCAGAACGCAAC
TGGATCTCGAGCGGCGGAGTGTCCGCAACGGGGTGAAGGCGGTTGCGGGAAGGCGCAACATCGCGGACCCATCCAGGCGCACCGCGCTTCTCGACCGCGGG
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TACGTTTCAACATATATGCGGATATTCACCATGCTGCGTGGAAATACGCGGCTGAGGCAAGCAACCCACTATGTACACGCGCGCAATATCGCCGGTTTCGTCA
AGTTCGCGGAGCGCATGTGCGCCCAAGCGTCTGTAATCCGCTCGTAAAGTGTATCTTGT

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*To whom correspondence should be addressed

⁺Present address: Department of Biological Sciences, University of Warwick, Coventry CV4 7AL, UK

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