

Corrigendum

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

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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*.

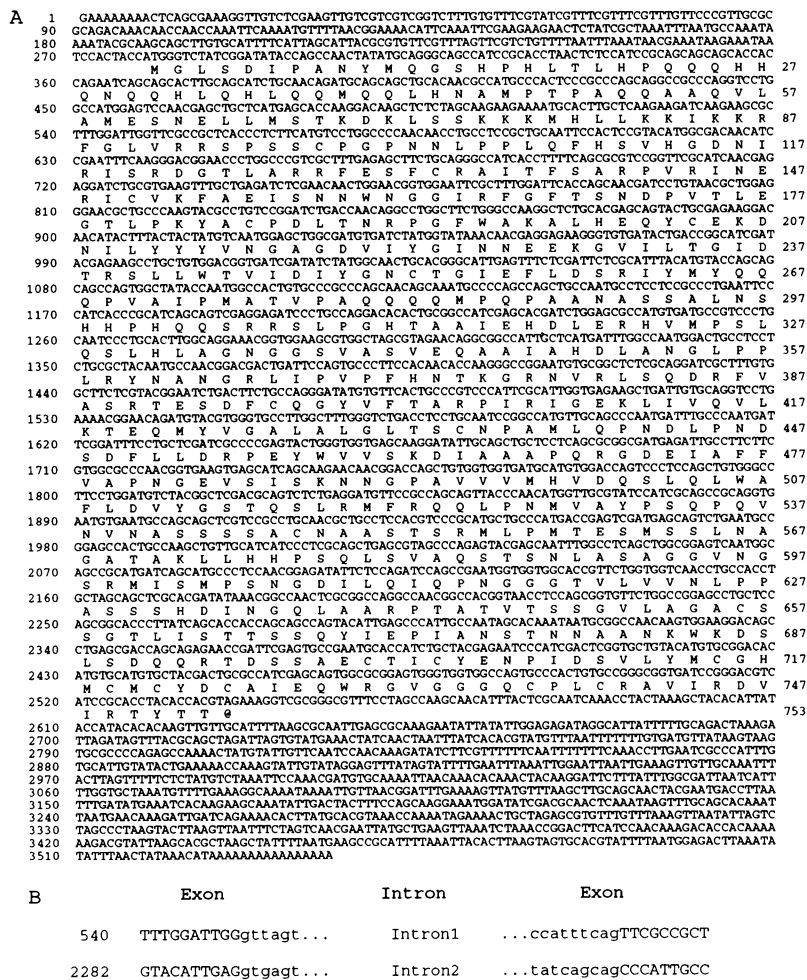


Fig. 1. Nucleotide sequence of the *neu* cDNA and of the predicted Neu protein. This figure replaces Figure 6 of the paper by Boulianne *et al.* (1991). (A) Numbers on the left refer to the first nucleotide of each line; numbers on the right indicate the last amino acid of each line. The protein sequence 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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