

Nucleotide sequence of the apocytochrome B gene in white sturgeon mitochondrial DNA

James R. Brown, Teresa L. Gilbert¹, David J. Kowbel, Patrick J. O'Hara¹, Norman E. Buroker², Andrew T. Beckenbach and Michael J. Smith

Institute of Molecular Biology and Biochemistry, Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia V5A 1S6, Canada

Submitted April 18, 1989

EMBL accession no. X14944

The apocytochrome B gene (below) of white sturgeon (*Acipenser transmontanus*) mitochondrial DNA and some flanking sequences were subcloned into M13MP18/MP19 or puc19 (1, Buroker et al. in preparation). Nucleotide sequence was determined using the dideoxy nucleotide chain termination method (2). In this primitive vertebrate, the arrangement and transcriptional polarity of the D-loop region and the genes tRNA(Pro), tRNA(Thr), apocytochrome B and tRNA(Glu) are consistent with that observed in higher vertebrates including *Xenopus laevis* (3,4,5). Sturgeon and *X. laevis* apocytochrome B genes have nucleotide and amino acid identities of 73.0 % and 79.2 %, respectively.

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M A N I R K T H P L L K I I N G A F I D L P T P S N I S V W W N F
ATGGCAAACATCCGAAAAACACACCCACTCTAAATATTAATGGAGCATTATTGATCTCCCCACACCCCTCCAACATCCCGTGATGAAATTTTG 100
G S L L G L C L I T Q I L T G L F L A M H Y T A D I S T A F S S V A
GCTCACCTCTGGGCCTCTGCCTTATCACACAAATCCTAACAGGATTATTTCTTGCAATACACTACACAGCTGACATTTCAACAGCCTCTCCTCTGTCGC 200
H I C R D V N Y G W L I R N I H A N G A S F F F I C L Y L H V A R
CCACATCTCCGAGATGTGAATTCAGGATGACTAATTCGAAACATTCATGCAACGGGGCCTTTCTTCTCATCTGCTGTATCTTCACGTTGGCAGCA 300
G M Y Y G S Y L Q K E T W N I G V I L L L L T M H T A F V G Y V L
GGTATATACTACGGCTCATACCTCCAAAAAGAAACCTGAAACATCGGAGTAATCCTCTTGCTTCTCACCATAATAACCGCCTTCGTAGGATATGACTGC 400
P W G Q M S F W G A T V I T N L L S A F P D I G D T L V Q W I W G G
CCTGAGGACAAATGTCAATTTGAGGGCAACCGTATCATCAACCTCCTCCGCTTCCCGGACATCGCGGACACACTAGTTCAATGAATCTGAGGCG 500
F S V D N A T L T R F F A F H F L L P F V I A G A S H I H L L F L
CTTTTCAGTAGACAATGCCACCTTACCCGATTCTTCGGCTTCCACTTTCTCCTACCATTGTAATCGCCGGAGCTAGCATAATCCACCTCTTATTCCTA 600
H Q T G S S N P T G L N S D A D K V T F H P Y F S Y K D L F G F T
CACCAAACCGAATCAAAACACCAAGGACTGACTCAGACCGGACAAAGTAACATTCACCCATATTTCTCATCAAAAGACCTCTTCGGATTTCCTT 700
L M L V G L T S V A L F S P H L L G D P D N F T P A N P L V T P P H
TAATGCTAGTCGGACTCACCTCTGTGGCACTATTTCCCCCAACCTCCTGGGTGACCCAGACAACCTTTACACCAGCAACCCCTTGTACACACCCCA 800
J K P E W Y F L F A Y A I L R S I P N K L G G V L A L L F S I L V
CATCAAACCGAATGATCTTTCTTTCCTAGCCCTATCTCCGATCCATCCCAACAACTGGGGGAGTACAGCCCTTCTATTTCCATTTAGTC 900
L M L V P H L H T S K Q R G N T F R P L S Q I L F W A L V A D H L
CTAATATTAGTACCAACTACTCCACCTCTAAACAACGAGGAAACACATTCCGACCCCTCTCTCAAATCCTATTCTGGGCCCTAGTAGCCGACATACTAG 1000
V L T W I G G Q P V E H P F V L I G Q V A S T V Y F A L F L I A L P
TACTCACATGAATGGAGGCCAACCGTCAACACCCATTCTGCTTAATCGGACAAGTAGCCCTCCACAGCTTAATTTTCGCCCTATTTCTAATCGCCCTCCC 1100
L T G W L E N K A L N W H
CCTGACCGGCTGACTAGAAAATAAAGCCTTAAACTGAAAC 1140

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Acknowledgements

This work was supported by NSERC, B.C. GREAT Award and SFU Special Research Grant to ATB and MJS.

¹ZymoGenetics Inc., 4225 Roosevelt Way NE, Seattle, WA 98105 and ²School of Medicine, Department of Pediatrics, RD-20, University of Washington, Seattle, WA 98195, USA

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