

# Distinct regions in the 3' untranslated region are responsible for targeting and stabilizing utrophin transcripts in skeletal muscle cells

Anthony O. Gramolini, Guy Bélanger, and Bernard J. Jasmin

Department of Cellular and Molecular Medicine, Faculty of Medicine, and Center for Neuromuscular Disease, University of Ottawa; and Ottawa Health Research Institute, Ottawa, Ontario K1H 8M5, Canada

In this study, we have sought to determine whether utrophin transcripts are targeted to a distinct subcellular compartment in skeletal muscle cells, and have examined the role of the 3' untranslated region (UTR) in regulating the stability and localization of utrophin transcripts. Our results show that utrophin transcripts associate preferentially with cytoskeleton-bound polysomes via actin microfilaments. Because this association is not evident in myoblasts, our findings also indicate that the localization of utrophin transcripts with cytoskeleton-bound polysomes is under developmental influences. Transfection of LacZ reporter constructs containing the utrophin 3'UTR showed that this

region is critical for targeting chimeric mRNAs to cytoskeleton-bound polysomes and controlling transcript stability. Deletion studies resulted in the identification of distinct regions within the 3'UTR responsible for targeting and stabilizing utrophin mRNAs. Together, these results illustrate the contribution of posttranscriptional events in the regulation of utrophin in skeletal muscle. Accordingly, these findings provide novel targets, in addition to transcriptional events, for which pharmacological interventions may be envisaged to ultimately increase the endogenous levels of utrophin in skeletal muscle fibers from Duchenne muscular dystrophy (DMD) patients.

## Introduction

Duchenne muscular dystrophy (DMD)\* is the most prevalent inherited neuromuscular disorder affecting ~1 in every 3,500 male births (Emery, 1991). The disease results from mutations and/or deletions in the X-linked dystrophin gene which prevents production of a large cytoskeletal protein of the spectrin superfamily (Ahn and Kunkel, 1993; Worton, 1995). Although the exact function of dystrophin remains unclear, it has been shown to serve as a link between the internal actin cytoskeleton and the extracellular matrix via a complex of dystrophin-associated pro-

teins (Matsumura and Campbell, 1994; Blake et al., 1996). Through these interactions, dystrophin is thought to maintain the integrity of muscle fibers during cycles of muscle contraction and relaxation.

Several years ago, a multiexonic gene on chromosome 6 that encodes a large cytoskeletal protein showing extensive sequence identity with dystrophin was identified (Love et al., 1989; Tinsley et al., 1992). Interestingly, this protein, now referred to as utrophin, is more ubiquitously distributed than full-length dystrophin. In skeletal muscle fibers, utrophin also displays a clear difference in its pattern of distribution as compared with dystrophin. Indeed, whereas dystrophin is known to be expressed along the entire length of the sarcolemma in normal muscle fibers, utrophin preferentially accumulates at the level of the neuromuscular junction in both normal and DMD muscles (Matsumura and Campbell, 1994; Blake et al., 1996; Gramolini et al., 2000) where it may contribute to the full differentiation of the postsynaptic apparatus (Deconinck et al., 1997; Grady et al., 1997). Because of its high degree of identity with dystrophin and its capacity to bind dystrophin-associated proteins (Matsumura et al., 1992), it has been suggested that upregulation of utrophin into extrasynaptic regions of DMD muscle fibers could serve as an

Address correspondence to Bernard J. Jasmin, Dept. of Cellular and Molecular Medicine, University of Ottawa, 451 Smyth Rd., Ottawa, Ontario K1H 8M5, Canada. Tel.: (613) 562-5800 Ext. 8383. Fax: (613) 562-5636. E-mail: jasmin@uottawa.ca

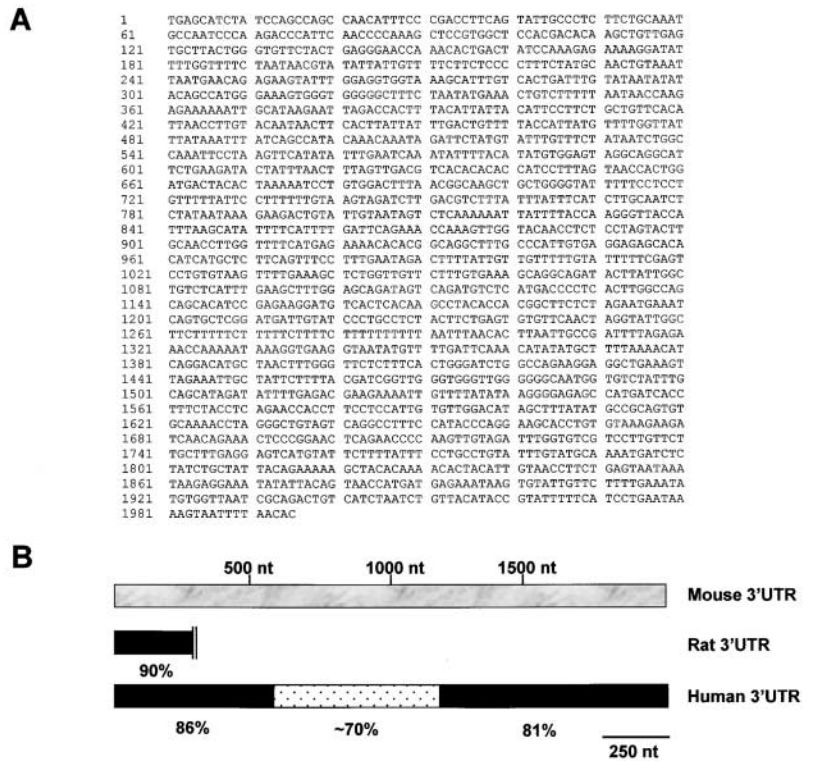
A.O. Gramolini and G. Bélanger contributed equally to this work.

A.O. Gramolini's present address is Howard Hughes Medical Institute and Dept. of Cell Biology, Duke University Medical Center, Durham, NC 27710.

\*Abbreviations used in this paper: AChR, acetylcholine receptor; COL, colchicine; Cy-D, cytochalasin D; DMD, Duchenne muscular dystrophy; LDH, lactate dehydrogenase; RT, reverse transcription; UTR, untranslated region.

Key words: Duchenne muscular dystrophy; neuromuscular junction; 3'UTR; posttranscriptional mechanisms; polysomes

**Figure 1. Complete sequence of the utrophin 3'UTR.** (A) Sequence of the mouse utrophin 3'UTR. (B) Comparison between the mouse 3'UTR and the available rat and human sequences. The percentage of identity with the mouse sequence is also shown.



adequate therapeutic strategy for this disease (Blake et al., 1996; Gramolini et al., 2000). Indeed, a series of experiments using transgenic mouse model systems has shown that increased expression of utrophin along dystrophic muscle fibers functionally compensates for the lack of dystrophin, and hence prevents the development of the muscle pathology (see, for example, Tinsley et al., 1996). Therefore, it is of interest to understand the mechanisms presiding over utrophin expression in attempts to ultimately increase expression of the endogenous gene product throughout DMD muscle fibers.

We have recently undertaken a series of experiments to gain insights into the nature of these mechanisms (Gramolini et al., 2000). In a first set of studies, we have shown that utrophin transcripts display an asymmetric distribution along skeletal muscle fibers, as they are clearly enriched within the postsynaptic sarcoplasm (Gramolini et al., 1997; Vater et al., 1998). Subsequent work further demonstrated that local transcriptional activation of the utrophin gene within myonuclei located in the postsynaptic sarcoplasm accounts, at least in part, for the preferential accumulation of utrophin mRNAs within this region of muscle fibers (Gramolini et al., 1997, 1998, 1999a; Khurana et al., 1999). However, under distinct experimental conditions we have also observed that utrophin may be regulated via posttranscriptional events (Gramolini et al., 1999b). In particular, we have recently shown that increased mRNA stability accounts for the higher levels of utrophin seen in slow versus fast skeletal muscles, thereby implicating the contribution of posttranscriptional events in the overall regulation of utrophin expression (Gramolini et al., 2001). In this context, it is interesting to note that posttranscriptional as well as translational regulatory mech-

anisms have recently been shown to contribute to the development and maintenance of neuromuscular junctions in *Drosophila* (Sigrist et al., 2000).

The targeting of distinct mRNAs to specific subcellular compartments has recently emerged as a key posttranscriptional event involved in the control of protein expression and localization. For instance, mRNAs such as *bicoid*, *oskar*, and *Vg1* become localized to a specific pole in developing *Xenopus* and *Drosophila* oocytes (see, for example, Pondel and King, 1988; Kim-Ha et al., 1993; Forristall et al., 1995). Interestingly, similar mRNA targeting mechanisms have also been observed in a variety of mammalian cells (see, for example, Bruckenstein et al., 1990; Burgin et al., 1990; Cripe et al., 1993; Kislauskis et al., 1994). In some cases, the subcellular localization of mRNAs has been shown to involve their targeting to specific pools of polysomes which associate with the cytoskeleton through regulatory sequences contained within the 3'UTR (Hesketh et al., 1994; Veyrune et al., 1996; Tsai et al., 1997; Bagni et al., 2000; Mori et al., 2000). Such subcellular localization of mRNAs is now recognized as a key step that facilitates the sorting and targeting of proteins, while also promoting their assembly into macromolecular complexes (for review see St Johnston, 1995; Hovland et al., 1996; Bassell and Singer, 1997; Hazelrigg, 1998; Jansen, 2001). With this in mind, we have begun to examine in the present study whether posttranscriptional regulatory mechanisms control utrophin expression in skeletal muscle cells. Specifically, we have: (a) sought to determine whether utrophin transcripts are targeted to a distinct subcellular compartment; and (b) examined the role of the utrophin 3' untranslated region (UTR) in regulating the stability and localization of utrophin transcripts in skeletal muscle cells.

Table I. LDH activity in various polysomal fractions

Fraction	Control (n = 12)	COL (n = 4)	Cy-D (n = 8)	3'UTR (n = 12)	Myoblast (n = 7)
Free	95.0 ± 0.6	90.0 ± 3.7	95.1 ± 0.8	93.1 ± 1.0	93.2 ± 1.5
Cytoskeletal	3.3 ± 0.6	9.0 ± 3.8	3.5 ± 0.5	4.1 ± 0.8	3.9 ± 1.1
Membrane	0.7 ± 0.2	1.1 ± 0.6	1.4 ± 0.4	3.0 ± 0.5	3.0 ± 0.5

Aliquots from each polysomal fraction were assayed for LDH. As expected, the preferential activity of LDH within the free (cytosolic) polysomal fraction. Data are expressed as a percent of the total activity. The heading for each column represents the different experiments performed in this study, i.e., control myotubes, myotubes treated with COL or Cy-D, myotubes transfected with reporter constructs containing the utrophin 3'UTR, and myoblasts used for examining the effects of differentiation.

## Results

### The utrophin 3'UTR

Cloning and sequencing of the utrophin 3'UTR revealed that it is a relatively large region spanning 1,995 nucleotides (Fig. 1 A). A detailed analysis of this RNA fragment showed that it contains several regions of interest. For example, there are six AU-rich elements located at nucleotide positions 479, 487, 613, 760, 840, and 1292, which consist of the sequence AUUUA (St Johnston, 1995; Hesketh, 1996; Veyrune et al., 1997). Alignment of the full-length 3'UTR using several data banks revealed a high degree of homology with a partial utrophin 3'UTR from rat (Fig. 1 B). Specifically, the homology between mouse and rat is ~90% through the first 281 nt, after which there is no available sequence information for the rat 3'UTR. Interestingly, significant homology was also observed between the mouse 3'UTR and a human sequence from chromosome 6 containing the utrophin gene. In this case, the overall sequence identity between the mouse and human 3'UTRs is close to 80%, with certain regions showing even higher homology (Fig. 1 B). In particular, there is ~87% homology between nucleotides 352 and 583 of the mouse and human sequences. However, our comparison also revealed that the utrophin 3'UTR is quite distinct from the dystrophin 3'UTR. Indeed, we could not find any significant homology between these two 3'UTRs (<10%) despite the high sequence identity seen in the coding regions of these two genes.

### Utrophin transcripts are enriched in a cytoskeletal-bound polysomal fraction

Initially, we examined the distribution of utrophin mRNAs in different pools of polysomes by using subcellular fractionation methods (Hesketh et al., 1994; Kislauskis et al., 1994; Hovland et al., 1995; Veyrune et al., 1997). Three distinct pools, corresponding to free, cytoskeletal-, and membrane-bound polysomes, were biochemically isolated. For these experiments, we first used several approaches to confirm that we had successfully isolated different pools of polysomes. Specifically, we monitored lactate dehydrogenase (LDH) activity as previously used in this case as a positive control for the free polysomal fraction because it contains cytosolic elements (Vedeler et al., 1991; Hovland et al., 1995; Mahon et al., 1995). Analysis of aliquots taken from the various subcellular fractions and from each sample showed that >90% of the total LDH activity was present in the free polysomal fraction (Table I). These results are in excellent agreement with previous findings (Vedeler et al., 1991; Hovland et al.,

1995; Mahon et al., 1995). In addition, we examined the distribution of utrophin among the different polysomal fractions. As shown in Fig. 2 A, utrophin levels were clearly enriched within the cytoskeletal fraction as revealed by Western blot analysis. Finally, we also monitored in these fractions the presence of mRNAs encoding the acetylcholine receptor (AChR)  $\alpha$ -subunit. Because these transcripts encode a membrane protein (Hovland et al., 1995), we observed, as expected, that AChR  $\alpha$ -subunit mRNAs were significantly more abundant in the membrane-bound polysomal fraction (Fig. 2 B).

Having established that this subcellular fractionation procedure yielded three distinct pools of polysomes, we next determined the relative distribution of utrophin transcripts in

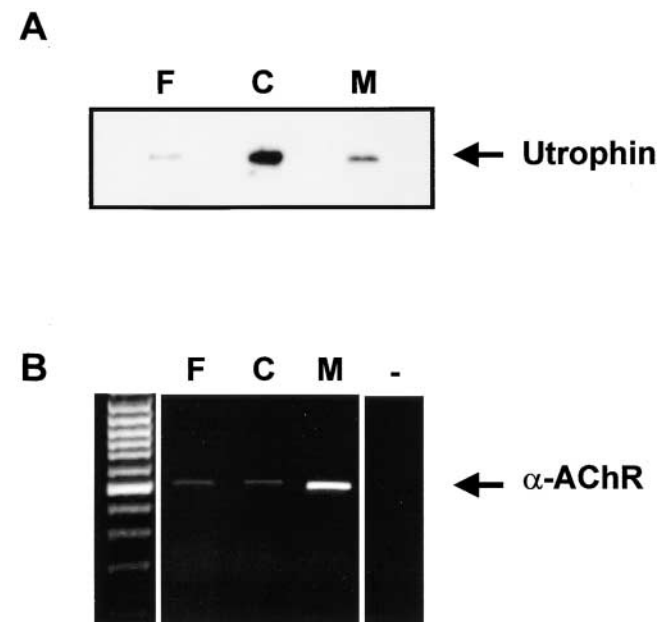
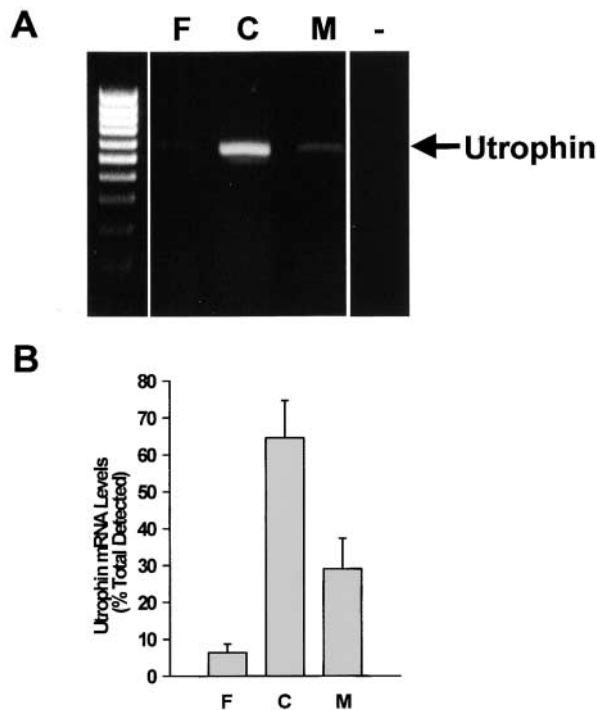


Figure 2. **Characterization of the polysomal fractions.** Markers of the three distinct pools of polysomes were used to ensure the validity of the subcellular fractionation procedure. Activity of the cytosolic enzyme LDH was determined for the free polysomal fraction (text and Table I). (A) shows the levels of utrophin in the free (F), cytoskeletal (C)-, and membrane (M)-bound polysomal fractions as determined by Western blot analysis. (B) shows a representative ethidium bromide-stained agarose gel of RT-PCR products corresponding to  $\alpha$ -AChR mRNAs obtained from the three fractions. The left lane is a 100-bp molecular mass marker. (-), negative control lane. Note the accumulation of utrophin in the cytoskeletal-bound fraction (B) and the enrichment of transcripts encoding the  $\alpha$ -subunit of AChR in the membrane-bound polysomal fraction (C).

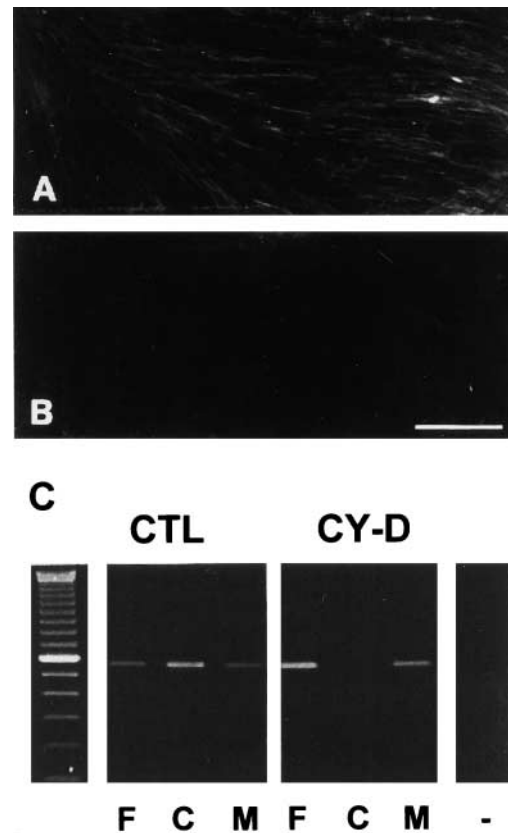


**Figure 3. Utophin mRNAs preferentially associate with cytoskeletal-bound polysomes.** (A) shows a representative ethidium bromide-stained agarose gel of RT-PCR products corresponding to utrophin mRNAs obtained from free (F), cytoskeletal (C)-, and membrane (M)-bound polysomal fractions. The left lane is a 100-bp molecular mass marker. (-), negative control lane. Note the accumulation of utrophin transcripts in the cytoskeletal-bound fraction. (B) Utophin transcript levels in each fraction were determined and expressed as a percent of the total. Shown are the results of a minimum of six independent experiments.

free, cytoskeletal-, and membrane-bound polysomal fractions. Interestingly, in these experiments we observed that utrophin mRNAs were enriched within the cytoskeletal-bound polysomal fraction in 4-d-old myotubes (Fig. 3 A). In fact, our analysis revealed that ~65% of the total content of utrophin transcripts was present within this fraction as compared with the free and membrane-bound fractions (Fig. 3 B).

#### Utophin transcripts associate with actin filaments

To further characterize the association of utrophin transcripts with cytoskeletal-bound polysomes, we next disrupted the integrity of actin filaments or microtubules. Short-term treatments of myotubes with cytochalasin D (Cy-D) resulted in the depolymerization of actin filaments as shown by fluorescence labeling using rhodamine-conjugated phalloidin (Fig. 4, compare A and B). Examination of the relative content of utrophin transcripts in polysomal fractions isolated from control versus treated myotubes revealed a dramatic redistribution of utrophin mRNAs. In comparison to the findings seen in control myotubes, utrophin transcripts were clearly enriched in the cytoplasmic fraction after Cy-D treatment. These findings not only confirm the association of utrophin mRNAs with the cytoskeleton (Fig. 3), but further indicate that actin filaments play an essential role in maintaining a link between these transcripts

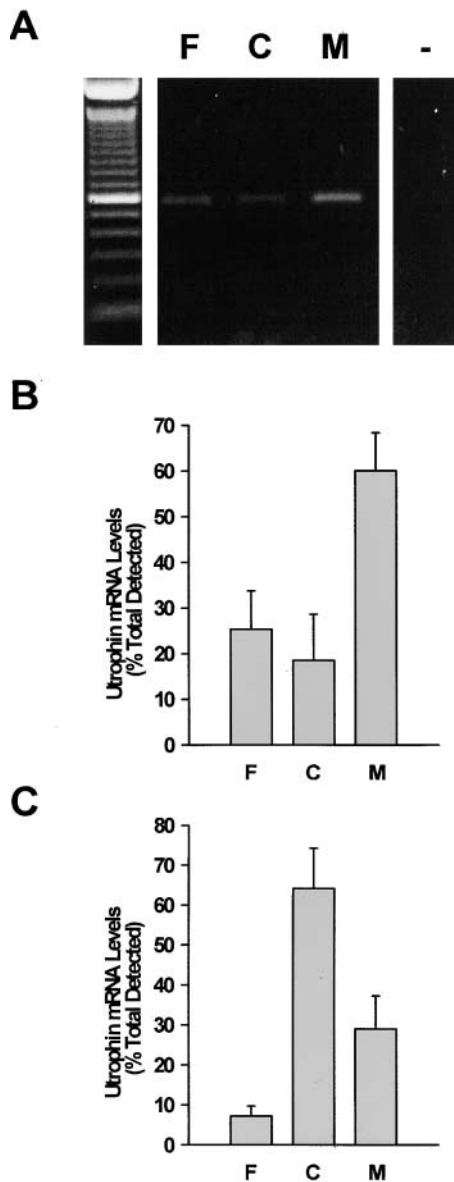


**Figure 4. Utophin mRNAs associate with actin microfilaments.** (A and B) Representative examples of phalloidin-stained myotubes without and following exposure to Cy-D, respectively. Note the absence of fluorescence following Cy-D treatment. (C) Representative ethidium bromide-stained agarose gels of utrophin RT-PCR products obtained from RNA isolated from free (F), cytoskeletal (C)-, and membrane (M)-bound polysomes, along with a negative control (-). Left panel corresponds to polysomal fractions isolated from control (CTL) myotubes, revealing that utrophin mRNAs preferentially associate with the cytoskeleton. Right panel represents myotubes treated with CY-D showing a redistribution of utrophin mRNAs into the free polysomal fraction. (-), negative control lane. The left lane is a 100-bp molecular mass marker. Shown are representative results of a minimum of five independent experiments. Bar, 230  $\mu$ m.

and cytoskeletal-bound polysomes (Fig. 4 C). In these experiments, we verified that the 3-h Cy-D treatment did not affect the overall steady-state levels of utrophin mRNA, thereby demonstrating that the disappearance of utrophin transcripts from the cytoskeletal-bound polysomal fraction could not be ascribed to a change in mRNA stability, and that it was caused by a redistribution of the existing transcripts.

On the other hand, treatment of myotubes with colchicine (COL) failed to induce a redistribution of utrophin transcripts among the distinct pools of polysomes. In these experiments, we did verify by immunofluorescence that the COL treatment had successfully induced the depolymerization of microtubules (unpublished data). Because the results are similar to those observed in control myotubes (Fig. 3), these data indicate that the preferential localization of utrophin mRNAs within the cytoskeletal-bound pool of polysomes does not require intact microtubules.





**Figure 5. Utrophin mRNAs do not preferentially associate with cytoskeletal-bound polysomes in myoblasts.** (A) Representative ethidium bromide-stained agarose gels of PCR products corresponding to utrophin cDNAs obtained from free (F), cytoskeletal-bound (C), and membrane (M)-bound polysomal fractions. The left lane is a 100-bp molecular mass marker. (-), negative control lane. Note the lack of preferential accumulation of utrophin transcripts within the cytoskeletal-bound fraction. (B) Utrophin transcript levels in each polysomal fraction were determined and expressed as a percent of the total. Shown are the results of a minimum of seven independent experiments. (C) Utrophin transcript levels in polysomal fractions were also determined in myotubes treated with agrin and expressed as a percent of the total. Shown are the results of a minimum of four independent experiments.

### Redistribution of utrophin transcripts during myogenic differentiation

Because the association of specific mRNAs with specific subcellular domains may be developmentally regulated (Cripe et al., 1993), and because utrophin expression is moderately increased during myogenic differentiation (Gramolini and Jasmin, 1999), we also determined in separate experiments

the distribution of utrophin transcripts between the three pools of polysomes in myoblasts versus myotubes. As shown in Fig. 5, utrophin mRNAs are clearly not enriched in the cytoskeletal-bound polysomal fraction in myoblasts. By comparison to myotubes (Fig. 3), in which ~65% of all utrophin mRNAs are found within cytoskeletal-bound polysomes, <20% are present in this polysomal fraction in myoblasts. Therefore, these data suggest that the association of utrophin transcripts with cytoskeletal-bound polysomes and actin microfilaments is regulated during myogenic differentiation. In contrast, agrin treatment of myotubes, which is known to induce the formation of AChR clusters that contain other synaptic components (Burden, 1998; Sanes and Lichtmann, 1999) including utrophin (Campanelli et al., 1994; Guo et al., 1996), failed to alter the distribution of utrophin mRNAs amongst the three pools of polysomes (compare Figs. 5 C and 3).

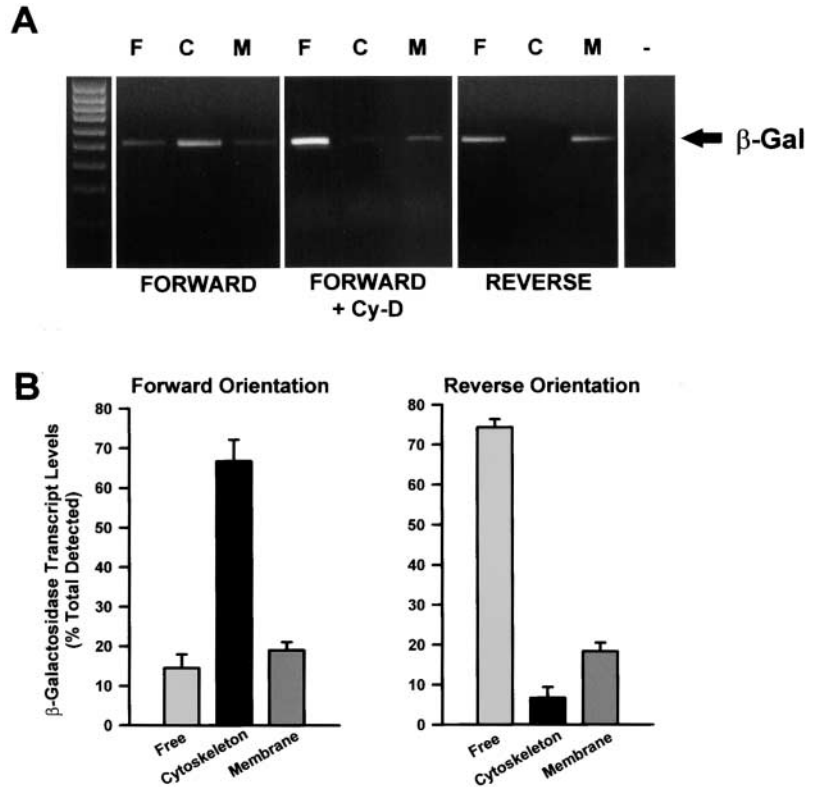
### Role of the 3'UTR in targeting utrophin transcripts to cytoskeletal-bound polysomes

Given that previous studies have indicated that mRNAs associate with the cytoskeleton via their 3'UTR (for review see Veyrune et al., 1997), we next investigated the role of the 3'UTR in the targeting of utrophin transcripts in skeletal muscle. To this end, we isolated the utrophin 3'UTR by PCR and subsequently generated  $\beta$ -galactosidase reporter constructs by inserting the 3'UTR in forward or reverse (used as a control) orientation, downstream of the LacZ gene (see Fig. 7 C). These expression vectors were then transfected into skeletal muscle cells grown in culture. The three distinct polysomal fractions were subsequently isolated and the presence of  $\beta$ -galactosidase transcripts was analyzed in each fraction.

In these experiments, analysis of the various subcellular fractions showed that the utrophin 3'UTR, cloned in the forward orientation, was capable of directing  $\beta$ -galactosidase transcripts to the cytoskeletal pool of polysomes (Fig. 6 A). Quantitative analyses revealed that ~65% of the total content of  $\beta$ -galactosidase transcripts was present within the cytoskeletal-bound polysomal fraction (Fig. 6 B), a value nearly identical to that observed for endogenous utrophin transcripts (Fig. 3 B). In addition, we noted in these experiments that disruption of the actin filament network with Cy-D, led to a redistribution of  $\beta$ -galactosidase transcripts as observed with the endogenous utrophin mRNAs (compare Figs. 4 and 6 A). In contrast to the localization within the cytoskeletal-bound polysomal fraction of  $\beta$ -galactosidase transcripts containing the utrophin 3'UTR in the forward orientation, cultures transfected with  $\beta$ -galactosidase expression constructs containing the 3'UTR in the reverse orientation failed to be targeted to this pool of polysomes (Fig. 6 A). With the reverse orientation construct, we observed that ~75% of all  $\beta$ -galactosidase transcripts were enriched within the free polysomal fraction (Fig. 6 B). This pattern of distribution was also seen with the parental  $\beta$ -galactosidase expression vector that only contains its own 3'UTR (unpublished data). As a control for these experiments, we verified in these myotubes (except for those treated with Cy-D) that endogenous utrophin mRNAs were indeed present within cytoskeletal-bound polysomes. Together, these results indi-

**Figure 6. The 3'UTR of utrophin mRNA targets LacZ transcripts to cytoskeletal-bound polysomes.**

(A) shows representative examples of ethidium bromide-stained agarose gels of  $\beta$ -galactosidase PCR products obtained from free (F), cytoskeletal (C)-, and membrane (M)-bound polysomes following transfections with constructs containing the utrophin 3'UTR in the forward or reverse orientation. (Left) Muscle cultures were transfected with the reporter construct containing the utrophin 3'UTR in the forward orientation. Note that in these myotubes, chimeric transcripts preferentially associate with cytoskeletal-bound polysomes. (Middle) Cultures were treated with Cy-D which disrupts this association as seen with endogenous utrophin mRNAs. (Right)  $\beta$ -galactosidase constructs containing the utrophin 3'UTR in the reverse orientation are not targeted to cytoskeletal-bound polysomes. (B) The levels of  $\beta$ -galactosidase transcripts for each polysomal fraction were determined and expressed as a percentage of the total  $\beta$ -galactosidase mRNA levels detected. Shown are the results obtained from a minimum of five independent experiments.



cate that the 3'UTR is critical in targeting utrophin transcripts to their appropriate subcellular location.

### Domains necessary for targeting utrophin transcripts

Having established that the full-length 3'UTR leads to an association of utrophin mRNAs with cytoskeletal-bound polysomes and actin filaments, we became interested in further characterizing the region(s) within the 3'UTR necessary for this targeting. Therefore, we generated several additional reporter constructs that contained, downstream of the LacZ gene, truncated fragments of the utrophin 3'UTR (Fig. 7 C). These constructs were subsequently transfected into muscle cells, and polysomal fractions were isolated and analyzed for the presence of  $\beta$ -galactosidase transcripts. As illustrated in Fig. 7, A and B, we determined in these experiments that elements contained within nucleotides 969 to 596 account for  $\sim 1/2$  of the localization of chimeric mRNAs to cytoskeletal-bound polysomes. Similarly, the 3'UTR fragment containing nucleotides 596–332 appeared responsible for the remaining targeting effect, as reporter constructs containing the first 332 nucleotides, or less (with constructs 161 and 86) of the 3'UTR, failed to direct  $\beta$ -galactosidase mRNAs to this pool of polysomes. Therefore, a region containing  $>600$  nucleotides appears critical for targeting  $\beta$ -galactosidase transcripts to cytoskeleton-bound polysomes.

### A distinct region in the 3'UTR regulates the stability of utrophin transcripts

In a final series of experiments, we used the same reporter constructs to determine the impact of the utrophin 3'UTR on the stability of  $\beta$ -galactosidase transcripts. For these studies, we transfected muscle cells in culture with the various expression vectors and subsequently exposed the cells to ac-

tinomycin D to inhibit transcription. At different time points thereafter, muscle cell cultures were analysed to determine the levels of  $\beta$ -galactosidase mRNAs. In comparison to parental  $\beta$ -galactosidase mRNAs, which displayed a half-life of  $\sim 4$  h under these conditions, these experiments revealed that the utrophin 3'UTR was capable of conferring a more stable half-life to  $\beta$ -galactosidase transcripts (Fig. 8). Indeed, we determined that the half-life of  $\beta$ -galactosidase transcripts that contained the full-length utrophin 3'UTR was  $\sim 21$  h (Fig. 8), a value similar to that seen recently under similar experimental conditions for endogenous utrophin mRNAs (Gramolini and Jasmin, 1999). Furthermore, we also identified in these experiments a region that appears critical for conferring this relatively stable half-life to  $\beta$ -galactosidase transcripts. Using the different reporter constructs containing different lengths of the utrophin 3'UTR (Fig. 7 C), we determined that constructs 86 and 161 failed to extend the longevity of  $\beta$ -galactosidase mRNAs, whereas the reporter constructs containing the first 332, 596, and 969 nucleotides showed similar half-lives as those seen using the full-length 3'UTR. Therefore, it appears that the element(s) contained within nucleotides from position 161 to 332 in the 3'UTR is necessary to regulate the relatively stable half-life of utrophin transcripts in skeletal muscle cells.

### Discussion

Similar to several other transcripts encoding synaptic proteins in muscle (for review see Duclert and Changeux, 1995; Burden, 1998), utrophin mRNAs display an asymmetric distribution along skeletal muscle fibers as they accumulate preferentially within the postsynaptic sarcoplasm (Gramolini et al., 1997; Vater et al., 1998). Such a pattern of distri-

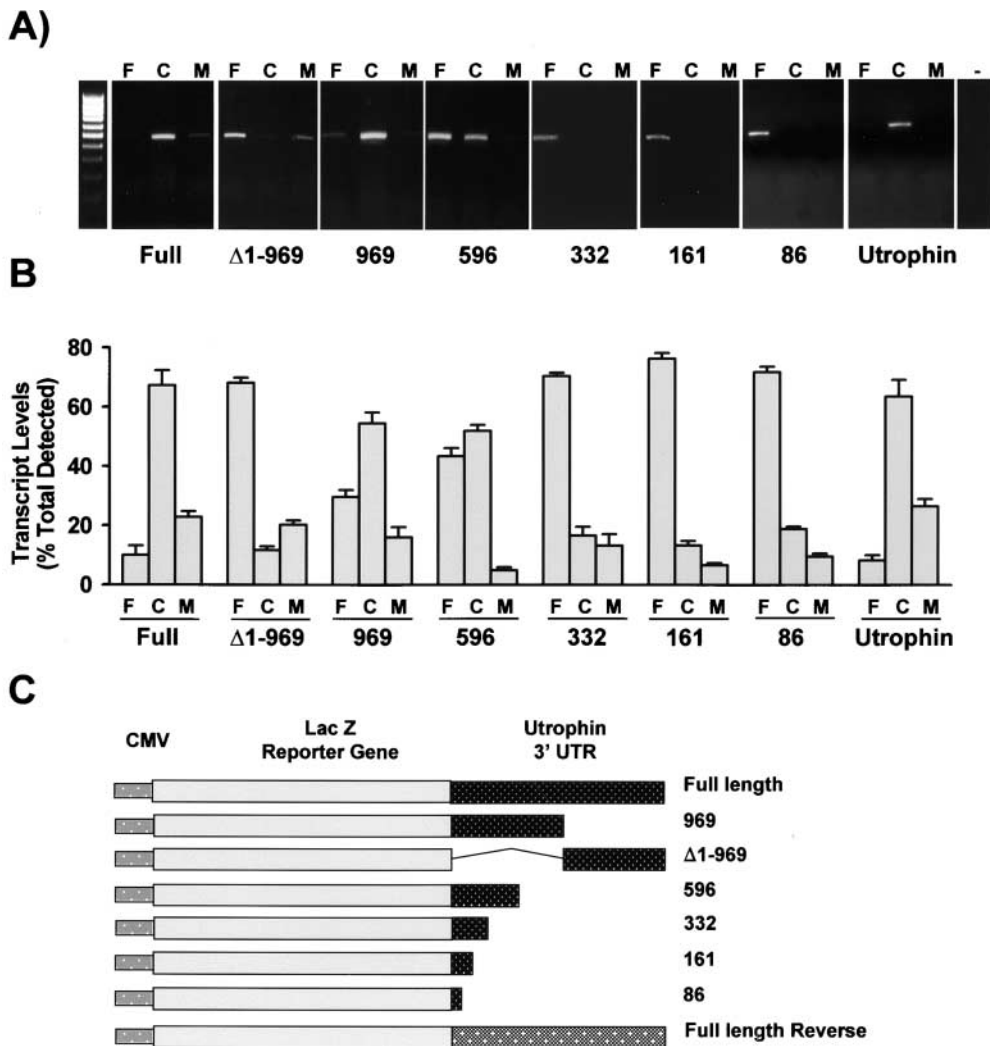
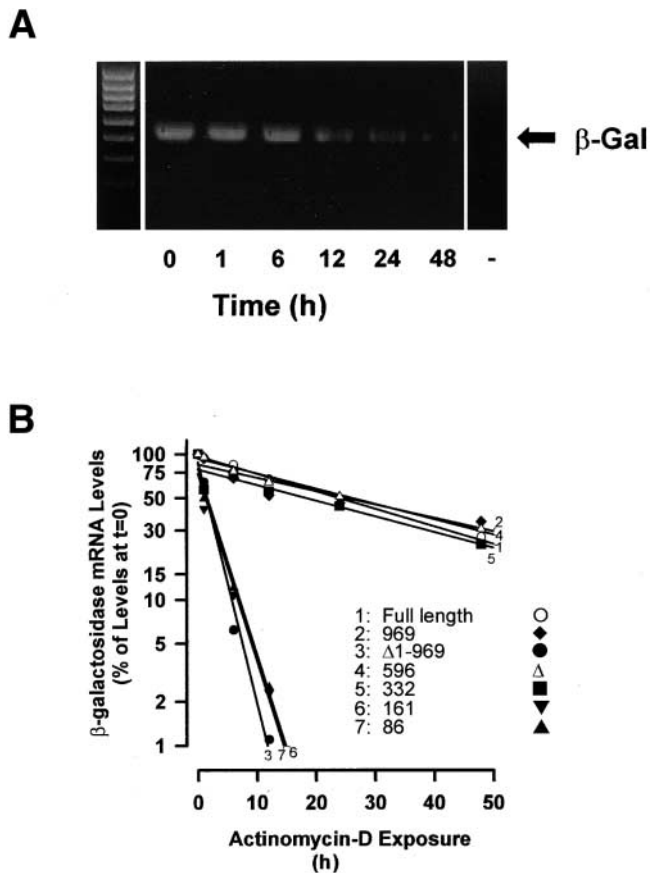


Figure 7. **Targeting domain within the utrophin 3' UTR.** (A) Representative examples of ethidium bromide-stained agarose gels corresponding to  $\beta$ -galactosidase RT-PCR products obtained from free (F), cytoskeletal (C)-, and membrane (M)-bound polysomal fractions after transfections with reporter constructs containing truncated fragments of the 3' UTR. Note that  $\beta$ -galactosidase constructs containing nucleotide sequence 332–596 are still targeted to cytoskeletal-bound polysomes and that this localization is lost with a smaller 3' UTR fragment (332 nt). (B) The levels of  $\beta$ -galactosidase transcripts for each polysomal fraction were determined and expressed as percentage of the total  $\beta$ -galactosidase mRNA levels detected. Shown are representative examples of a minimum of five experiments. (C) shows the reporter constructs used in these studies. The utrophin 3' UTR sequences were inserted downstream of the LacZ gene. Nucleotide positions are denoted on the right.

tribution has been shown to result, at least partially, from the local activation of the utrophin gene in myonuclei located in the vicinity of the postsynaptic apparatus (Gramolini et al., 1997, 1998). However, previous studies using several other experimental systems, have led to the notion that the compartmentalized expression of mRNAs in specific cellular compartments requires their interaction with cytoskeletal elements (Bassell and Singer, 1997; Bassell et al., 1999; Lipshitz and Smibert, 2000). Additionally, it has become apparent that in the cytoplasm, specific mRNAs are localized to a distinct class of polysomes that are attached to cytoskeletal elements rather than localizing to free polysomes (Hesketh, 1996; Bassell and Singer, 1997). Because the postsynaptic sarcoplasm of muscle fibers contains a differentiated set of microtubules (Jasmin et al., 1990) as well as a specialized actin meshwork (Hall et al., 1981), we became interested in determining whether utrophin transcripts were enriched in a

particular subcellular compartment of polysomes through interactions with the cytoskeleton. Using a sequential detergent/salt extraction procedure, we show that in myogenic cells, utrophin mRNAs are concentrated in a pool of cytoskeletal-bound polysomes and that this specific enrichment depends on the integrity of the actin microfilaments. Therefore, it is tempting to speculate that these mechanisms also operate *in vivo* and act to complement the local transcriptional regulation of the utrophin gene in order to ensure the efficient local expression of utrophin mRNAs at the neuromuscular junction.

In our experiments, we also observed that the association of utrophin transcripts with cytoskeletal elements is under developmental influence because, as opposed to our findings with myotubes, utrophin mRNAs were clearly not enriched within the cytoskeletal-bound polysomal fraction in undifferentiated myoblasts. Interestingly, recent studies have indi-



**Figure 8. The utrophin 3'UTR regulates the stability of  $\beta$ -galactosidase transcripts.**  $\beta$ -Galactosidase reporter constructs containing the full-length utrophin 3'UTR were transfected into muscle cells in culture. The stability of  $\beta$ -galactosidase transcripts was determined by exposing cultures to actinomycin D at time zero. Samples were collected at various time points and total RNA was subsequently extracted and subjected to RT-PCR. A shows a representative ethidium bromide-stained agarose gel corresponding to  $\beta$ -galactosidase RT-PCR products. (-), negative lane. (B) Quantitation of these results revealed that the half-life of  $\beta$ -galactosidase transcripts containing the full-length utrophin 3'UTR is  $\sim 22$  h (O; line 1). Similar results were obtained with constructs containing the first 332 nt of the utrophin 3'UTR (lines 2, 4, and 5). Note also that the stability of the chimeric mRNAs was reduced with smaller fragments (lines 6 and 7) or when the region from nt 1 to 969 was absent from the 3'UTR (line 3). Shown are the pooled results from four independent experiments.

cated that other transcripts that are found in association with distinct polysomal fractions are also regulated during myogenic development. For example, transcripts encoding vimentin or the poly (a<sup>+</sup>)-binding protein do not show any association with the cytoskeleton in myoblasts; however, following myogenic differentiation, these transcripts become preferentially localized to the cytoskeleton (Adamou and Bag, 1992; Cripe et al., 1993). Thus, it appears that the subcellular localization of some mRNAs, including utrophin, undergoes profound changes during remodelling of the cytoskeleton which accompanies myogenic differentiation. Consistent with such a mechanism, a recent study has further revealed that actin polymerization during the early stages of synaptogenesis acts as an intracellular scaffold that orchestrates the assembly of the postsynaptic apparatus dur-

ing the formation and growth of the neuromuscular junction (Dai et al., 2000). As a result, it is possible that the sorting of utrophin mRNAs to specific subcellular compartments could in fact play an important role in establishing and maintaining the local synthesis of utrophin at the neuromuscular junction during synapse formation.

Having established that utrophin mRNAs are specifically targeted to a particular subcellular compartment in skeletal muscle cells, we next investigated the mechanism by which these transcripts are separated from those translated on the rough endoplasmic reticulum or free polysomes. We focussed on the 3'UTR as this region is known to contain cis-acting elements that are responsible for directing the intracellular trafficking of various mRNAs (Kim-Ha et al., 1993; Hesketh et al., 1994; Kislauskis et al., 1994; Partridge et al., 1999; Keibler and DesGroseillers, 2000). In our experiments, the ability of the utrophin 3'UTR to redirect the localization of  $\beta$ -galactosidase mRNAs to cytoskeletal-bound polysomes indicates that utrophin transcripts are subject to an active intracellular sorting and targeting process. To characterize more precisely the cis-acting elements involved in this targeting mechanism, we generated several reporter constructs that contain deleted fragments of the utrophin 3'UTR and examined the polysomal association of the chimeric LacZ transcripts. These studies highlighted the crucial contribution of the regions between nucleotides 332 and 969 of the utrophin 3'UTR for the targeting of LacZ mRNAs to cytoskeletal-bound polysomes. A detailed examination of elements contained within this region revealed the presence of several AU-rich regions, including two adjacent ones, that have been shown previously to be necessary for the appropriate targeting of *c-myc* transcripts to cytoskeletal-bound polysomes in fibroblasts (Veyrune et al., 1996). Therefore, it appears likely that these consensus sequences are also critical in regulating the targeting of utrophin transcripts to the cytoskeleton in skeletal muscle cells.

Comparison of the utrophin 3'UTR across species revealed a very high degree of sequence homology, particularly between nucleotides 352 and 583 of the mouse and human sequences (Fig. 1 B). This high level of conservation suggests that this region may indeed be critical for regulating the targeting of utrophin transcript in both mouse and human skeletal muscle. The exact mechanism by which these sequences act to target transcripts to cytoskeletal-bound polysomes remains unknown, but it is likely that specific RNA-binding proteins interact with these cis-acting elements, resulting in the recruitment and targeting of transcripts to the intracellular actin network. As utrophin mRNAs are specifically targeted to cytoskeletal-bound polysomes in myotubes but not in myoblasts, it appears plausible that the abundance of these RNA-binding proteins may vary during myogenic differentiation as to correctly target utrophin transcripts to their appropriate subcellular compartment. Therefore, it will be important in future studies to identify the putative RNA-binding proteins that interact with the utrophin 3'UTR in attempts to further characterize the role of the 3'UTR in the control of utrophin expression. Similarly, it may be interesting to examine whether the 5'UTR and coding sequence also plays a role in targeting utrophin transcripts in muscle cells, although the large size of the coding region may make it difficult to study in its entirety.



It is well established that in addition to directing the subcellular localization of mRNAs, the 3'UTR controls the turnover rate of presynthesized mRNAs through interactions with trans-acting factors and cytoskeletal elements (Bassell and Singer, 1997; Tsai et al., 1997; Veyrune et al., 1997). In recent work, we have shown that the half-life of utrophin transcripts in skeletal muscle cells is  $\sim 20$  h (Gramolini and Jasmin, 1999). In the present study, we determined that specific regions of the utrophin 3'UTR were sufficient to confer a similar and relatively stable half-life to the LacZ transcript. In fact, deletion analyses revealed that nucleotides between position 161 and 332 of the utrophin 3'UTR are important for mediating this effect. Interestingly, this region, responsible for mediating transcript stability, is different than the elements responsible for targeting utrophin transcripts to the cytoskeletal-bound polysomes (nucleotides 332–969; see above). Nonetheless, this observation is entirely consistent with previous studies that have examined the localization and stability of *c-myc* transcripts in fibroblasts (Veyrune et al., 1996). In particular, mutations of specific AU-rich regions in the *c-myc* 3'UTR were shown to disrupt the subcellular targeting of the transcript without affecting mRNA stability (Veyrune et al., 1996). It should also be pointed out that since we were able to confer a relatively stable half-life to the reporter transcripts that was nearly identical ( $\sim 20$  h) to that measured for endogenous utrophin mRNAs under similar conditions (Gramolini and Jasmin, 1999), it appears that the 3'UTR contains most, if not all, the regulatory elements necessary to control the stability of utrophin transcripts in skeletal muscle cells.

Based on utrophin's ability to functionally compensate for the lack of dystrophin in animal models of DMD, a number of studies have examined the regulatory events controlling utrophin expression in skeletal muscle. Until now, these studies have focussed primarily on transcriptional mechanisms (see, for example, Gramolini et al., 1997, 1998, 1999a; Burton et al., 1999; Khurana et al., 1999; Galvagni and Oliviero, 2000). Taken together with our recent findings obtained *in vivo* and demonstrating the importance of mRNA stability in the control of the levels of utrophin and its transcript in slow versus fast muscles (Gramolini et al., 2001), the results of the present study illustrate the key contribution of posttranscriptional events in the overall regulation of utrophin in skeletal muscle cells. Accordingly, these findings provide novel targets, in addition to transcriptional events, for which pharmacological interventions may be envisaged to ultimately increase the endogenous levels of utrophin in DMD muscle fibers.

## Materials and methods

### Generation of utrophin 3'UTR reporter constructs

The full-length utrophin 3'UTR was generated by reverse transcription (RT)-PCR using RNA isolated from C2C12 cells and primers designed against the mouse utrophin sequence (Fig. 1 A; Blake et al., 1995; Guo et al., 1996). The 3'UTR fragment was subsequently inserted downstream of the reporter gene LacZ in the pCMV Sport  $\beta$ -galactosidase expression vector (GIBCO BRL) using available NcoI and EcoRI cloning sites. Additional constructs containing varying lengths of the utrophin 3'UTR (Fig. 7 C) were also generated by PCR amplification. All plasmids were sequenced to verify the identity of the constructs. For both transfection and direct gene transfer experiments, plasmid DNA was prepared using QIAGEN kits.

### Tissue culture and cellular fractionation

Mouse C2C12 muscle cells were cultured, maintained, differentiated, and transfected using calcium phosphate, as described in detail previously (Gramolini et al., 1998). In our studies, myoblasts were examined when they were 50% confluent, whereas myotubes were analyzed after 4 d in differentiation media. Agrin treatment of myotubes was performed as described in Gramolini et al. (1998). For experiments involving the inhibition of RNA synthesis, cultures were incubated with 4  $\mu$ g/ml of actinomycin D in culture media (Tennyson et al., 1996; Gramolini and Jasmin, 1999). Samples were collected for up to 40 h after drug exposure. Unless otherwise specified, all culture reagents were obtained from GIBCO BRL.

The procedure to isolate subcellular fractions was similar to that described by Hesketh et al. (1994) and Hovland et al. (1995). In brief, muscle cells were washed three times with PBS and harvested in 1.0 ml of lysis buffer containing 10 mM Tris, pH 7.6, 0.25 M sucrose, 25 mM KCl, 5 mM MgCl<sub>2</sub>, 0.5 mM CaCl<sub>2</sub>, and 0.5% Nonidet P-40. Lysates were then centrifuged at 1,000 g for 5 min and the supernatant, containing the free polysomal fraction, was removed and stored on ice. To isolate the cytoskeletal-bound polysomal fraction, the pellet was washed in lysis buffer, resuspended in a second lysis buffer that contained 130 mM KCl and 0.5% NP-40, and then incubated for 10 min at 4°C. The extract was centrifuged at 2,000 g for 5 min and the supernatant removed and stored on ice. The membrane-bound polysomal fraction was harvested by incubating at room temperature for 15 min the cell pellet in a third lysis buffer containing 130 mM KCl, 0.5% Nonidet P-40, and 0.5% deoxycholate. This cell suspension was centrifuged at 3,000 g for 5 min and the resulting supernatant, yielding the membrane-bound fraction, was removed and placed on ice. An aliquot of each of the three fractions was taken to measure the activity of LDH using a commercially available kit (Sigma-Aldrich). All fractions were stored at  $-80^{\circ}\text{C}$  for further analysis.

To examine the association of utrophin transcripts with the cytoskeleton, myotube cultures were treated for 3 h, before the collection of subcellular fractions, with compounds known to disrupt the integrity of distinct components of the cytoskeleton. Specifically, myotubes were treated with 2  $\mu$ M Cy-D (Tsakiridis et al., 1994) or 50  $\mu$ M COL (Bassell et al., 1994) to depolymerize actin filaments or the microtubule network, respectively. To verify that these drug treatments had indeed resulted in the depolymerization of microfilaments and microtubules, myotubes were processed for fluorescence experiments using rhodamine-conjugated phalloidin or a monoclonal antibody directed against  $\alpha$ -tubulin (Molecular Probes), respectively.

### RNA extraction and RT-PCR

Total RNA was extracted from muscle cells in culture and from the polysomal fractions using TriPure as recommended by the manufacturer (Boehringer Mannheim). Final RNA pellets were washed twice with 75% ethanol, resuspended in 20  $\mu$ l RNase-free water, and stored at  $-20^{\circ}\text{C}$ . From each stock RNA sample, the RNA was further diluted to a final concentration of 50 ng/ $\mu$ l. 2  $\mu$ l of this final dilution was used for RT-PCR. For cultures transfected with  $\beta$ -galactosidase expression constructs, the RNA samples were treated with RQ DNase I (Promega) at 37°C for 1.5 h and then heated at 65°C for 20 min (Boudreau-Larivière et al., 2000).

RT-PCR was used to determine the relative abundance of transcripts among the different polysomal fractions and was performed as described in detail elsewhere (Jasmin et al., 1995; Gramolini et al., 1998). In brief, RT was performed for 45 min at 42°C using random hexamers, and heated to 99°C for 5 min to terminate the reaction. Utrophin cDNAs were specifically amplified by PCR using primers designed on the basis of the mouse utrophin sequence as described previously (Jasmin et al., 1995; Gramolini et al., 1998). These primers generate a 548-bp fragment. cDNAs encoding the  $\alpha$ -subunit of the AChR were amplified using primers designed on the basis of the mouse sequence (5':5'-GACTATGGAGGAGTGAAAA-3'; and 3':5'-TGGAGGTGGAAGGGATTAGC-3') that generate a 576-bp PCR product. cDNAs encoding  $\beta$ -galactosidase were amplified as described (Boudreau-Larivière et al., 2000). The primers used to amplify  $\beta$ -galactosidase were 5':5'-GTGACGGCAGTTATCTGG-3' and 3':5'-ATGATGCTCGTGACGGTT-3'. These primers generate a 506-bp PCR product. Amplification of the selected cDNAs was performed in a DNA thermal cycler (Perkin Elmer Cetus Co.). Each cycle of amplification consisted of denaturation at 94°C for 1 min, primer annealing at 65°C for 1 min, and extension at 72°C for 1 min. Typically, 26–30 cycles of amplification were performed. In separate experiments, we ascertained that these cycle numbers were within the linear range of amplification. Negative controls consisted of RT mixtures in which total RNA was replaced with RNase-free water.

PCR products were visualized on a 1% agarose gel containing ethidium bromide. The 100-bp molecular mass markers (MBI Fermentas and GIBCO

BRL) were used to estimate the molecular mass of the PCR products. For quantitative PCR experiments, PCR products were separated and visualized on agarose gels containing the fluorescent dye Vista green (Amersham Pharmacia Biotech) as described in Gramolini et al., (1998). The labeling intensity of the PCR product, which is linearly related to the amount of DNA, was subsequently quantitated using a Storm PhosphorImager and the accompanying software (Molecular Dynamics)

We thank John Lunde and Jun Wu for expert technical assistance.

This work was supported by grants from the Association Française Contre les Myopathies, the Muscular Dystrophy Association, the Ontario Neurotrauma Foundation, and the Canadian Institutes of Health Research to B.J. Jasmin. During the course of this work, A.O. Gramolini was supported by a Strategic Area of Development Fellowship from the University of Ottawa (Ottawa, Ontario, Canada), and is now supported by a Canadian Institutes of Health Research Postdoctoral Fellowship. B.J. Jasmin is a Canadian Institutes of Health Research Investigator.

Submitted: 31 January 2001

Revised: 1 August 2001

Accepted: 3 August 2001

## References

- Adamou, J., and J. Bag. 1992. Alteration of translation and stability of mRNA for the poly(A)-binding protein during myogenesis. *Eur. J. Biochem.* 209:803–812.
- Ahn, A.H., and L.M. Kunkel. 1993. The structural and functional diversity of dystrophin. *Nat. Genet.* 3:283–291.
- Bagni, C., L. Mannucci, C.G. Dotti, and F. Amaldi. 2000. Chemical stimulation of synaptosomes modulates  $\alpha$ -Ca<sup>2+</sup>/calmodulin-dependent protein kinase II mRNA association to polysomes. *J. Neurosci.* 20:1–6.
- Bassell, G.J., and R.H. Singer. 1997. mRNA and cytoskeletal filaments. *Curr. Opin. Cell Biol.* 9:109–115.
- Bassell, G.J., R.H. Singer, and K.S. Kosik. 1994. Association of Poly(A) mRNA with microtubules in cultured neurons. *Neuron.* 12:571–582.
- Bassell, G.J., Y. Oleynikov, and R.H. Singer. 1999. The travels of mRNAs through all cells large and small. *FASEB J.* 13:447–454.
- Blake, D.J., J. Schofield, R.A. Zuellig, D.C. Gorecki, S.R. Phelps, E.A. Barnard, Y.H. Edwards, and K.E. Davies. 1995. G-utrophin, the autosomal homologue of dystrophin Dp116, is expressed in sensory ganglia and brain. *Proc. Natl. Acad. Sci. USA.* 92:3697–3701.
- Blake, D.J., J.M. Tinsley, and K.E. Davies. 1996. Utrophin: A structural and functional comparison to dystrophin. *Brain Pathol.* 6:37–47.
- Boudreau-Larivière, C., R.Y.Y. Chan, J. Wu., and B.J. Jasmin. 2000. Molecular mechanisms underlying the activity-linked alterations in acetylcholinesterase mRNAs in developing versus adult rat skeletal muscles. *J. Neurochem.* 74: 2250–2258.
- Bruckenstein, D., P.J. Lein, D. Higgins, and R.T.J. Fremieu. 1990. Distinct spatial localization of specific mRNAs in cultured sympathetic neurons. *Neuron.* 5:809–819.
- Burden, S.J. 1998. The formation of neuromuscular synapses. *Genes Dev.* 12:133–148.
- Burgin, K.E., M.N. Waxman, S. Rickling, S.A. Westgate, W.C. Mobley, and P.T. Kelly. 1990. In situ hybridization histochemistry of Ca<sup>2+</sup>/calmodulin-dependent protein kinase in developing rat brain. *J. Neurosci.* 10:1788–1798.
- Burton, E.A., J.M. Tinsley, P.J. Holzfield, N.R. Rodriguez, and K.E. Davies. 1999. A second promoter provides an alternative target for therapeutic up-regulation of utrophin in Duchenne muscular dystrophy. *Proc. Natl. Acad. Sci. USA.* 96:14025–14030.
- Campanelli, J.T., S.L. Roberds, K.P. Campbell, and R.H. Scheller. 1994. A role for dystrophin-associated glycoproteins and utrophin in agrin-induced AChR clustering. *Cell.* 77:663–674.
- Cripe, L., E. Morris, and A.B. Fulton. 1993. Vimentin mRNA location changes during muscle development. *Proc. Natl. Acad. Sci. USA.* 90:2724–2728.
- Dai, Z., X. Luo, H. Xie, and H.B. Peng. 2000. The actin-driven movement and formation of acetylcholine receptor clusters. *J. Cell Biol.* 150:1321–1334.
- Deconinck, A.E., A.C. Potter, J.M. Tinsley, S.J. Wood, R. Vater, C. Young, L. Metzinger, A. Vincent, C.R. Slater, and K.E. Davies. 1997. Postsynaptic abnormalities at the neuromuscular junctions of utrophin-deficient mice. *J. Cell Biol.* 136:883–894.
- Duclert, A., and J.P. Changeux. 1995. Acetylcholine receptor gene expression at the developing neuromuscular junction. *Physiol. Rev.* 75:339–368.
- Emery, A. 1991. Population frequencies of inherited neuromuscular disorder—A world survey. *Neuromuscul. Disord.* 1:19–29.
- Forristall, C., M.D. Pondel, L. Chen, and M.L. King. 1995. Patterns of localization and cytoskeletal association of two vegetally localized RNAs, Vg1 and Xcat-2. *Development.* 121:201–208.
- Galvagni, F., and S. Oliviero. 2000. Utrophin transcription is activated by an intronic enhancer. *J. Biol. Chem.* 275:3168–3172.
- Grady, R.M., J.P. Merlie, and J.R. Sanes. 1997. Subtle neuromuscular defects in utrophin-deficient mice. *J. Cell Biol.* 136:871–882.
- Gramolini, A.O., and B.J. Jasmin. 1999. Regulation of utrophin expression during myogenic differentiation. *Nucleic Acids Res.* 27:3603–3609.
- Gramolini, A.O., C.L. Dennis, J.M. Tinsley, G.S. Roberston, J. Cartaud, K.E. Davies, and B.J. Jasmin. 1997. Local transcriptional control of utrophin expression at the neuromuscular synapse. *J. Biol. Chem.* 272:8117–8120.
- Gramolini, A.O., E.A. Burton, J.M. Tinsley, M.J. Ferns, A. Cartaud, J. Cartaud, K.E. Davies, J.A. Lunde, and B.J. Jasmin. 1998. Muscle and neural isoforms of agrin increase utrophin expression in cultured myotubes via a transcriptional regulatory mechanism. *J. Biol. Chem.* 273:736–743.
- Gramolini, A.O., L.A. Angus, L. Schaeffer, E.A. Burton, J.M. Tinsley, K.E. Davies, J.P. Changeux, and B.J. Jasmin. 1999a. Induction of utrophin gene expression by heregulin in skeletal muscle cells: Role of the N-box motif and GA-binding protein. *Proc. Natl. Acad. Sci. USA.* 96:3223–3227.
- Gramolini, A.O., G. Karpati, and B.J. Jasmin. 1999b. Discordant expression of utrophin and its transcript in human and mouse skeletal muscles. *J. Neuro-pathol. Exp. Neurol.* 58:235–244.
- Gramolini, A.O., J. Wu, and B.J. Jasmin. 2000. Regulation and functional significance of utrophin expression at the mammalian neuromuscular synapse. *Microsc. Res. Tech.* 49:90–100.
- Gramolini, A.O., G. Bélanger, J. Thompson, J.V. Chakkalakal, and B.J. Jasmin. 2001. Increased expression of utrophin in slow vs fast muscles involves post-transcriptional mechanisms acting through the 3'UTR. *Am. J. Physiol. Cell Physiol.* 281:C1300–C1309.
- Guo, W.X., M. Nichol, and J.P. Merlie. 1996. Cloning and expression of full length mouse utrophin: The differential association of utrophin and dystrophin with AChR clusters. *FEBS Lett.* 398:259–264.
- Hall, Z.W., B.W. Lubit, and J.H. Schwartz. 1981. Cytoplasmic actin in postsynaptic structures at the neuromuscular junction. *J. Cell Biol.* 90:789–792.
- Hazlerigg, T. 1998. The destinies and destinations of RNAs. *Cell.* 95:451–460.
- Hesketh, J. 1996. Sorting of messenger RNAs in the cytoplasm mRNA localization and the cytoskeleton. *Exp. Cell Res.* 225:219–236.
- Hesketh, J., G. Campbell, M. Piechaczek, and J.M. Blanchard. 1994. Targeting of c-myc and  $\beta$ -globin coding sequences to cytoskeletal-bound polysomes by c-myc 3' untranslated region. *Biochem. J.* 298:143–148.
- Hovland, R., G. Campbell, I. Pryme, and J. Hesketh. 1995. The mRNAs for cyclin A, c-myc, and ribosomal proteins L4 and S6 are associated with cytoskeletal-bound polysomes in HepG2 cells. *Biochem. J.* 310:193–196.
- Hovland, R., J.E. Hesketh, and I.F. Pryme. 1996. The compartmentalization of protein synthesis: Importance of cytoskeleton and role in mRNA targeting. *Int. J. Biochem. Cell Biol.* 28:1089–1105.
- Jansen, R.P. 2001. mRNA localization: message on the move. *Nat. Cell Biol.* 4:247–256.
- Jasmin, B.J., J.-P. Changeux, and J. Cartaud. 1990. Compartmentalization of cold-stable and acetylated microtubules in the subsynaptic domain of chick skeletal muscle fibre. *Nature.* 344:673–675.
- Jasmin, B.J., H. Alameddine, J.A. Lunde, F. Stetzkowski-Marden, H. Collin, J.M. Tinsley, K.E. Davies, F.M.S. Tome, D.J. Parry, and J. Cartaud. 1995. Expression of utrophin and its mRNA in denervated *mdx* mouse muscle. *FEBS Lett.* 374:393–398.
- Khurana, T.S., A.G. Rosmarin, J. Shang, T.O.B. Krag, S. Das, and S. Gammeltoft. 1999. Activation of utrophin promoter by heregulin via the ets-related transcription factor complex GA-binding protein  $\alpha/\beta$ . *Mol. Biol. Cell.* 10:2075–2086.
- Kim-Ha, J., P. Webster, J. Smith, and P. MacDonald. 1993. Multiple RNA regulatory elements mediate distinct steps in localization of oskar mRNA. *Development.* 119:169–178.
- Keibler, M.A., and L. DesGroseillers. 2000. Molecular insights into mRNA transport and local translation in the mammalian nervous system. *Neuron.* 25: 19–28.
- Kislauskis, E.H., X. Zhu, and R.H. Singer. 1994. Sequences responsible for intracellular localization of  $\beta$ -actin messenger RNA also affect cell phenotype. *J. Cell Biol.* 127:441–451.
- Lipshitz, H.D., and C.A. Smibert. 2000. Mechanisms of RNA localization and translational regulation. *Curr. Opin. Genet. Dev.* 10:476–488.

- Love, D.R., D.F. Hill, G. Dickson, N.K. Spurr, B.C. Byth, R.F. Marsden, F.S. Walsh, Y.H. Edwards, and K.E. Davies. 1989. An autosomal transcript in skeletal muscle with homology to dystrophin. *Nature*. 339:55–58.
- Mahon, P., J. Beattie, A. Glover, and J. Hesketh. 1995. Localisation of metallothionein isoforms mRNAs in rat hepatoma (H4) cells. *FEBS Lett.* 373:76–80.
- Matsumura, K., and K.P. Campbell. 1994. Dystrophin-associated complex: Its role in the molecular pathogenesis of muscular dystrophies. *Muscle Nerve*. 17:2–15.
- Matsumura, K., J.M. Ervasti, K. Ohlendieck S.D. Kahl, and K.P. Campbell. 1992. Association of dystrophin-related protein with dystrophin-associated proteins in mdx mouse muscle. *Nature*. 360: 588–591.
- Mori Y., K. Imaizumi, T. Katayama, T. Yoneda, and M. Tohyama. 2000. Two cis-acting elements in the 3' untranslated region of alpha-CaMKII regulate its dendritic targeting. *Nat. Neurosci.* 3:1079–1084.
- Partridge, K.A., A. Johannessen, A. Tauler, I.F. Pryme, and J.E. Hesketh. 1999. Competition between the signal sequence and a 3'UTR localisation signal during redirection of beta-globin mRNA to the endoplasmic reticulum: Implications for biotechnology. *Cytotechnology*. 30:37–47.
- Pondel, M.D., and M.L. King. 1988. Localized maternal mRNA related to transforming growth factor beta mRNA is concentrated in a cyokeratin-enriched fraction from *Xenopus* oocytes. *Proc. Natl. Acad. Sci. USA*. 85:7612–7616.
- Sanes, J.R., and J.W. Lichtmann. 1999. Development of the vertebrate neuromuscular junction. *Annu. Rev. Neurosci.* 22:389–442.
- Sigrist, S.J., P.R. Thiel, D.F. Reiff, P.E.D. Lachance, P. Lasko, and C.M. Schuster. 2000. Postsynaptic translation affects the efficacy and morphology of neuromuscular junctions. *Nature*. 405:1062–1065.
- St Johnston, D. 1995. The intracellular localization of messenger RNAs. *Cell*. 81: 161–170.
- Tennyson, C.N., Q.W. Shi, and R.G. Worton. 1996. Stability of the human dystrophin transcript in muscle. *Nucleic Acids Res.* 24:3059–3064.
- Tinsley, J.M., D.J. Blake, A. Roche, U. Fairbrother, J. Riss, B.C. Byth, A.E. Knight, J. Kendrick-Jones, G.K. Suthers, D.R. Love, Y.H. Edwards, and K.E. Davies. 1992. Primary structure of dystrophin-related protein. *Nature*. 360:591–593.
- Tinsley, J.M., A.C. Potter, S.R. Phelps, R. Fisher, J.I. Trickett, and K.E. Davies. 1996. Amelioration of the dystrophic phenotype of mdx mice using a truncated utrophin transgene. *Nature*. 384:349–353.
- Tsai, K.C., V.V. Cansino, D.T. Kohn, R.L. Neve, and N.I. Perrone-Bizzozero. 1997. Post-transcriptional regulation of the GAP-43 gene by specific sequences in the 3' untranslated region of the mRNA. *J. Neurosci.* 17:1950–1958.
- Tsakiridis, T., M. Vranic, and A. Klip. 1994. Disassembly of the actin network inhibits insulin-dependent stimulation of glucose transport and prevents recruitment of glucose transporters to the plasma membrane. *J. Biol. Chem.* 269:29934–29942.
- Vater, R., C. Young, L.V.B. Anderson, S. Lindsay, D.J. Blake, K.E. Davies, R.A. Zuellig, and C.R. Slater. 1998. Utrophin mRNA expression in muscle is not restricted to the neuromuscular junction. *Mol. Cell. Neurosci.* 10:229–242.
- Vedeler, A., I. Pryme, and J. Hesketh. 1991. The characterization of free, cytoskeletal and membrane-bound polysomes in Krebs II ascites and 3T3 cells. *Mol. Cell. Biochem.* 100:183–193.
- Veyrune, J.-L., G.P. Campbell, J. Wiseman, J.-M. Blanchard, and J. Hesketh. 1996. A localisation signal in the 3' untranslated regions of c-myc mRNA targets c-myc mRNA and  $\beta$ -globin reporter sequences to the perinuclear cytoplasm and cytoskeletal-bound polysomes. *J. Cell Sci.* 109:1185–1194.
- Veyrune, J.-L., J. Hesketh, and J.-M. Blanchard. 1997. 3' untranslated regions of c-myc and c-fos mRNAs: multifunctional elements regulating mRNA translation, degradation and subcellular localization. *In Progress in Molecular and Subcellular Biology*. P. Jeanteur, editor. Springer-Verlag, Berlin. 35–63.
- Worton, R. 1995. Muscular dystrophies: diseases of the dystrophin-glycoprotein complex. *Science*. 270:755–760.