Erratum

Cloning and characterization of the *C.elegans* histidyl-tRNA synthetase gene

by Y.G.Amaar and D.L.Baillie

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The publishers wish to apologise for the incomplete printing of figure 1 which accompanied this paper. The figure is reprinted in full below.

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1  GAGCTCAATAGCGATCTCAACAATTTGGAACTTCTTGAAAAAATGTCACAACCTCCCAGATCTCGGGCAAAATGACAAGTTTAAAAAGGGAGCCGAAGAACTGAAGGTGTTAATTGAGTACCTCAATGTCGATGGAGTGACCACTGTTCG 841
2  GAGCTCAATAGCGATCTCAACAATTTGGAACTTCTTGAAAAAATGTCACAACCTCCCAGATCTCGGGCAAAATGACAAGTTTAAAAAGGGAGCCGAAGAACTGAAGGTGTTAATTGAGTACCTCAATGTCGATGGAGTGACCACTGTTCG 1350
3   S  S  I  A  I  S  T  I  W  N  F  L  K  K  C  H  N  L  P  D  L  G  Q  N  D  K  F  K  K  G  A  E  E  L  K  V  L  I  E  Y  L  N  V  D  G  V  T  T  V  R 291
4                                                                          *                 *                 *        *

1  ATACGAACCATCCCTTGCCAGAGGTCTTGATTATTATACAGGTGCAATCTATGAAGCAGTCGCTCCTA                                                    AAGCTCTTGAAGGAACTGCTGTTGAAAACTCAGAGG 945
2  ATACGAACCATCCCTTGCCAGAGGTCTTGATTATTATACAGGTGCAATCTATGAAGCAGTCGCTCCTAgtatgtttttaaatattgaatcgactatcaaattgtttaatttcagAAGCTCTTGAAGGAACTGCTGTTGAAAACTCAGAGG 1500
3   Y  E  P  S  L  A  R  G  L  D  Y  Y  T  G  A  I  Y  E  A  V  A  P                                                    K  A  L  E  G  T  A  V  E  N  S  E  325
4            *  *  *  *  *  *  *  *  *  *  *     *  *  *     *

1  ATACTGCTGGACAACCAGTCGGAGTAGGATCAGTAGCTGCCGGTGGACGATACGATGGATTGGTTAAAATGTTCGACTCAAAAGCCAATGTTCCATGTTGCGGTGTTTCTTTTGGTATCGAACGTCTGTTTGCTATCATGGAAGCTCGAC 1095
2  ATACTGCTGGACAACCAGTCGGAGTAGGATCAGTAGCTGCCGGTGGACGATACGATGGATTGGTTAAAATGTTCGACTCAAAAGCCAATGTTCCATGTTGCGGTGTTTCTTTTGGTATCGAACGTCTGTTTGCTATCATGGAAGCTCGAC 1650
3  D  T  A  G  Q  P  V  G  V  G  S  V  A  A  G  G  R  Y  D  G  L  V  K  M  F  D  S  K  A  N  V  P  C  C  G  V  S  F  G  I  E  R  L  F  A  I  M  E  A  R  375
4                                                                  *                                 *     *     M3

1  AGAAAGTTGCCATTCGTACGACGCAAACCGAAGTCTATGTTGCATCTGCTCAAAAGAATTTGGTCAGGGATCGCAAGAAGTTGGTAAAGATGCTTCGATCTGCTGGAACTCAAGGACTGAAAATGGCACTGAAGGCTAATCCGAAATTGT 1245
2  AGAAAGTTGCCATTCGTACGACGCAAACCGAAGTCTATGTTGCATCTGCTCAAAAGAATTTGGTCAGGGATCGCAAGAAGTTGGTAAAGATGCTTCGATCTGCTGGAACTCAAGGACTGAAAATGGCACTGAAGGCTAATCCGAAATTGT 1800
3  Q  K  V  A  I  R  T  T  Q  T  E  V  Y  V  A  S  A  Q  K  N  L  V  R  D  R  K  K  L  V  K  M  L  R  S  A  G  T  Q  G  L  K  M  A  L  K  A  N  P  K  L  425
4                 *                                 *                                                   *

1  TAACGTCAATTCCAGTATGCCTGAGGAAAGACCGTATTCCGTCTTGCTATTGTTATTATGAGAGCAGAGCTAAGATGAGTGTCAGTGCGAAATGTGTCACCAGAGACGAACAG                                          1358
2  TAACGTCAATTCCAGTATGCCTGAGGAAAGACCGTATTCCGTCTTGCTATTGTTATTATGAGAGCAGAGCTAAGATGAGTGTCAGTGCGAAATGTGTCACCAGAGACGAACAGgtaatttttctaatatatttttttccgatatcaccaat 1950
3  L  T  S  I  P  V  C  L  R  K  D  R  I  P  S  C  Y  C  Y  Y  E  S  R  A  K  M  S  V  S  A  K  C  V  T  R  D  E  Q                                          463
4

1                 ACTATTAAACTCGACCAGCTGATCACTGCCGTTCGTGACACTCTTGCGCCCTCTAAACAATCGATAATTTCTTGTTTTCTTAGCTTTCTAATTCTCTGCGTTCACCTCACTTCAGCTTTTATGTCCCTCTTTCCA 1493
2  ttaaaatattttcagACTATTAAACTCGACCAGCTGATCACTGCCGTTCGTGACACTCTTGCGCCCTCTAAACAATCGATAATTTCTTGTTTTCTTAGCTTTCTAATTCTCTGCGTTCACCTCACTTCAGCTTTTATGTCCCTCTTTCCA 2100
3                  T  I  K  L  D  Q  L  I  T  A  V  R  D  T  L  A  P  S  K  Q  S  I  I  S  C  F  L  S  F  L  I  L  C  V  H  L  T  S  A  F  M  S  L  F  P  508
4

1  GTCATCATAATTCATATTTCCTGTTTTATTGATTTTTGCATAGTCGGTGTTTGACTTGTTTGTTTTTCTCCTTTTTTTGTTCCAGATTTCATATTTATTTTTGTTGGTTTGAAAATTCAGAACTTATCACAAAAAAAAAAA          1634
2  GTCATCATAATTCATATTTCCTGTTTTATTGATTTTTGCATAGTCGGTGTTTGACTTGTTTGTTTTTCTCCTTTTTTTGTTCCAGATTTCATATTTATTTTTGTTGGTTTGAAAATTCAGAACTTATCAC                  2230
3   V  I  I  I  H  I  S  C  F  I  D  F  C  I  V  G  V  *                                                                                                525
4
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```
1
2  cgagctaacgaattgtaggtttactagtttttcgtacattgttaatttaaacgaaattcagtcagaaacaaacaaataatcgtttaattccaaaattagatagactttttacatgtatcgtttttttcgcatttttgaacaaataaagg 150
3
4

1
2  atacccggttcatgtctgatcttctattttaatgaaacgcgtttgcaatccgcatagttttctcaccaaattcatgaaaattgtgacgaactttcacatcttcagtaaaatgtttcgaagcctgtattacgagtaggctggctttctcag 300
3
4

1
2  ttcggcaggctgaagaaactgtaaaaccgcggattgcatatgcacagagaagtggacgacgagtattcttgaataacatgaaattccaccaatacatgctttttcagatcaaagagaaagtcgcactgATGCAAGCGAAAAGAAAGGAGG 450
3                                                                                                                                  M  Q  A  K  R  K  E   7
4                                                                                                                                                 *

1          CCGGTGCACCCGAAAAACCCGGAAAGTTTGTTCTGAAAACAGGAAAGGGAACTCGTGACTACGGACCAGCTCAATCGGCTCTTCGCAATTCTGTGTTACAGACAGTCACTGAAACATTCAATAGATATGGTGCAGAGACCA 141
2  CAGGCGAGACCGGTGCACCCGAAAAACCCGGAAAGTTTGTTCTGAAAACAGGAAAGGGAACTCGTGACTACGGACCAGCTCAATCGGCTCTTCGCAATTCTGTGTTACAGACAGTCACTGAAACATTCAATAGATATGGTGCAGAGACCA 600
3  A  G  E  T  G  A  P  E  K  P  G  K  F  V  L  K  T  G  K  G  T  R  D  Y  G  P  A  Q  S  A  L  R  N  S  V  L  Q  T  V  T  E  T  F  N  R  Y  G  A  E  T   57
4                *                          *  *  *     *  *  *     *                                                          *        .  *  M1

1  TTGATACACCAGTATTCGAGCTTCGTGATGTTCTGATGGGAAAATATGGCGAGGAAGGAGGAAAACTTGTATATGATCTTCAAGATCAAGGAGGAGAGCTTCTATCATTGCGTTATGATCTCACTGTTCCATTTGCACGATACTTGGCAA 291
2  TTGATACACCAGTATTCGAGCTTCGTGATGTTCTGATGGGAAAATATGGCGAGGAAGGAGGAAAACTTGTATATGATCTTCAAGATCAAGGAGGAGAGCTTCTATCATTGCGTTATGATCTCACTGTTCCATTTGCACGATACTTGGCAA 750
3  I  D  T  P  V  F  E  L  R  D  V  L  M  G  K  Y  G  E  E  G  G  K  L  V  Y  D  L  Q  D  Q  G  G  E  L  L  S  L  R  Y  D  L  T  V  P  F  A  R  Y  L  A  107
4  *  *  *  *  *  *  *  *           *     *  *  *  *  *           *  *     *     *     *  *  *  *  *  *     *  *  *  *  *  *  *  *  *  *  *  *     *

1  TGAACAAAATCACGAATATTACAAGATATCAAATTGCGAAAGTATACAGAAGAGATCAACCTGTAATGTCTCGTGGACGGTACCGCGAGTTCTATCAATGCGATTTTGATATTGCCGGACAGTATGACCTTATGCTTCCGGAGCTGAGTG 441
2  TGAACAAAATCACGAATATTACAAGATATCAAATTGCGAAAGTATACAGAAGAGATCAACCTGTAATGTCTCGTGGACGGTACCGCGAGTTCTATCAATGCGATTTTGATATTGCCGGACAGTATGACCTTATGCTTCCGGAGCTGAGTG 900
3  M  N  K  I  T  N  I  T  R  Y  Q  I  A  K  V  Y  R  R  D  Q  P  V  M  S  R  G  R  Y  R  E  F  Y  Q  C  D  F  D  I  A  G  Q  Y  D  L  M  L  P  E  L  S  157
4  *  *                 *  *     *  *  *  *  *  *  *  *           *        *  *     M2          *  *  *     *  *              *     *

1  TCTGGGAATTGTTGATGAGTTGCTCACGAAACTGGAAATTGGAGAGTTTTTCATTAAT                                                                CTCAATCACCGTCTTGATCCTCGAAGGAATGTTTGCCGTTTC 541
2  TCTGGGAATTGTTGATGAGTTGCTCACGAAACTGGAAATTGGAGAGTTTTTCATTAATgtaaggctatttgttgaacaatcattttaattcgaattgtgttgtttcagCTCAATCACCGTCTTGATCCTCGAAGGAATGTTTGCCGTTTC 1050
3  V  W  E  L  L  M  S  C  S  R  N  W  K  L  E  S  F  S  L  I                                                                S  I  T  V  L  I  L  E  G  M  F  A  V  S 191
4                                                   *                                                                                 *  *     *     *

1  CGGTATTCCTGCTAAAGATTTCAAAACAATTTGCTCATCGGTCGATAAGCTTGACAAAACTCCATGGGAAGATGTTGAACAAGAAATGATTAATGAAAAGTTCCTAACTAAAGAGCAGACTGGAAAGCTGGGAGAACTTGTTCGATTCGA 691
2  CGGTATTCCTGCTAAAGATTTCAAAACAATTTGCTCATCGGTCGATAAGCTTGACAAAACTCCATGGGAAGATGTTGAACAAGAAATGATTAATGAAAAGTTCCTAACTAAAGAGCAGACTGGAAAGCTGGGAGAACTTGTTCGATTCGA 1200
3   G  I  P  A  K  D  F  K  T  I  C  S  S  V  D  K  L  D  K  T  P  W  E  D  V  E  Q  E  M  I  N  E  K  F  L  T  K  E  Q  T  G  K  L  G  E  L  V  R  F  E 241
4   *                    *     *     *  *  *  *  *  *     **     *     *     *  *     *  *           *             *     *
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Figure 1. Most of the cDNA sequence (1), the genomic sequence (2), the deduced amino acid sequence (3) of the *C.elegans* histidyl-tRNA synthetase gene are shown. Lower case letters indicate the 5′ untranslated region and the location of the three introns identified. The putative TATA box, (tatta), the CCAAT box, (ccaaat), the trans-splice site (tttttcag), the three motifs (M1, M2, M3) are underlined, as is the poly (A) tail. The (*) (4) shows identical amino acids among *C.elegans*, human, and *S.cerevisiae* histidyl-tRNA synthetases.