

Molecular Cloning and Developmental Expression of the Rat Cardiac-Specific Isoform of Troponin I

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A. F. MARTIN AND J. ORLOWSKI. Molecular Cloning and Developmental Expression of the Rat Cardiac-Specific Isoform of Troponin I. *Journal of Molecular and Cellular Cardiology* (1991) 23, 583-588. Troponin I is the subunit of the troponin complex in striated muscle which inhibits actomyosin ATPase activity. We have isolated a full-length cDNA clone for rat cardiac troponin I and determined its nucleic acid sequence. The amino acid sequence deduced from this clone shows 88%-92% similarity with previously reported amino acid sequences for rabbit (Wilkinson and Grand, 1978) and bovine (Leszyk *et al.*) cardiac troponin I. Examination of cardiac troponin I mRNA abundance during development revealed a 15-fold induction in its expression in the adult heart compared to that in embryonic (14 day) heart muscle. Furthermore, expression of cardiac troponin I mRNA was restricted to heart muscle and was not detected in skeletal muscle at any developmental stage.

KEY WORDS: Troponin I; Cardiac; cDNA clone; mRNA; Developmental expression.

Introduction

Troponin I is a component of the troponin complex, which with tropomyosin, plays a central role in the calcium dependent regulation of myosin and actin interaction in striated muscle. Three tissue specific isoforms of troponin I with different functional properties have been identified in fast and slow skeletal muscle and cardiac muscle by amino acid sequencing (Wilkinson and Grand, 1978). Analysis of sequence diversity indicates that these tissue specific isoforms of troponin I are the products of different genes. The amino acid sequences of rabbit (Wilkinson and Grand, 1978) and bovine (Leszyk *et al.*, 1988) cardiac troponin I differ from that of skeletal troponin I in that they contain an additional 26-33 amino acids at the amino terminus of the protein. A serine residue in the amino terminal region of rabbit cardiac troponin I (ser 20) has been shown to be phosphorylated in the intact heart by cAMP dependent protein kinase in response to β -adrenergic stimulation (England, 1976; Moir *et al.*, 1980). An increase in the phosphorylation of troponin I at serine 20 can be

correlated with the increased contractile force observed in response to inotropic agents (Moir *et al.*, 1980). This suggests that phosphorylation of troponin I at this site may be involved in the modulation of contractile function in cardiac muscle.

The gene for avian fast skeletal troponin I, from quail (Baldwin *et al.*, 1985) and chicken (Nikovits *et al.*, 1986) has been isolated and sequenced. Recently, the nucleotide sequences of cDNAs encoding mouse fast skeletal troponin I and rat slow skeletal troponin I have been reported (Koppe *et al.*, 1989). We report here the isolation and nucleotide sequence determination of a cDNA for the rodent cardiac troponin I and its mRNA expression during the development of the heart.

Materials and Methods

Screening of a cDNA library and sequencing of clones

A rat heart λ gt11 library was purchased from Clontech (Palo Alto, CA, USA0. 1×10^6

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plaques were screened using standard screening techniques (Maniatis *et al.*, 1982) with a 20 base oligonucleotide, containing 3 deoxyinosine substitutions (5' C-A-(A,G)-G-T-(I,C)-A-A(A,G)-A-A-I-G-A-I-G-A-(T,C)-A-C 3'), synthesized to a conserved amino acid sequence (GlnValLysLysGluAspThr) at the carboxyl terminus of troponin I. Hybridization of the filters with the end-labeled oligonucleotide probe was performed using conditions described by Boyd *et al.* (1984). Positive clones were identified and plaque purified. One of these clones, Tn2C, encompassing the entire coding region of the TnI, was subcloned into the plasmid vector IBI30 (International Biotechnologies Inc.). Sequencing was performed by the dideoxynucleotide chain termination method (Sanger *et al.*, 1977) utilizing the T7 polymerase (Pharmacia) reagent kit. Oligonucleotides to IBI30 sequence adjacent to the cloning site were used to obtain initial sequence in both directions. Four additional oligonucleotides, synthesized to the internal sequence of the Tn2C clone as it was obtained, were used to complete the sequence of both strands of the TnI cDNA. Sequence comparisons were performed by the DNAnalyze program (Wernke and Thompson, 1989).

RNA preparation, electrophoresis and hybridization

Total cellular RNA was isolated by the procedure of Chomczynski and Sacchi (1987). RNA samples (10 µg each) were denatured with formaldehyde, fractionated on 1.2% formaldehyde-agarose gels (Fig. 2) or denatured with glyoxal and fractionated on 1% agarose gels (Fig. 3) and transferred onto Nytran membranes (Schleicher and Schuell). The filters were baked, prehybridized and hybridized with the oligo-labeled (Feinberg and Vogelstein, 1983) troponin I cDNA (Tn2C, 0.72 Kb) according to the manufacturer's protocol. The filters were washed in $0.1 \times \text{SSC}$ (SSC is 150 mM NaCl, 15 mM $\text{Na}_3\text{C}_6\text{H}_5\text{O}_7$), 0.1% SDS at 50°C for 1–2 h. As a check to confirm that equal amounts of RNA (10 µg) were loaded in each lane, the blots were probed with a 30-mer oligonucleotide corresponding to rat 18 S ribosomal RNA. Only blots which showed approxi-

mately equal amount of RNA in all lanes were used in this study.

Results

Several positive clones were obtained from our screening of the $\lambda\text{gt}11$ rat heart library with an oligonucleotide made to a conserved amino acid sequence at the carboxyl terminus of troponin I. The complete nucleotide sequence and its deduced amino acid sequence of one of these clones, Tn2C, is given in Figure 1. This cDNA consisted of 633 nts of coding sequence, 54 nts of 5' untranslated sequence and 62 nts of 3' untranslated sequence. Although there is no upstream stop codon in this reading frame, we selected the first ATG codon as the translation initiation site because of the extensive homology of the deduced amino acid sequence with the amino acid sequence of bovine (Leszyk *et al.*, 1988) cardiac troponin I (92%) and rabbit (Wilkinson and Grand, 1978) cardiac troponin I (88%). Comparison of the deduced amino acid sequence of rat cardiac troponin I with the amino acid sequences of fast and slow skeletal troponin I indicated a 57% similarity to fast skeletal troponin I and a 64% similarity with slow skeletal troponin I.

Analysis of the expression of mRNA for cardiac troponin I on Northern blots (Fig. 2) demonstrates that cardiac troponin I mRNA is expressed specifically in cardiac muscle as an approximately 950 bp transcript. Cross hybridization of the cardiac troponin I cDNA was not seen with RNA from fast or slow skeletal muscle on Northern blots (Fig. 2), even under conditions of relatively low stringency ($2 \times \text{SSC}$, 37°C). We have also examined the expression of cardiac troponin I mRNA at various stages of development in cardiac and skeletal muscle (Fig. 3). Cardiac troponin I mRNA is present in 14 day embryonic hearts at low levels and shows a continuous increase in the level of expression with age. The level of expression of cardiac troponin I mRNA shows an approximately 10-fold induction by 25 days post birth and continues to increase up to 55 days at which time an approximately 15-fold increase is observed relative to levels at 14 days gestation as estimated by densitometry. Expression of cardiac troponin I mRNA was not observed in skeletal muscle at any stage of development.

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CTTC TAAGACCCCTC CAGGAATCTG CAATCCCATT CTCTACCTCT GGAGATCAGC
      10      20
MetAlaAspGluSerSerAspSerAlaGlyGluProGlnProAlaProAlaProValArg
ATGGCGGACGAGAGCAGCGATTCTGGCTGGGGAACCCAGCCGGCGCTGCTCTGTCCGA
      30      40
ArgArgSerSerAlaAsnTyrArgAlaTyrAlaThrGluProHisAlaLysLysLysSer
CGTCGCTCCTCGGCCAACTACCGAGCCTATGCCACCGAGCCACATGCCAAGAAAAGTCT
      50      60
LysIleSerAlaSerArgLysLeuGlnLeuLysThrLeuMetLeuGlnIleAlaLysGln
AAGATCTCCGCCTCCAGAAAATTCTAGTTGAGAGCTCTGATGCTGCAGATTGCGAGCAG
      70      80
GluMetGluArgGluAlaGluGluArgArgGlyGluLysGlyArgValLeuSerThrArg
GAGATGGAGCGTGAGGCAGAGGAGCGACGTGGAGAGAGGGCCGCTTCTGAGCACCGCT
      90     100
CysGlnProLeuValLeuAspGlyLeuGlyPheGluGluLeuGlnAspLeuCysArgGln
TGCCAGCCCTTGGTGTGGATGGGCTGGGCTTTGAGAGCTTCAGGACCTATGCCGGCAG
     110     120
LeuHisAlaArgValAspLysValAspGluGluArgTyrAspValGluAlaLysValThr
CTTCACGCTCGTGTGGACAAAGTGGATGAAGAGAGATACGACGTGGAGCAAAAGTCACC
     130     140
LysAsnIleThrGluIleAlaAspLeuThrGlnLysIleTyrAspLeuArgGlyLysPhe
AAGAACATCACTGAGATTGCAGATCTGACCCAGAAGATCTATGACCTGCGTGCCAGTTT
     150     160
LysArgProThrLeuArgArgValArgIleSerAlaAspAlaMetMetGlnAlaLeuLeu
AAGCGGCCCACTCTCCGAGAGTGAGATCTCGGCAGATGCCATGATGCAGGCACTACTG
     170     180
GlyThrArgAlaLysGluSerLeuAspLeuArgAlaHisLeuLysGlnValLysLysGlu
GGGACCCGGGCCAAGGAATCCTTGGACCTGAGGGCCACCTCAAGCAGGTGAAGAGGGAG
     190     200
AspThrGluLysGluAsnArgGluValGlyAspTrpArgLysAsnIleAspAlaLeuSer
GACACTGAGAAGGAACCGGGAGGTGGGAGACTGGCGCAAGATATCGATGCACTAAGT
     210
GlyMetGluGlyArgLysLysLysPheGluGly--*
GGAAATGGAGGCCGAAGAAAAAGTTTGAGGGCTGA GCCCATGGCT CTCACACTGT
GCTCTGAAGG GCATCTCTGA GGATAAATT TCTTTAACT GGAAAAAATA
AAAAAAAAAA AAAAAAACgg aattc

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FIGURE 1. The complete cDNA sequence for rat cardiac troponin I. The bottom line is the nucleic acid sequence and the top line is the deduced amino acid sequence. Numbers refer to the amino acid sequence. The star indicates the termination codon and the polyadenylation sequence is underlined. The bars indicate amino acid sequences conserved in all published amino acid sequences for cardiac (Wilkinson and Grand, 1978, Leszyk *et al.*, 1988), slow skeletal (Wilkinson and Grand, 1978, Koppe *et al.*, 1989) and fast skeletal troponin I (Wilkinson and Grand, 1978, Baldwin *et al.*, 1985, Nikovits *et al.*, 1986, Koppe *et al.*, 1989).

Discussion

This paper describes the nucleotide and amino acid sequence of rodent cardiac troponin I and its mRNA expression during the development of the heart. Several of the functional domains of troponin I have been identified by a number of groups using a variety of experimental approaches (see Leavis and Gergely, 1984 and Zot and Potter, 1987 for reviews). Using the amino acid residue numbers for the rat cardiac troponin I sequence, the region of troponin I encompassing residues 128–149 has been shown to inhibit actomyosin ATPase and to contain the actin binding site and a calcium dependent troponin C binding site (Syska *et al.*, 1976, and

Van Eyk and Hodges, 1988). Leszyk *et al.* (1988) have compared the amino acid sequences of cardiac, fast and slow skeletal troponin I and demonstrated that this region is highly conserved. Several other regions of homology at the carboxyl terminus, residues 177–185, 189–195 and 200–207 in rat cardiac troponin I (Fig. 1), are completely conserved in all known sequences of troponin I although their precise function has not been defined.

A comparison of the amino acid sequence at the amino terminal cardiac specific region of troponin I of rat, bovine and rabbit cardiac troponin I is given in Figure 4. Fifty per cent of the variable amino acid residues between cardiac troponin Is occur in this region. the

functional significance of the additional amino acids present at the amino terminus of cardiac troponin I is postulated to reside in the rapid phosphorylation of serine 23,24 by cAMP dependent protein kinase in the intact heart in response to inotropic agents that increase cAMP (England, 1976; Moir *et al.*, 1980). Phosphorylation of troponin I at this site has been shown to modify the affinity of the Ca^{2+} specific site of cardiac troponin C in the troponin complex for calcium (Robertson *et al.*, 1982). Thus it is postulated that troponin I phosphorylation which occurs in response to β -adrenergic stimulation in beating hearts may be responsible for the increased rate of

relaxation seen following this inotropic intervention. As shown in Figure 4 the sequence of the phosphorylation site in rat cardiac troponin I is similar to that of bovine cardiac troponin I (Leszyk *et al.*, 1988) and contains two serines (residues 23,24) whereas rabbit cardiac troponin I has only one serine (residue 20) in this region. In the serine containing peptide isolated from bovine heart (Swiderek *et al.*, 1988) both serine residues were found to be phosphorylated although the first, residue 23, was phosphorylated to a lesser extent than the second serine. The extent to which one or both serine residues are phosphorylated in response to β -adrenergic stimulation in the heart remains to be determined.

A number of developmentally regulated transitions in the expression of isoforms of the contractile proteins in cardiac tissue have been reported (Swynghedauw, 1986; Wade and Kedes, 1989). For rodent troponin I, recent studies using immunological techniques have indicated that two antigenically distinct isoforms of troponin I are expressed in a temporal manner during cardiac development (Sabry and Dhoot, 1989; Saggin *et al.*, 1989). The slow skeletal isoform of troponin I predominates in fetal heart and is replaced gradually by the cardiac isoform in the adult. These results are consistent with our findings of low mRNA levels for the cardiac troponin I in fetal heart, increasing approximately 15-fold upon reaching adulthood. This developmental induction of cardiac troponin I mRNA expression indicates that a pretranslational mechanism plays a significant role in determining the isoform composition of troponin I in the heart. However, the molecular signals responsible for altering the expression of the troponin I isoforms in heart muscle are not known. The time course of troponin I isoform switching is similar to the transitions observed for the α - and β -myosin heavy chain isoforms in rat heart (Hoh *et al.*, 1978; Lompre *et al.*, 1981). Substantial evidence from *in vivo* and *in vitro* studies has implicated thyroid hormone as the primary physiological modulator for the inverse regulation of these genes (Hoh *et al.*, 1978; Martin *et al.*, 1982; Chizzonite and Zak, 1984; Gustafson *et al.*, 1987; Izume *et al.*, 1986). Thus, it is possible that thyroid hormone may also be a modulator of cardiac troponin I isoform expression, although this remains to be tested.

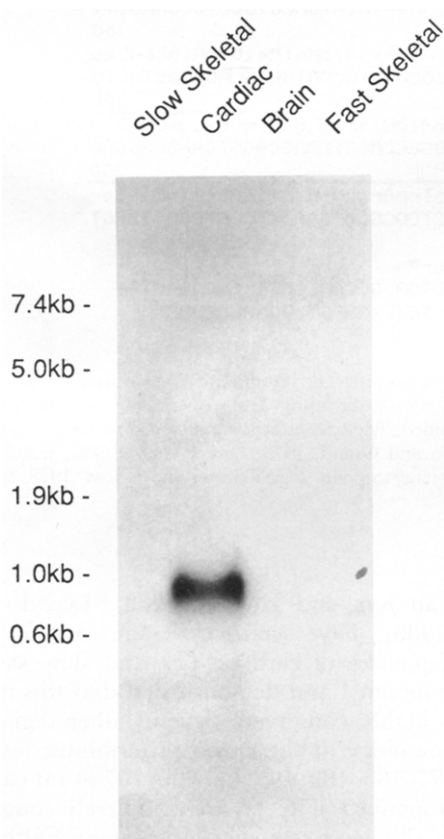
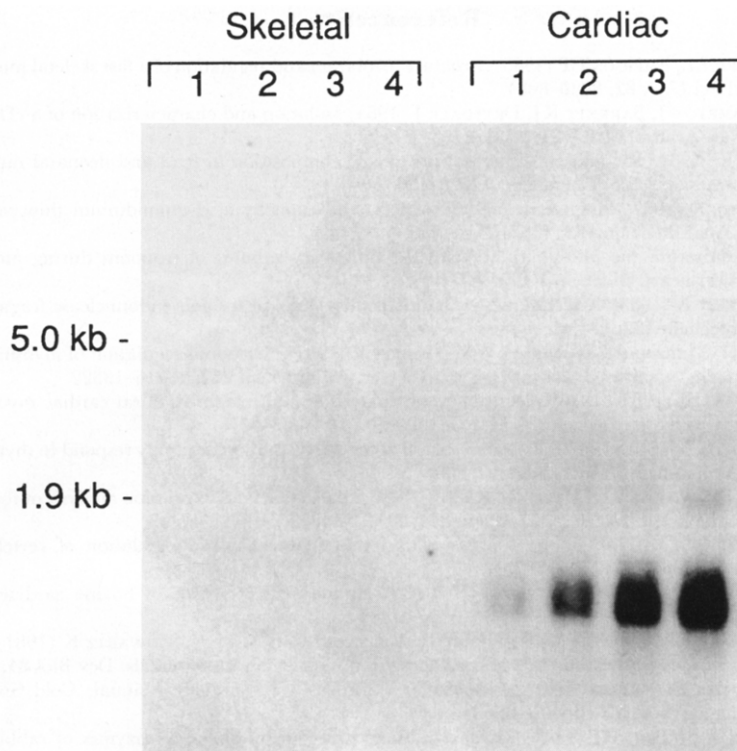


FIGURE 2. Northern blot analysis of RNA from rat slow skeletal (soleus), cardiac and fast skeletal (white vastus lateralis) muscles and rat brain. The total RNA (10 μg) was fractionated on a formaldehyde-agarose gel and transferred to a Nytran filter. The blots were hybridized with the full-length (0.72 kb) [^{32}P]-labeled troponin I cDNA (Tn2C). The autoradiogram shown was exposed to the blot for a 12 h period.



RABBIT A l a A s p G l u S e r A r g A s p A l a A l a G l y G l u A l a L y s P r o A l a P r o A l a
RAT A l a A s p G l u S e r S e r A s p S e r A l a G l y G l u P r o G l n P r o A l a P r o A l a
BOVINE A l a A s p A r g S e r G l y G l y S e r T h r A l a G l y A s p T h r V a l P r o A l a P r o P r o
 * * * * * * *

RABBIT * * * * * * 30
 V a l A r g A r g S e r A s p A r g A l a T y r A l a T h r G l u
RAT P r o V a l A r g A r g A r g S e r S e r A l a A s n T y r A r g A l a T y r A l a T h r G l u
BOVINE P r o V a l A r g A r g A r g S e r S e r A l a A s n T u r A r g A l a T u r A l a T h r G l u

FIGURE 4. Comparison of the deduced amino acid sequence of the cardiac specific amino terminal region of rat cardiac troponin I with that of rabbit (Wilkinson and Grand, 1979) and bovine (Leszyk *et al.*, 1988) cardiac troponin I. Stars indicate differences from the rat cardiac troponin I sequence. Blank spaces denote amino acid deletions.

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