Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dismutase

Ye-Shih Ho and James D. Crapo

Laboratory of Molecular Biology, Division of Allergy, Critical Care and Respiratory Medicine, Department of Medicine, Duke University Medical Center, Durham, NC 27710, USA

Submitted July 30, 1987

Accession no. Y00497

cDNA clones coding for rat manganese-containing superoxide dismutase (Mn SOD) have been isolated from a Sprague-Dawley rat liver cDNA library constructed in vector λ gt11 (Clontech Laboratories, Inc., Palo Alto, CA) by cross hybridization with human cDNA (sequences shown in Figure 1) (1). The nucleotide sequence of a truncated clone is identical between residues 188 and 994 of the full-length cDNA clone except for a C to G substitution at residue 512 leading to substitution of histidine by glutamine at amino acid residue 143. The nucleotide sequences of the 3' noncoding region after residue 994 of these two cDNA clones are different. From comparing the deduced amino acid sequence and the known amino-terminal of mature human Mn SOD, the first 24 amino acids of the primarily translated precursor may constitute the leader peptide for transport to the mitochondria (2). Amino acid sequences of the rat and human Mn SODs are 89% homologous with the leader peptides and mature proteins 50% and 93% homologous, respectively (1).

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      ~20          ~10          1
G CGCCTACGCA Met Leu Cys Arg Ala Ala Cys Ser Ala Gly Arg Arg Leu Gly Pro Ala Ala Ser Thr Ala Gly Ser Arg His Lys His 89
      ATG TTG TGT CGG GCG GCG GCG TGC AGC GCG AGA AGA CTG GGC CCC GCG GCC AGT ACC GCG GCG TCC CGG CAC AAG CAC
      10          20          30
Ser Leu Pro Asp Leu Pro Tyr Asp Tyr Gly Ala Leu Glu Pro His Ile Asn Ala Gln Ile Met Gln Leu His His Ser Lys His His Ala 179
      AGC CTC CCT GAC CTG CCT TAC GAC TAT GGC GCG CTG GAG CDG CAC ATT AAC GCG CAG ATC ATG CAG CTG CAC CAC AGC AAG CAC CAC GCG
      40          50          60
Thr Tyr Val Asn Asn Leu Asn Val Thr Glu Glu Lys Tyr His Glu Ala Leu Ala Lys Gly Asp Val Thr Thr Gln Val Ala Leu Gln Pro 269
      ACC TAC GTG AAC AAT CTG AAC GTC ACC GAG GAG AAG TAC CAC GAG GCG CTG GCC AAG GGA GAT GTT ACA ACT CAG GTT GCT CTT CAG CCT
      70          80          90
Ala Leu Lys Phe Asn Gly Gly Gly His Ile Asn His Ser Ile Phe Trp Thr Asn Leu Ser Pro Lys Gly Gly Gly Glu Pro Lys Gly Glu 359
      GCA CTG AAG TTC AAT GGC GGG GGC CAT ATC AAT CAC AGC ATT TTC TGG ACA AAC CTG AGC CCT AAG GGT GGT GGA GAA CCC AAA GGA GAG
      100          110          120
Leu Leu Glu Ala Ile Lys Arg Asp Phe Gly Ser Phe Glu Lys Phe Lys Glu Lys Thr Ala Val Ser Val Gly Val Gln Gly Ser Gly 449
      TTG CTG GAG GCT ATC AAG CGT GAC TTT GGG TCT TTT GAG AAG TTT AAG GAG AAA CTG ACA GCT GTG TCT GTG GGA GTC CAA GGT TCA GGC
      130          140          150
Trp Gly Trp Leu Gly Phe Asn Lys Glu Gln Gly Arg Leu Gln Ile Ala Ala Cys Ser Asn His Asp Pro Leu Gln Gly Thr Thr Gly Leu 539
      TGG GGC TGG CTT GGC TTC AAT AAG GAG CAA GGT GCG TTA CAG ATT GCC GCC TGT TCT AAT CAC GAC CCA CTG CAA GGA ACC ACA GGC CTT
      160          170          180
Ile Pro Leu Leu Gly Ile Asp Val Trp Glu His Ala Tyr Tyr Leu Gln Tyr Lys Asn Val Arg Pro Asp Tyr Leu Lys Ala Ile Trp Asn 629
      ATT CCA CTG CTG GGG ATT GAT GTG TGG GAG CAC GCT TAC TAT CTT CAG TAT AAA AAC GTC ACA GCT GAT TAT CTG AAA GCC ATT TGG AAT
      190          200          210
Val Ile Asn Trp Glu Asn Val Ser Gln Arg Tyr Ile Val Cys Lys Lys
      GTA ATC AAC TGG GAG AAT GTT AGC CAA AGA TAC ATA GTT TGC AAG AAG TGA AGCCCTCCG CCAGGCTGTG TGTCAGGCC GTGGTGGGTG TTTTGTG 727
      220          230          240
GTA GTGTAGAGCA TTGAGCACT GTGCTGAGC TGTTGTAATC TTCAATGATG CCTATGACCA TATGTGTAAG CATACAGITTA TGATAATTC TTAATTAAT GTATT 835
      250          260          270
GTTAG GCAACTGTTT GAGAAGCA TACACTTGGT GTGAGCTGCT CTTGATTGAA CATTTCATT ABAGGCTTGA ATTGCTTGGG GCGTGTCACT GTCACTATAA GGC 943
      280          290          300
CATCAAA GATATTCATT CTCTGTGTTG GGGCTGTGG GAGGCTGTA ATCCTGTCT ACTGCAGITTA GGAAGGAGGAG GAGTTACCC CCCCCCGAG AATTGTTGAA T 1051
      310          320          330
AATAAATA GAGAAGTAA TAGTCTCTT TTGTGTAA AATTGCTATT TTTCATAAGT AATCCTTTGT TTAGCGGATA TCACCTAGTG GTCTTTATT ATGGCCAG 1160
      340          350          360
TTCACTTG ACTCGTACA CACTGATGCT CTCACTTTCA TGAGCTTTTG TTGTCGACA TACGGGGCT GTGAGTACA TACCACTTA TTTCATATT C
      370          380          390
TTTCAAGAA ACATCATTTT TTCACTTGA ACGTGTAACT AGGCTAAGGA TGGATGAGT GTTAGAGCTT TTGCTGTCT TATGTGAGGC CTTGGGCTCT ACCTCACTA 1269
      400          410          420
C TGAACAATC AACAGACCCA AGCTAGGCTC CTGACTGACA ACTGTTAATT CAGAGAGGAG TGACATTGTG CCTCTGGGT TTTTATAGG CTGAGATGCA AAAACTG 1377
      430          440          450
TTA CCTGTCTAT TAAACCCAG TGTGATTGT ATGAAGTGC TCAAGATGA CAAAGTAT 1438

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Figure 1. Nucleotide and deduced amino acid sequences of rat manganese-containing superoxide dismutase cDNAs. Variations in the nucleotide and deduced amino acid sequences of a truncated cDNA clone are indicated in italics below the sequences of the full-length cDNA clone.

ACKNOWLEDGEMENT: This research was supported by grants from NIH (HL39585) and RJR Nabisco, Inc.

REFERENCES: (1) Ho, Y.S. and Crapo, J.D. Manuscript in preparation. (2) Barra, D., et al. (1984) *J. Biol. Chem.* **259**, 12595-12601.