Developmental Biology. In the article "A thyroid hormone-regulated gene in *Xenopus laevis* encodes a type III iodothyronine 5-deiodinase" by Donald L. St. Germain, Robert A. Schwartzman, Walburga Croteau, Akira Kanamori, Zhou Wang, Donald D. Brown, and Valerie Anne Galton, which appeared in number 16, August 2, 1994, of *Proc. Natl. Acad. Sci.* USA (**91**, 7767–7771), the authors request that the following correction be noted. The cDNA sequence and deduced amino acid sequence of XL-15 reported in Fig. 1 is incorrect. The correct cDNA sequence, shown below in a corrected Fig. 1, has an additional deoxycytidylic acid nucleotide after position 162. The open reading frame of the XL-15 cDNA is thus extended in the 5′ direction by 207 nt and encodes a protein with a predicted size of 271 amino acids and a molecular mass of 30 kDa. Included in the open reading frame is the in-frame TGA triplet, noted previously, which encodes selenocysteine. As shown in the corrected Fig. 1, homology between the XL-15 and G21 cDNAs and proteins is found only in the central and 3′ regions of the open reading frame. The XL-15 cDNA sequence has been corrected in the GenBank data base (accession no. L28111).

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   1  CGGAGGGGGTGAGGGCTGAGCACCATGTTGCACTGCGCGGGACCCCACACCGGTAAACTT
                                M  L  H  C  A  G  P  H  T  G  K  L
  61  GTGAAACAGGTGGCCGCCTGCTGCCTGCTGCTGCCCCGCTTCCTGCTCACGGGGCTGATG
      V  K  Q  V  A  A  C  C  L  L  L  P  R  F  L  L  T  G  L  M
 121  CTGTGGCTGCTGGATTTCCAGTGTATCAGGAGGAGGGTCCTGCTGACCGCCAGGGAGGAG
      L  W  L  L  D  F  Q  C  I  R  R  R  V  L  L  T  A  R  E  E
 181  AGCACCGCCGAGCACGAAGACCCCCCGCTGTGCGTGTCCGACTCCAACCGAATGTGCACC
      S  T  A  E  H  E  D  P  P  L  C  V  S  D  S  N  R  M  C  T
 241  GTGGAGTCGCTGCGAGCCGTGTGGCACGGGCAGAAGCTGGACTACTTCAAGTCGGCGCAC
      V  E  S  L  R  A  V  W  H  G  Q  K  L  D  Y  F  K  S  A  H
 301  CTGGGCTGCTCGGCGCCCAACACGGAGGTGGTGATGCTGGAAGGGCGCAGGCTGTGCAAG
      L  G  C  S  A  P  N  T  E  V  V  M  L  E  G  R  R  L  C  K
 361  ATCCTGGACTTCTCCCAGGGCAAGAGACCGCTGGTTGTCAATTTCGGCAGCTGCACCTGA
      I  L  D  F  S  Q  G  K  R  P  L  V  V  N  F  G  S  C  T  SC
 421  CCCCCGTTCATGGCTCGCCTGCAAGCCTATCGCCGCCTGGCAGCCCAGCACGTTGGCATC
      P  P  F  M  A  R  L  Q  A  Y  R  R  L  A  A  Q  H  V  G  I
 481  GCGGATTTCCTGCTGGTGTACATAGAAGAAGCGCACCCGTCAGACGGCTGGCTCAGCACC
      A  D  F  L  L  V  Y  I  E  E  A  H  P  S  D  G  W  L  S  T
 541  GACGCCTCCTACCAAATCCCCCAGCACCAGTGCCTGCAGGACCGCCTGGCCGCGGCTCAG
      D  A  S  Y  Q  I  P  Q  H  Q  C  L  Q  D  R  L  A  A  A  Q
 601  CTCATGCTCCAAGGGGCGCCCGGCTGCCGGGTGGTGGTGGACACCATGGACAACTCCTCC
      L  M  L  Q  G  A  P  G  C  R  V  V  V  D  T  M  D  N  S  S
 661  AACGCCGCCTACGGTGCCTACTTTGAGAGACTTTACATCGTCCTGGAGGGCAAAGTGGTG
      N  A  A  Y  G  A  Y  F  E  R  L  Y  I  V  L  E  G  K  V  V
 721  TACCAGGGGGGTCGGGGGCCGGAGGGCTACAAGATCTCTGAACTGAGGATGTGGCTGGAG
      Y  Q  G  G  R  G  P  E  G  Y  K  I  S  E  L  R  M  W  L  E
 781  CAGTACCAGCAGGGCTTGATGGGGACCAAGGGCAGCGGCCAAGTGGTCATTCAAGTGTAA
      Q  Y  Q  Q  G  L  M  G  T  K  G  S  G  Q  V  V  I  Q  V  *
 841  TTGTCATCAGCAGCAGCAGCACCAAGGCAACGGGACACAATAACCACCACCAGCAGCAGC
 901  AGCAGTATTATTACTATTGTTATTATTATTGTCATTATTATAGAGGCAGGTGGAACCTGT
 961  TAGGTGAAGTGACTGAAAGTACACAAAAAGTGCGACCAAACGACTCCTTTCTTTAAATCC
1021  CAGTGCGACAAATAGTAGTAAACTGCAACAAGGGAAAGGCATCCCATCTGCGCACCTCGG
1081  GCTCAATCGCAACTTCCAACACGTCCAGTCCCCCCGACTCATCAGGGAGTTGCCATTGAA
1141  CAAATGCCGGAGGGTCGCGGTTCAGATGTCATTGCGAGAATAATAAGCTACAGTGGCTGT
1201  CTGTCTGTCCCCAGCTGTGTGTGCGACTAAGCCGCTGTGTGAAGTGGGGCGGGAGTACAA
1261  GGTGCGTGTGACTGGAGCCACCCACTCCGACTCTGCAGGTGTTTGCAAATGACGACCGAT
1321  TTTGAAATGGTCTCACGGCCAAAAACTCGTGTCCGACATCAACCCCCTTCCTCAAACTAC
1381  CTGCAGGCTCCGGTGTCGGGCTCCTCCAGTCCAGTAGATTTATTTATGTGATTTTTGTAA
1441  GCAGACTTTTATATAAAGGATTTTTTACGATTAAAAACATGACCACATAAAAAAAAAAAA
1501  AAAAAAAAAAA
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FIG. 1. Nucleotide and deduced amino acid sequence of the XL-15 cDNA. Underlined nucleotide sequences in the open reading frame represent five regions with significant homology to the rat G21 5′DI cDNA (7). Underlined amino acid residues have been conserved between the XL-15 and G21 proteins. The underlined nucleotides in the 3′-untranslated region between 1307 and 1352 are similar to the selenocysteine insertion element required to translate the UGA codon into a selenocysteine residue (22). The double-underlined nucleotides are identical to the eukaryotic consensus sequences of this element (22).