Volume 17 Number 13 1989 Nucleic Acids Research

Nucleotide sequence of a cDNA encoding a third distinct *Xenopus* immunoglobulin heavy chain isotype

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Submitted June 2, 1989 EMBL accession no. X15114

The nucleotide sequence of a Xenopus laevis immunoglobulin heavy chain cDNA is presented. The clone was isolated from a non-mitogen stimulated spleen cDNA library using a mixed 33mer J_H oligonucleotide probe (1). The inferred amino acid sequence of the constant region (C_H) is consistent with four domains (exons), as has been reported for Xenopus IgM and IgX (2,3). Conserved cysteine (C) and tryptophan (W) residues are underlined; the two potential N-glycosylation sites are circled. The immunoglobulin cDNA reported here is probably representative of the IgY isotype (4), since avian IgY (5) also possesses four C_H domains, exhibits a paucity of potential N-glycosylation sites and terminates with the dipeptide, G-K (glycine-lysine). The V_H segment is a member of a hitherto undescribed V_H subgroup.

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   Leader                                  ┌──V_H──→
1  TTTGTGCTCTCATTTCTCTCCGAAGTCAAATCTGATATTGAGCTTGTTCAGCCAAGTTCAGAAATCAAATCACCCGGTGAGAGTATTAAACTG
     F  V  L  S  F  L  S  E  V  K  S  D  I  E  L  V  Q  P  S  S  E  I  K  S  P  G  E  S  I  K  L

94 TCCTGCAAGACATCAGGTTACACATTCACCAACTACTGGATACACTGGATACAGCAGGTTCCTGGGAAAGGATTGCAATGGATAGGCAGAATA
     S  C  K  T  S  G  Y  T  F  T  N  Y  W  I  H  W  I  Q  Q  V  P  G  K  G  L  Q  W  I  G  R  I

187 TATCCTGGAGATGCAGATACAGACTACTCATCCTCATACCAAGGAAGGTGCCACATTAGCACTGATAATCCACAAAGCACAACATTCCTGCAA
     Y  P  G  D  A  D  T  D  Y  S  S  S  Y  Q  G  R  C  H  I  S  T  D  N  P  Q  S  T  T  F  L  Q

                                        ┌──D_H──→          ┌──J_H──→
280 CTGAACAATCTAAAAGTGGAGGACACTGCCATTTATTACTGTGCTAGAGAAGGGAGTGGGAGTCTACTTTGACTACTGGGGACAAGGGACCATG
     L  N  N  L  K  V  E  D  T  A  I  Y  Y  C  A  R  E  G  V  G  V  Y  F  D  Y  W  G  Q  G  T  M

                  ┌──C_H──→
373 GTCACCGTCACTTCAGCAACCCTGCATGCTCCATCAGTGTTTCCCTTGAGGCCCTGCTGTGGATCTTCGAGCTCCGACTCTCACGTCACCATT
     V  T  V  T  S  A  T  L  H  A  P  S  V  F  P  L  R  P  C  C  G  S  S  S  S  D  S  H  V  T  I

466 GGTTGTTTGTCTACTGGATTCCTTCCTGCACCAGTAGATGTCAAATGGAACTCAGGAAGCATAACAAGTGGATTAAAGAACTTTCCAGCTGTT
     G  C  L  S  T  G  F  L  P  A  P  V  D  V  K  W  N  S  G  S  I  T  S  G  L  K  N  F  P  A  V

559 CTGCAGCAAAGTGGCCTCTTTGCATCCAGCAGCCAACTCACCATCCCTCTGTCTGACTGGAAGGCCAAAAAATCCTTTGAGTGTAATGTGCAA
     L  Q  Q  S  G  L  F  A  S  S  S  Q  L  T  I  P  L  S  D  W  K  A  K  K  S  F  E  C  N  V  E

652 CACAAACCAACCAGTACCAAAGTCACTCAAAAGATAGAATGCCAAGATGAACCTGAACCAATTGAACCAACTGTGGAGATTTTGCAAGGACCT
     H  K  P  T  S  T  K  V  T  Q  K  I  E  C  Q  D  E  P  E  P  I  E  P  T  V  E  I  L  Q  G  P

745 TGTGCTTCTTCTAAATCAGTTGAATTGCTCTGTCTTATCACTGGATATGCTCCCTCAGAAATCAAAGTGCACTGGCTGCTCAATGGCCAGGTC
     C  A  S  S  K  S  V  E  L  L  C  L  I  T  G  Y  A  P  S  E  I  K  V  H  W  L  L  N  G  Q  V

838 ACAAATATTTCTCCGTCCAACAGCAAACCCTGTAAGGAAGAGAATGGGACATTTTCCTCCAGAAGTAAAGTGTCTGTTCCAAAGGAAGACTGG
     T  (N  I  S) P  S  N  S  K  P  C  K  E  E  (N  C  T) F  S  S  R  S  K  V  S  V  P  K  E  D  W

931 AATTCCGAAGATTCCTACACTTGCAAGGTCACCCACCCTGCTTCCCACACTAAGACTGAAGCCAGCACCAAAAAATGTGATGAAACAGCCATA
     N  S  E  D  S  Y  T  C  K  V  T  H  P  A  S  H  T  K  T  E  A  S  T  K  K  C  D  E  T  A  I

1024 ACTCCAAAGGTAGATGTTCTTCCTCCATCTCCCAAAGATCTGCTTGTTACCAAAGAAGCCAAAGTGTACTGTGTGATCTCCAGGATGGCAAGT
     T  P  K  V  D  V  L  P  P  S  P  K  D  L  L  V  T  K  E  A  K  V  Y  C  V  I  S  R  M  A  S

1117 ACAGACGACTTAACTGTGCAATGGTCACGTAGTGATGGCAAGAAAGCCCTTGCATTTGATTCAGCCCCGGAAAAAGCATATGATGGAACATTC
     T  D  D  L  T  V  Q  W  S  R  S  D  G  K  K  A  L  A  F  D  S  A  P  E  K  A  Y  D  G  T  F

1210 ACTGTAAAAAGCACTTTGAAAATAAGTCCTGGGGACTGGGAAAACAAAAAACAATTTAACTGCAAAGTTGTACACCCTGATCTTCCATCACCA
     T  V  K  S  T  L  K  I  S  P  G  D  W  E  N  K  K  Q  F  N  C  K  V  V  H  P  D  L  P  S  P

1303 ATAGAAAAGTCAATACAAAAAAGTCAAGATCCAGGAACAGAACCAACAATCACCTTGCTGCCACCTTCAGATGATGAACTTAGAAATGATTTT
     I  E  K  S  I  Q  K  S  Q  D  P  G  T  E  P  T  I  T  L  L  P  P  S  D  D  E  L  R  N  D  F

1396 ATAAGTCTTATCTGCATGCTGAAAAACTTCAGACCCCAAGATATCTATGTATTTTGGAAAAAAGATGGTGTTACTCTAGAGGAAGACTACTAC
     I  S  L  I  C  M  L  K  N  F  R  P  Q  D  I  Y  V  F  W  K  K  D  G  V  T  L  E  E  D  Y  Y

1489 ATGACTACTACTCCTGTTTTGGAAGAAGAAGAAGAGGGTTTCATCTCATTTAGTAAACTCACCATCGCTAGATCAGACTGGATGAGAGGAGCT
     M  T  T  T  P  V  L  E  E  E  E  E  G  F  I  S  F  S  K  L  T  I  A  R  S  D  W  M  R  G  A

1582 ACTTATAGCTGCATTGCTGCACACAACACGATCAGTCAGAGAGACATCAAGAAAAATAGGGGTAAATGAGTCTTGAATTCTGTGTTCGTAATT
     T  Y  S  C  I  A  A  H  N  T  I  S  Q  R  D  I  K  K  N  R  G  K  .
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Acknowledgments M. Shamblott and R. Litman for technical help. Supported by NIH GM38656. CTA is supported by a Sloan Fellowship for molecular studies of evolution.

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