Tissue Specific Expression of the Retinoic Acid Receptor-β2: Regulation by Short Open Reading Frames in the 5'-Noncoding Region

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Abstract. The 40-S subunit of eukaryotic ribosomes binds to the capped 5'-end of mRNA and scans for the first AUG in a favorable sequence context to initiate translation. Most eukaryotic mRNAs therefore have a short 5'-untranslated region (5'-UTR) and no AUGs upstream of the translational start site; features that seem to assure efficient translation. However, ∼5-10% of all eukaryotic mRNAs, particularly those encoding for regulatory proteins, have complex leader sequences that seem to compromise translational initiation. The retinoic-acid-receptor-β2 (RARB2) mRNA is such a transcript with a long (461 nucleotides) 5'-UTR that contains five, partially overlapping, upstream open reading frames (uORFs) that precede the major ORF. We have begun to investigate the function of this complex 5'-UTR in transgenic mice, by introducing mutations in the start/stop codons of the uORFs in RARβ2-lacZ reporter constructs. When we compared the expression patterns of mutant and wild-type constructs we found that these mutations affected expression of the downstream RARβ2-ORF, resulting in an altered regulation of RARβ2-lacZ expression in heart and brain. Other tissues were unaffected. RNA analysis of adult tissues demonstrated that the uORFs act at the level of translation; adult brains and hearts of transgenic mice carrying a construct with either the wild-type or a mutant UTR, had the same levels of mRNA, but only the mutant produced protein. Our study outlines an unexpected role for uORFs: control of tissue-specific and developmentally regulated gene expression.

Introduction. The 5' and 3' untranslated regions (UTRs) of many eukaryotic mRNAs play an important role in the regulation of gene expression by modulating mRNA stability and translational efficiency. In fact, the expression of many genes is primarily regulated at the posttranscriptional level (for review see Jackson, 1993).

The initiation of protein synthesis is often the rate-limiting step and determines how much protein is synthesized from one mRNA. According to the scanning model for translational initiation, the 40 S preinitiation complex binds to the 5'-cap site of the mRNA, and then migrates until it encounters the first AUG in a favorable context to initiate translation. However, in many eukaryotic genes, the first AUG is not the translational start site of the major open reading frame. In particular mRNAs that encode for proteins with a proposed function in cell growth and differentiation, often have one or more AUGs or small upstream open reading frames (uORFs) that precede the major ORF (Kozak, 1991). These AUGs or uORFs usually inhibit translation from downstream, although some cases have been described where uORFs stimulated translation of the major ORF.

The retinoic acid receptor-β (RARβ) gene is one of those genes. It encodes a ligand-activated transcription factor and belongs to the superfamily of nuclear hormone receptors (Evans, 1988). Retinoic acid (RA) plays a critical role during embryonic development, homeostasis, and cell differentiation (for review see Eichele, 1993). Retinoic acid receptors act as molecular switches to transform the RA signal into a transcriptional response.

The RARβ gene encodes at least four different transcripts which are derived by differential splicing and promoter usage (Zelent et al., 1991; van der Leede et al., 1992; Nagpal et al., 1992). These transcripts contain common DNA and hormone-binding domains, but differ in the 5'-UTR and the NH2-terminal part of the receptor. The RARβ2 isoform has an unusually long 5'-UTR (461 nucleotides) that can form stable secondary structures and contains five small uORFs preceding the major ORF (de The et al., 1987; Reynolds et al., 1991; Zelent et al., 1991). Interestingly, uORF2, uORF4, and uORF5 have a staggered organization of overlapping start and stop codons. Similarly overlapping uORFs can be found in other regulatory genes, like homeobox genes. It has been suggested that such an arrangement might be part-
particularly suitable for translational regulation (Kessel and Gruss, 1988).

We (Reynolds et al., 1991; Zimmer and Zimmer, 1992) and others (Mendelsohn et al., 1991; Shen et al., 1992) have used RARβ2-lacZ reporter constructs in transgenic mice, to study the regulation of the RARβ2 gene in normal embryos and after RA treatment. Our constructs were made by fusing the lacZ coding region to the NH2-terminus of the RARβ2 gene, leaving the 5′ UTR intact. The expression pattern of the reporter gene constructs was tightly regulated during embryogenesis and closely followed that of the endogenous gene in most tissues. This was surprising, because it indicated that the 5′ UTR did not inhibit translation, as one might have expected. However, close examination of the published reports revealed some striking differences. For example, Mendelsohn et al. (1991) and Shen et al. (1992) both noted lacZ expression in the heart wall, which we never observed in our transgenics. Mendelsohn et al. (1991) and Shen et al. (1992) used constructs with a truncated 5′-UTR, thus indicating that this region might have indeed an important regulatory function that is not evident in all tissues.

To address the role of the uORFs, we generated RARβ2-lacZ reporter constructs with mutations in all upstream AUGs or with mutations in overlapping start and stop codons. The expression patterns in transgenic mice of the mutant constructs were compared with a construct carrying the wild-type 5′-UTR (Reynolds et al., 1991; Zimmer and Zimmer, 1992). We found that expression of the mutant constructs was differently regulated in heart and brain, suggesting that the uORFs play an important role in regulating tissue specific expression of the RARβ2 mRNA.

Materials and Methods

Constructs

Mutations in the RARβ2-UTR were introduced using an oligonucleotide directed mutagenesis system (Amersham Corp., Arlington Heights, IL) according to the manufacturer’s recommendations. The template for mutagenesis was a PstI fragment from the wild-type reporter construct RLZ79 (Reynolds et al., 1991) inserted into M13mp18. The following oligonucleotides were used for site directed mutagenesis: M24-CCCGA ATCTA CTCTC; uORF5-ACGAA CTCCT 1ICAAA ATTTC CAGC~; uORF3-CC.AAA TGATC AATTA CCATT; uORF4- CCGGA ACAA GAATT ATGAC; M24-CCCGA ATCTA CTCTC. Mutations were verified by di-deoxy sequencing and the mutated PstI fragment was reinserted into RLZ79 after partial PstI digestion.

Generation and Analysis of Transgenic Mice

Transgenic mice were established and embryos were analyzed for B-gal expression essentially as described (Sambrook et al., 1989). 10 μg of total RNA were hybridized with 1.5 × 105 cpm of probe in hybridization buffer (40 mM Pipes, pH 6.4; 1 mM EDTA; 0.4 M NaCl; 80% formamide) at 50°C for 16 h. Subsequently, 300 μl RNAse digestion mixture (10 mM Tris, pH 7.4; 300 mM NaCl; 5 mM EDTA; 2 μg/ml RNAse Ti; 40 μg/ml RNAse A), was added and incubated at 37°C for 60 min. The protected RNA was precipitated after inactivation of RNAses by proteinase K digestion and phenol/chloroform extractions, dissolved in formamide loading buffer and separated on a 6% sequencing gel (Sequagel). Subsequently, the gels were dried and analyzed using a Bio-Imaging Analyzer (Pujil BAS 2000). Expression levels were quantitated using the "Radioaktive" function and also independently after importing the raw data into a Macintosh Quadra 800 computer using the public domain NIH Image program (written by Wayne Rasband at the U.S. National Institutes of Health and available from the Internet by anonymous ftp from zippy.nlm.nih.gov or on floppy disk from National Technical Information Service, 5285 Port Royal Rd., Springfield, VA 22161, part number PB93-904866).

Results

The 5′-UTR Is Highly Conserved between Mouse and Human

The short upstream open reading frames in the RARβ2 5′-UTR are highly conserved between mouse and human (Fig. 1; de The et al., 1987; Reynolds et al., 1991; Zelent et al., 1991), which indicates that this region has an important function. Particularly striking is the overlapping arrangement of uORF2, uORF4, and uORF5. The stop codon of uORF2 overlaps with the uORF4 start codon, and the uORF4 stop codon overlaps with the AUG of uORF5 (Fig. 1). The organization of these uORFs is almost identical in mouse and humans. However, because of a frameshift mutation in uORF3/uORF5, the amino acid sequence of the human and mouse uORF5 peptides and the COOH-terminal half of the uORF3 peptides would be different.

Mutations in Overlapping Start and Stop Codons

Results in Altered Regulation of LacZ Expression in Heart and Brain

The reporter constructs used in this study were derived from the RARβ2-lacZ expression vector RLZ79 (Reynolds et al., 1991). This construct contained about 1.25 kb of RARβ genomic sequences, including the RARβ promoter, the RARβ 5′-UTR and the first 29 amino acids of the RARβ2-ORF, to which the lacZ coding region was fused (Fig. 2). Consequently, translation of the lacZ gene was subject to potential control mechanisms located within the 5′-UTR. We analyzed the expression pattern in transgenic founder embryos and transgenic lines. Transgenic founder embryos...
Comparison of the human and mouse RARβ2 5'-UTRs. Shown are the sequences from the transcriptional start site (de The et al., 1990) to the RARβ2-AUG and the conceptual translation of all five uORFs. The amino acid sequence of uORF5 is indicated in bold letters, because uORF3 and uORF5 are in the same reading frame.

Figure 1. Comparison of the human and mouse RARβ2 5'-UTRs. Shown are the sequences from the transcriptional start site (de The et al., 1990) to the RARβ2-AUG and the conceptual translation of all five uORFs. The amino acid sequence of uORF5 is indicated in bold letters, because uORF3 and uORF5 are in the same reading frame.

were particularly informative. We routinely obtained between 10% and 30% transgenic embryos from every litter, enabling us to examine several independently derived founder animals within a single experiment. Transgenic lines were most useful for following the expression patterns during development.

The first mutation tested, M24, had a two nucleotide exchange in the uORF2 stop codon and the uORF4 start codon (Fig. 2), thus extending uORF2 (162 bp vs 63 bp) and deleting uORF4. Four transgenic lines that expressed the transgene were derived with this construct. The expression patterns did not change in M24 embryos. Thus, the mutation in M24 alters the regulation of expression of the RARβ2-lacZ gene in heart and telencephalon.

Two of the four lines also expressed at high levels in the peritoneum of day 12.5 embryos (Fig. 3 E). However, we believe that this high level of expression can not be attributed to the mutation, because we also found lacZ expression in the peritoneum in ~35% of all RLZ79 embryos analyzed.

The second construct, M45, had a single nucleotide exchange to mutate the uORF4 stop codon and the overlapping uORF5 start codon. As uORF4 and the major ORF are in the same reading frame, the possibility exists that a larger fusion protein of uORF4 and RARβ2-lacZ is made. In construct M0, the AUGs of uORF1 to uORF4 are mutated by changing the adenine to a thymidine, while in uORF5 the thymidine was mutated to an adenine.

Figure 2. Schematic representation of reporter plasmids employed in this study. The RARβ2-lacZ expression vector RLZ79 (Reynolds et al., 1991) contained ~1.25 kb of RARβ genomic sequences, including the RARβ2 promoter, the RARβ2 5'-UTR and the first 29 amino acids of the RARβ2-ORF, to which the lacZ coding region was fused. Translation of the lacZ gene was subject to potential control mechanisms located within the 5'-UTR. Open reading frames in the 5'-UTR are indicated as lines. The exchange of two nucleotides in mutation M24 eliminates the uORF2 stop codon and the uORF4 start codon. As a consequence, uORF2 terminates further downstream, and uORF5 is deleted. The single nucleotide exchange in M45, mutates the uORF4 stop codon and the uORF5 start codon. As uORF4 and the major ORF are in the same reading frame, the possibility exists that a larger fusion protein of uORF4 and RARβ2-lacZ is made. In construct M0, the AUGs of uORF1 to uORF4 are mutated by changing the adenine to a thymidine, while in uORF5 the thymidine was mutated to an adenine.
Figure 3. Mutations in the uORFs result in altered regulation of lacZ expression in the heart and brain of transgenic embryos. Whole mount staining of representative embryos at day 9.5 p.c. and 12.5 p.c. are shown in the upper panel (A, D, G, and K) and the middle panel (B, E, H, and L), respectively. Note lacZ expression in the telencephalon (arrows) of embryos derived with M24, M45, or M0. M45 embryos also expressed at high levels in the hearts of day 9.5 embryos (asterisk) while M24 expressed only weakly at this stage. Sagittal (C, F, and M) and transverse (I) sections show high levels of lacZ expression in the heart wall and also in papillary muscles of day 12.5 p.c. M24 and M45 embryos. M0 expressed only in a few cells (M).

mental stages and also at low levels in the brain. The M45 expression pattern in other tissues was similar to the wild-type construct, although staining in the spinal cord of some M45 embryos was weaker (Fig. 3). These results suggest that the uORFs inhibit expression of the RARβ2-ORF in a tissue specific manner in heart and brain.

β-gal staining in the heart of M24 and M45 embryos was particularly strong in the heart wall and weaker in papillary muscle fibers (Fig. 3, F and I). This distribution is not an artifact caused by incomplete penetration of the staining solution, as we found a similar pattern when the staining was performed with sections (data not shown).

Both mutations exhibited a distinct temporal expression pattern in heart and brain during development and also in adults (see Table I). For example, M24 embryos expressed lacZ in the heart only at moderate levels at day 9.5 p.c., when compared to M45 embryos. However, at day 12.5 p.c. and in adults, lacZ staining in the heart was very similar with both constructs. In the brain, β-gal activity of M24 embryos and adult mice was very high throughout all developmental stages, while M45 transgenics showed much weaker lacZ staining.

Deletion of All uORFs

The mutations in M24 and M45 suggest that the altered regulation of lacZ expression is tissue specific. However, the possibility exists that the presence of uORFs that were not af-
Table 1. LacZ Expression in Heart and Brain of Transgenic Lines and Founder Embryos

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<th>Construct</th>
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Expression of 5'-UTR mutants in the heart (H) or the brain (B) of transgenic mice. The number of transgenic lines or transgenic founder embryos that were analyzed for each construct is indicated. –, no expression; +, weak expression; ++, strong expression; ++++, very strong expression; nd, not done.

* Of 22 founder embryos and two transgenic lines analyzed, only one expressed in the telencephalon.

† We examined one transgenic line throughout embryonic development and in adults, and the litters from three independently derived transgenic founder females on days 10.5 or 12.5 p.c., respectively.

...ected by these mutations may prevent translation of the major ORF in other tissues. It was therefore important to investigate the expression pattern of a reporter construct in which all uORFs were mutated. This was achieved by introducing single nucleotide exchanges into all upstream AUGs.

One transgenic line and 10 founder embryos were generated with M0 and analyzed at different developmental stages. Representative day 9.5 and day 12.5 embryos are shown in Fig. 3, K and L. The overall pattern of expression was very similar in RLZ79 and M0 embryos. However, M0 founders exhibited, as expected, lacZ activity in the heart and/or brain (Fig. 3, K–M), although expression in the heart was weaker.

Figure 4. Determination of RARβ2-lacZ RNA and protein levels in day 12.5 embryos. (A) Organization of the endogenous RARβ2 and the transgene. A BsaAI-Bsu36I fragment of the transgene was used to synthesize an antisense RNA probe. The endogenous RARβ mRNAs protect a 187-nt fragment (BsaAI to PstI). The transgene protects a 423-nt fragment (BsaAI to Bsu36I) of the RNA probe. (B) Total RNA from various transgenic embryos was hybridized to the radiolabeled RNA probe and digested with RNase as described in Materials and Methods. The protected fragments were separated on a sequencing gel (Sequagel) and analyzed using a Bio-Imaging Analyzer. Radiolabeled BluescriptSK+ DNA digested with HpaII was used as size-marker. Note that the probe overlaps with the AUG of uORF5. This AUG is mutated by a single nucleotide exchange in constructs M0. As a consequence RNA from M0 and M45 embryos is partially cleaved at this position to yield a smaller fragment (indicated by asterisk). (C) Quantitation of RARβ2-lacZ RNA and protein levels. Protein levels were determined enzymatically in at least three embryos (see Materials and Methods). RNA levels were estimated using a Bio-Imaging Analyzer (Fuji BAS 2000) and also independently after importing the raw data into a Macintosh Quadra 800 computer using the public domain NIH Image program.
was weaker compared to M24 and M45 embryos. These data support our hypothesis that the translational regulation by the uORFs is tissue specific.

It has previously been shown that uORFs can inhibit the translation of transfected constructs in cultured cells. To determine if the translation of the RLZ79 construct is also inhibited in our transgenic lines, we wanted to compare the amount of protein made from the RLZ79 and the mutant constructs quantitatively. Therefore, day 12.5 embryos were isolated and the lacZ-mRNA and protein levels were determined by RNAse protection and enzymatic assays, respectively. To facilitate the quantitation of RNA levels, we used a probe that simultaneously protected the endogenous RARB2 mRNA and the transgene (Fig. 4). Thus, the endogenous RARB expression level served as a reference. The comparison of RNA and protein levels revealed similar protein/RNA ratios in RLZ79, M0, and M45 embryos. However, translation of M24 was overall reduced, despite its strong expression in heart and telencephalon. These data indicate that the uORFs in the wild-type construct do not inhibit translation of the major open reading frame in most tissues.

mRNA, but Not Protein Expression, Is Similar in Mutant and Wild-Type Mice

To investigate whether the low lacZ levels in heart and brain of the wild-type construct could be accounted for by reduced mRNA levels, we analyzed RARB2-lacZ RNA and protein in hearts and brains of adult RLZ79 and M24 transgenic mice. Preliminary experiments showed that the lacZ activity was readily detectable in organ extracts from M24 transgenic mice, while we failed to detect any lacZ activity above background in the hearts and brains of RLZ79 transgenic mice, when measured in enzymatic assays. Therefore, lacZ activity was estimated by staining of organs from several mice of similar age (3–6 mo), either as whole mounts or after sectioning. RNAs were analyzed in parallel.

We found that RARB2-lacZ RNA levels were very similar in M24 and RLZ79 tissues (Fig. 5 B). However, β-gal staining patterns in both transgenic lines varied dramatically. In the brain, RLZ79 expressed β-gal activity only in a very small number of neurons, while M24 stained for β-gal in a large number of cells in the cortex (Fig. 5 A), the medial habenular nucleus, the striatum, and the telencephalic ependyma (Fig. 6). The β-gal activity in those few cells in the brains of RLZ79 mice that stained positive seemed to be similar to M24 mice. β-gal staining in the hearts was very strong in M24 transgenics, while RLZ79 transgenics were completely negative (Fig. 7). These data indicate that the uORFs inhibit translation of the RARB2-lacZ mRNA in heart and brain.

Figure 5. LacZ expression in brain and heart of adult mice. (A) Brain sections were cut after β-gal staining and the tissue was counterstained with neutral red as described in Materials and Methods. To visualize the β-gal staining, sections were photographed with a red filter (left panel). The right panel shows the same sections photographed under full light conditions. Non-transgenic controls showed no β-gal activity (top row). RLZ79 expressed only in very few cells in the cortex (middle row), while M24 (bottom row) expressed in a very large number of cells. (B) RNAse protection assays of hearts and brains. Analysis was performed as described in Fig. 3 and Materials and Methods. The wild-type RLZ79 mRNA is expressed in the brain at slightly higher levels than M24 although protein staining is detected in fewer cells (see also Fig. 6). Expression in the heart is comparable with both constructs. Note however, that we found no β-gal staining in RLZ79 hearts (Fig. 7).
Figure 6. *LacZ* expression in the medial habenular nucleus, striatum, and ependyma. To compare *lacZ* expression in deeper brain structures between RLZ79 and M24, frozen sections from adult brains were stained for β-gal activity. (A and B) Sections through the medial habenular nucleus of RLZ79 transgenic mice showed β-gal staining only in very few cells while M24 (C and D) expressed in almost all cells. A similar pattern was seen in the ependyma (arrows) and striatum (st), where RLZ79 (E and F) expressed in very few and M24 (G and H) in many cells. Note that RNase protection assays revealed higher RNA levels from RLZ79 than from M24 (Fig. 5).

**Discussion**

The complex 5'-UTR of the RARβ2 mRNA is highly conserved between mice and humans, indicating an important function. Such a complex leader is not unique for the RARβ2 mRNA, but can be found in ~5% of all vertebrate mRNAs, in particular those that encode for proteins with a proposed function in the regulation of cell growth and differentiation (Kozak, 1991). However, the role of these 5'-UTRs is unknown, although evidence suggests that they negatively interfere with translation (Marth et al., 1988; Rao et al., 1988; Arrick et al., 1991; Darveau et al., 1985). It was therefore very surprising to see that the mutation of RARβ2-uORFs yielded no increase in the overall protein synthesis.

Nevertheless, mutations in uORFs in the 5'-UTR of RARβ2-*lacZ* reporter gene constructs lead to differently regulated *lacZ* expression in hearts and brains of transgenic mice, while the expression in other tissues was very similar. Interestingly, every mutation tested effected the level and time of expression during embryogenesis differently. M45, for example, already expressed at high levels in the hearts of day 9.5 embryos, in contrast to M24 and M0. However, expression in the brain was higher with M24 and M0 than with M45, at all developmental stages. These results show that uORFs in the RARβ2-5'-UTR can modulate gene expression in a tissue specific and developmentally regulated manner.

The best studied example of translational regulation by uORFs is the control of *GCN4* gene expression in *Saccharomyces cerevisiae* (Mueller and Hinnebusch, 1986; Miller and Hinnebusch, 1989; Abastado et al., 1991; Dever et al., 1992). The *GCN4*-open reading frame (ORF) is preceded by four small uORFs. Ribosomes initially translate the first uORF and subsequently reinitiate at a downstream AUG. Under conditions of amino acid sufficiency, ribosomes reinitiate at AUG of uORF2-4, instead of the *GCN4-*AUG. The frequency of reinitiation at uORF2-4 is reduced in amino acid starved cells and thus, some ribosomes resume translation at the *GCN4*-AUG (Mueller and Hinnebusch, 1986; Abastado et al., 1991). The reinitiation efficiency is regulated by the protein kinase GCN2, which is activated by uncharged tRNAs and phosphorylates the eukaryotic initiation factor 2 (eIF-2). When phosphorylated, eIF-2 sequesters the guanine nucleotide exchange factor eIF-2B, and thus reduces the level of active ternary complexes (Dever et al., 1992). Phosphorylation of eIF-2 by the heme regulated kinase (HRF) or dsIF has initially been described as a mechanism regulating the general protein synthesis in mammalian cells (Farrell et al., 1977; Cooper and Farrell, 1977; De Benedetti and Baglioni, 1984; Chen et al., 1991). Reinitiation is thought to be more sensitive to reduced levels of ternary complexes than cap-dependent initiation events, because it is less efficient (Kozak, 1989). Thus, a molecular
mechanism involved in the regulation of the general protein synthesis can be used to control gene specific translation as well.

Surprisingly, very little is known about the role of uORFs in complex leaders of vertebrate genes. Experiments involving expression constructs in which all or parts of the 5'-UTR were deleted showed that these leaders impaired translation (Marth et al., 1988; Ra et al., 1988; Arrick et al., 1991; Darveau et al., 1985). Therefore, it has been speculated that these 5'-UTRs might serve to reduce translation levels and that alterations in the translational efficiency of some proto-oncogenes may contribute to the development of the neoplastic phenotype (Darveau et al., 1985; Marth et al., 1988; Rao et al., 1988). This idea was supported by the finding that overexpression of eIF-4F (or a 24-kD subunit eIF-4E; Lazaris et al., 1990; Koromilas et al., 1992) or the IFN-inducible dsRNA-dependent protein kinase (dsRNA-PK, Koromilas et al., 1992) results in malignant transformation, possibly by increasing the translation of normally poorly translated mRNAs.

Our results show that a translational mechanism involving uORFs can be a very effective means to control tissue- or cell-specific gene expression patterns. This suggests that the translational control involving complex 5'-UTRs may be used to fine tune tissue specific gene expression patterns, rather than modulating the general level of protein synthesis. The molecular basis for tissue specific translational control of the RARβ2 gene remains to be determined, but the distinct expression patterns of the mutations indicate that several factors may be involved. It is conceivable that specific differences in the composition of initiation and/or elongation factors permit the translational machinery to traverse the uORFs in some cells, but not in others. A tissue specific expression pattern has been reported for different eIF-4A genes (Nielsen and Trachsel, 1988) and eIF-4E (Jaramillo et al., 1991), but a comprehensive analysis for other factors is lacking. The activity of the translational machinery is modulated by posttranslational modifications, in particular through phosphorylation by several protein kinases (Tuazon et al., 1989; Hershey, 1991; Merrick, 1992; Samuel, 1992). It is conceivable that the tissue specific and developmentally coordinated activation or expression of these protein kinases may account for tissue specific differences in the ability of ribosomes to translate the RARβ2-ORF.

The high degree of evolutionary conservation indicates that the RARβ2 isoform has a unique and important function. Furthermore, the very good conservation of the regulatory 5'-UTR suggests that the precise control of RARβ2 translation in heart and brain is important. Interestingly, a relatively small number of cells in the brain expressed the wild-type construct at high levels, while most cells were negative. As judged by the staining intensity, β-gal levels in those cells were similar to that seen in the brain cells of mutant mice. Thus it appears that the regulation of RARβ2
translation in the brain is cell specific. A unique feature of the brain is the enormous number of specific cell-cell interactions, totaling as many as 10^12 (Kandel et al., 1991). It is evident that this complexity can be specified only through combinatorial effects of many genes in conjunction with epigenetic processes. Conceivably, synaptic inputs might influence the translation of regulatory proteins by modulating the translational machinery through the activity of G-coupled receptors. Such a mechanism could play an important role in fine tuning the expression of many genes in neurons and in the specification of neuronal identity.

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