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Corrigendum

The *Drosophila* neurogenic gene *neuralized* encodes a novel protein and is expressed in precursors of larval and adult neurons

by G.L.Boulianne, A.de la Concha, J.A.Campos-Ortega, L.Y.Jan and Y.N.Jan

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The *neuralized (neu)* cDNA sequence included in this paper was found to contain errors in the summer of 1992, when G.Feger began to study the gain-of-function phenotype of *neuralized* by putting *neu* behind a heat-shock promoter and resequencing part of the gene. Over the past 8 months G.Feger and E.Wolff have isolated several overlapping cDNA clones and genomic DNA clones and re-determined the *neu* coding sequence (Figure 1). The corrected cDNA sequence was further verified with G.L.Boulianne, who was in L.Y.Jan and Y.N.Jan's laboratory until 1991 and carried out the cloning and molecular analysis of *neu* as reported in the original paper. A.de la Concha and J.A.Campos-Ortega contributed to the genetic analysis of *neu* and some of the *in situ* hybridization experiments; these authors are not responsible for the mistakes of the molecular characterizations. G.L.Boulianne, L.Y.Jan and Y.N.Jan take full responsibility for these mistakes and regret any inconvenience caused by the errors in the published *neu* sequence.

The correct *neu* cDNA sequence (Figure 1) predicts a protein of 753 amino acids (rather than 411 amino acids as initially reported). We did not detect overall similarities to other proteins (GenBank release 75 and PIR protein database release 35) except for a putative Zn binding motif in the C-terminal domain of *neu*.

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A    1  GAAAAAAAACTCAGCGAAAGGTTGTCTCGAAGTTGTCGTCGGTCTTTGTGTTTCGTATCGTTTCGTTTCGTTTGTTCCCGTTGCGC
    90  GCAGACAAACAACCAACCAAATTCAAAATGTTTTAACGGAAAACATTCAAATTCGAAGAAGAACTCTATCGCTAAATTTAATGCCAAATA
   180  AAATACGCAAGCAGCTTGTGCATTTTCATTAGCATTACGCGTGTTCGTTTAGTTCGTCTGTTTTAATTTAAATAACGAAATAAGAAATAA
   270  TCCACTACCATGGGTCTATCGGATATACCAGCCAACTATATGCAGGGCAGCCATCCGCACCTAACTCTCCATCCGCAGCAGCAGCACCAC
                  M  G  L  S  D  I  P  A  N  Y  M  Q  G  S  H  P  H  L  T  L  H  P  Q  Q  Q  H  H  27
   360  CAGAATCAGCAGCACTTGCAGCATCTGCAACAGATGCAGCAGCTGCACAACGCCATGCCCACTCCCGCCCAGCAGGCCGCCCAGGTCCTG
         Q  N  Q  Q  H  L  Q  H  L  Q  Q  M  Q  Q  L  H  N  A  M  P  T  P  A  Q  Q  A  A  Q  V  L  57
   450  GCCATGGAGTCCAACGAGCTGCTCATGAGCACCAAGGACAAGCTCTCTAGCAAGAAGAAAATGCACTTGCTCAAGAAGATCAAGAAGCGC
         A  M  E  S  N  E  L  L  M  S  T  K  D  K  L  S  S  K  K  K  M  H  L  L  K  K  I  K  K  R  87
   540  TTTGGATTGGTTCGCCGCTCACCCTCTTCATGTCCTGGCCCCAACAACCTGCCTCCGCTGCAATTCCACTCCGTACATGGCGACAACATC
         F  G  L  V  R  R  S  P  S  S  C  P  G  P  N  N  L  P  P  L  Q  F  H  S  V  H  G  D  N  I  117
   630  CGAATTTCAAGGGACGGAACCCTGGCCCGTCGCTTTGAGAGCTTCTGCAGGGCCATCACCTTTTCAGCGCGTCCGGTTCGCATCAACGAG
         R  I  S  R  D  G  T  L  A  R  R  F  E  S  F  C  R  A  I  T  F  S  A  R  P  V  R  I  N  E  147
   720  AGGATCTGCGTGAAGTTTGCTGAGATCTCGAACAACTGGAACGGTGGAATTCGCTTTGGATTCACCAGCAACGATCCTGTAACGCTGGAG
         R  I  C  V  K  F  A  E  I  S  N  N  W  N  G  G  I  R  F  G  F  T  S  N  D  P  V  T  L  E  177
   810  GGAACGCTGCCCAAGTACGCCTGTCCGGATCTGACCAACAGGCCTGGCTTCTGGGCCAAGGCTCTGCACGAGCAGTACTGCGAGAAGGAC
         G  T  L  P  K  Y  A  C  P  D  L  T  N  R  P  G  F  W  A  K  A  L  H  E  Q  Y  C  E  K  D  207
   900  AACATACTTTACTACTATGTCAATGGAGCTGGCGATGTGATCTATGGTATAAACAACGAGGAGAAGGGTGTGATACTGACCGGCATCGAT
         N  I  L  Y  Y  Y  V  N  G  A  G  D  V  I  Y  G  I  N  N  E  E  K  G  V  I  L  T  G  I  D  237
   990  ACGAGAAGCCTGCTGTGGACGGTGATCGATATCTATGGCAACTGCACGGGCATTGAGTTTCTCGATTCTCGCATTTACATGTACCAGCAG
         T  R  S  L  L  W  T  V  I  D  I  Y  G  N  C  T  G  I  E  F  L  D  S  R  I  Y  M  Y  Q  Q  267
  1080  CAGCCAGTGGCTATACCAATGGCCACTGTGCCCGCCCAGCAACAGCAAATGCCCCAGCCAGCTGCCAATGCCTCCTCCGCCCTGAATTCC
         Q  P  V  A  I  P  M  A  T  V  P  A  Q  Q  Q  Q  M  P  Q  P  A  A  N  A  S  S  A  L  N  S  297
  1170  CATCACCCGCATCAGCAGTCGAGGAGATCCCTGCCAGGACACACTGCGGCCATCGAGCACGATCTGGAGCGCCATGTGATGCCGTCCCTG
         H  H  P  H  Q  Q  S  R  R  S  L  P  G  H  T  A  A  I  E  H  D  L  E  R  H  V  M  P  S  L  327
  1260  CAATCCCTGCACTTGGCAGGAAACGGTGGAAGCGTGGCTAGCGTAGAACAGGCGGCCATTGCTCATGATTTGGCCAATGGACTGCCTCCT
         Q  S  L  H  L  A  G  N  G  G  S  V  A  S  V  E  Q  A  A  I  A  H  D  L  A  N  G  L  P  P  357
  1350  CTGCGCTACAATGCCAACGGACGACTGATTCCAGTGCCCTTCCACAACACCAAGGGCCGGAATGTGCGGCTCTCGCAGGATCGCTTTGTG
         L  R  Y  N  A  N  G  R  L  I  P  V  P  F  H  N  T  K  G  R  N  V  R  L  S  Q  D  R  F  V  387
  1440  GCTTCTCGTACGGAATCTGACTTCTGCCAGGGATATGTGTTCACTGCCCGTCCCATTCGCATTGGTGAGAAGCTGATTGTGCAGGTCCTG
         A  S  R  T  E  S  D  F  C  Q  G  Y  V  F  T  A  R  P  I  R  I  G  E  K  L  I  V  Q  V  L  417
  1530  AAAACGGAACAGATGTACGTGGGTGCCTTGGCTTTGGGTCTGACCTCCTGCAATCCGGCCATGTTGCAGCCCAATGATTTGCCCAATGAT
         K  T  E  Q  M  Y  V  G  A  L  A  L  G  L  T  S  C  N  P  A  M  L  Q  P  N  D  L  P  N  D  447
  1620  TCGGATTTCCTGCTCGATCGCCCCGAGTACTGGGTGGTGAGCAAGGATATTGCAGCTGCTCCTCAGCGCGGCGATGAGATTGCCTTCTTC
         S  D  F  L  L  D  R  P  E  Y  W  V  V  S  K  D  I  A  A  A  P  Q  R  G  D  E  I  A  F  F  477
  1710  GTGGCGCCCAACGGTGAAGTGAGCATCAGCAAGAACAACGGACCAGCTGTGGTGGTGATGCATGTGGACCAGTCCCTCCAGCTGTGGGCC
         V  A  P  N  G  E  V  S  I  S  K  N  N  G  P  A  V  V  V  M  H  V  D  Q  S  L  Q  L  W  A  507
  1800  TTCCTGGATGTCTACGGCTCGACGCAGTCTCTGAGGATGTTCCGCCAGCAGTTACCCAACATGGTTGCGTATCCATCGCAGCCGCAGGTG
         F  L  D  V  Y  G  S  T  Q  S  L  R  M  F  R  Q  Q  L  P  N  M  V  A  Y  P  S  Q  P  Q  V  537
  1890  AATGTGAATGCCAGCAGCTCGTCCGCCTGCAACGCTGCCTCCACGTCCCGCATGCTGCCCATGACCGAGTCGATGAGCAGTCTGAATGCC
         N  V  N  A  S  S  S  S  A  C  N  A  A  S  T  S  R  M  L  P  M  T  E  S  M  S  S  L  N  A  567
  1980  GGAGCCACTGCCAAGCTGTTGCATCATCCCTCGCAGCTGAGCGTAGCCCAGAGTACGAGCAATTTGGCCTCAGCTGGCGGAGTCAATGGC
         G  A  T  A  K  L  L  H  H  P  S  Q  L  S  V  A  Q  S  T  S  N  L  A  S  A  G  G  V  N  G  597
  2070  AGCCGCATGATCAGCATGCCCTCCAACGGAGATATTCTCCAGATCCAGCCGAATGGTGGTGGCACCGTTCTGGTGGTCAACCTGCCACCT
         S  R  M  I  S  M  P  S  N  G  D  I  L  Q  I  Q  P  N  G  G  G  T  V  L  V  V  N  L  P  P  627
  2160  GCTAGCAGCTCGCACGATATAAACGGCCAACTCGCGGCCAGGCCAACGGCCACGGTAACCTCCAGCGGTGTTCTGGCCGGAGCCTGCTCC
         A  S  S  S  H  D  I  N  G  Q  L  A  A  R  P  T  A  T  V  T  S  S  G  V  L  A  G  A  C  S  657
  2250  AGCGGCACCCTTATCAGCACCACCAGCAGCCAGTACATTGAGCCCATTGCCAATAGCACAAATAATGCGGCCAACAAGTGGAAGGACAGC
         S  G  T  L  I  S  T  T  S  S  Q  Y  I  E  P  I  A  N  S  T  N  N  A  A  N  K  W  K  D  S  687
  2340  CTGAGCGACCAGCAGAGAACCGATTCGAGTGCCGAATGCACCATCTGCTACGAGAATCCCATCGACTCGGTGCTGTACATGTGCGGACAC
         L  S  D  Q  Q  R  T  D  S  S  A  E  C  T  I  C  Y  E  N  P  I  D  S  V  L  Y  M  C  G  H  717
  2430  ATGTGCATGTGCTACGACTGCGCCATCGAGCAGTGGCGCGGAGTGGGTGGTGGCCAGTGCCCACTGTGCCGGGCGGTGATCCGGGACGTC
         M  C  M  C  Y  D  C  A  I  E  Q  W  R  G  V  G  G  G  Q  C  P  L  C  R  A  V  I  R  D  V  747
  2520  ATCCGCACCTACACCACGTAGAAAGGTCGCGGGCGTTTCCTAGCCAAGCAACATTTACTCGCAATCAAACCTACTAAAGCTACACATTAT
         I  R  T  Y  T  T  @                                                                       753
  2610  ACCATACACACAAGTTGTTGCATTTTAAGCGCAATTGAGCGCAAAGAATATTATATTGGAGAGATAGGCATTATTTTTGCAGACTAAAGA
  2700  TTAGATAGTTTACGCAGCTAGATTAGTGTATGAAACTATCAACTAATTTATCACACGTATGTTTAATTTTTTTGTGATGTTATAAGTAAG
  2790  TGCGCCCCAGAGCCAAAACTATGTATTGTTCAATCCAACAAAGATATCTTCGTTTTTTCAATTTTTTTCAAACCTTGAATCGCCCATTTG
  2880  TGCATTGTATACTGAAAAACCAAAGTATTGTATAGGAGTTTATAGTATTTTGAATTTAAATTGGAATTAATTGAAAGTTGTTGCAAATTT
  2970  ACTTAGTTTTTCTCTATGTCTAAATTCCAAACGATGTGCAAAATTAACAAACACAAACTACAAGGATTCTTTATTTGGCGATTAATCATT
  3060  TTGGTGCTAAATGTTTTGAAAGGCAAAATAAAATTGTTAACGGATTTGAAAAGTTATGTTTAAGCTTGCAGCAACTACGAATGACCTTAA
  3150  TTTGATATGAAATCACAAGAAGCAAATATTGACTACTTTCCAGCAAGGAAATGGATATCGACGCAACTCAAATAAGTTTGCAGCACAAAT
  3240  TAATGAACAAAGATTGATCAGAAAACACTTATGCACGTAAACCAAAATAGAAAACTGCTAGAGCGTGTTTGTTTAAAGTTAATATTAGTC
  3330  TAGCCCTAAGTACTTAAGTTAATTTCTAGTCAACGAATTATGCTGAAGTTAAATCTAAACCGGACTTCATCCAACAAAGACACCACAAAA
  3420  AAGACGTATTAAGCACGCTAAGCTATTTTAATGAAGCCGCATTTTAAATTACACTTAAGTAGTGCACGTATTTTAATGGAGACTTAAATA
  3510  TATTTAACTATAAACATAAAAAAAAAAAAAAAAA
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B

	Exon	Intron	Exon
540	TTTGGATTGGgttagt...	Intron1	...ccatttcagTTCGCCGCT
2282	GTACATTGAGgtgagt...	Intron2	...tatcagcagCCCATTGCC

Fig. 1. Nucleotide sequence of the *neu* cDNA and of the predicted Neu protein. This figure replaces Figure 6 of the paper by Boulianne *et al.* (1991). **(A)** Numbers on the left refer to the first nucleotide of each line; numbers on the right indicate the last amino acid of each line. The protein sequence shown is a conceptual translation of the longest open reading frame within the cDNA sequence, which was determined by sequencing both strands of overlapping cDNAs as well as corresponding regions of the genomic DNA. The errors made in the previous publication include multiple frameshifts and other errors, which alter the conceptual translation, resulting in a smaller predicted protein. **(B)** Nucleotide sequence around the 5′ and 3′ exon/intron boundaries of the two introns.

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