

Structure and expression of rat muscle-specific enolase gene

Kenji Sakimura¹, Etsuko Kushiya¹, Yuka Ohshima-Ichimura², Hiromi Mitsui^{2,*} and Yasuo Takahashi¹

¹Department of Neuropharmacology, Brain Research Institute and ²Department of Biology, Faculty of Science, Niigata University, Niigata 951, Japan

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The structure of rat muscle-specific enolase ($\beta\beta$ enolase) gene was determined. It comprises 12 exons of various lengths (59–223 bp) spanning about 6 kbp and its exon–intron organization is similar to that of neuron-specific enolase ($\gamma\gamma$ enolase) gene. A transcriptional start site was identified by a combination of S1 nuclease mapping and primer extension analyses. In the 5'-flanking region we found a TATA-box-like sequence and several MyoD-binding motifs. The in vitro cell free transcription of the truncated genomic DNA fragment using HeLa cell extract showed that the transcription start site has been correctly identified and the promoter sequences work well.

Gene; Exon; Intron; Enolase; Transcription; Muscle

1. INTRODUCTION

The $\beta\beta$ isozyme of enolase (2-phospho-D-glycerate hydrolase, EC 3.2.1.11), a glycolytic enzyme, is present in mature muscle and known as muscle-specific enolase (MSE). A switch-over from non-neuronal enolase (NNE; $\alpha\alpha$ enolase) to MSE occurs during the final stage of cell differentiation and the amounts of MSE increase with the functional maturation of myotubes.

We previously cloned cDNA for rat NNE, neuron-specific enolase (NSE; $\gamma\gamma$ enolase) and MSE and determined their nucleotide sequences [1–3]. We have also isolated a genomic clone coding for rat NSE, elucidated its structural organization and studied its expression [4]. After we published a paper on MSE cDNA [1], Lamandé et al. reported a similar result [5]. In this paper, we describe the isolation of a genomic clone coding for rat MSE, the exon–intron organization and the expression of this gene in a cell-free transcription system.

2. MATERIALS AND METHODS

A rat genomic library was kindly provided by Dr J. Bonner. Two DNA fragments from cDNA for rat MSE (M 35) labeled with [α -³²P] α CTP by nick translation or random primed labelling, were used as the probes. The genomic library was screened by the plaque-hybridization technique of Benton-Davis using the probes [6]. The DNA inserts of positive clones were subcloned into pUC8 or pUC118 vectors. Restriction maps generated by digestion with appropriate

restriction enzymes and Southern blot hybridization analyses revealed the DNA fragments containing exons. Nucleotide sequences were determined by the method of Maxam-Gilbert [7] and dideoxy-sequencing method [8]. In order to determine the transcription initiation site, primer extension and S1 nuclease mapping analyses were carried out as described previously [4].

Preparation of the HeLa cell extract and in vitro transcription of MSE gene in this cell extract were performed by the procedure of Manley et al. [4,9]. Plasmid pMX1-4 as a template contained 1781 bp, 642 bp, 331 bp or 180 bp of the 5'-flanking region, exon 1, intron 1 and a portion of exon 2, of MSE gene. Each DNA template added was truncated at a unique restriction site (*Nco*I). Another template, plasmid pMX5 contained 141 bp of the 5' flanking region, a portion of the exon 1 (22 bp) and a spacer (187 bp). The reaction conditions were described in detail previously [4] and in the legend of Fig. 4.

3. RESULTS AND DISCUSSION

3.1. Isolation and characterization of the rat MSE gene

From the rat genomic library, 4 clones were obtained using cDNA probe containing 3'-noncoding region which contained the nucleotide sequence unique to MSE mRNA. Three overlapping clones out of 4 were isolated and designated λ ME1, λ ME2 and λ ME3 and used for further analyses (Fig. 1). DNA of each clone was digested with restriction endonucleases and analyzed by Southern blot hybridization. Furthermore, two DNA fragments from λ ME2 (E3-4 and E7-2) and three DNA fragments from λ ME3 (HB6-6, H4-6 and H2-9) were subcloned into the multicloning sites of pUC8 vector. The subcloned DNA fragments were subjected to further restriction endonuclease analysis and to sequencing by the procedures of Maxam-Gilbert and Sanger et al. Fig. 1 also shows the restriction endonuclease map and the structure of the rat MSE gene. The *Bam*HI-*Pst*I region (8.4 kbp) was sequenced except some parts of introns. The rat MSE gene is about 6 kbp long and

Correspondence address: Y. Takahashi, Department of Neuropharmacology, Brain Research Institute, Niigata University, Asahimachidori 1, Niigata 951, Japan

* Present address: Kyoto Pharmaceutical College, Yamashina, Kyoto 607, Japan

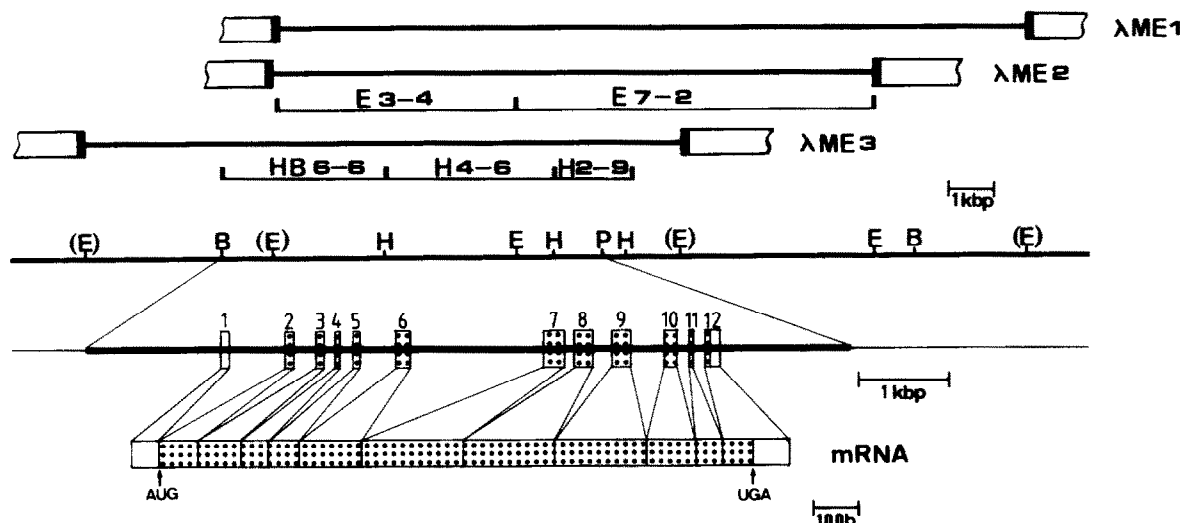


Fig. 1. Restriction map of the rat MSE gene cloned in λ phages and structure of the rat MSE gene. Three λ phage clones (λ ME1, λ ME2 and λ ME3) hybridized with MSE cDNA are shown with the subcloned DNA fragments from λ ME2 and λ ME3. A restriction endonuclease map and structure of MSE gene are indicated in the middle. Exons are shown by the numbered stippled and open boxes. Stippled boxes represent the coding regions and open boxes represent the noncoding regions. Thick bars show the introns and the flanking regions and these regions were sequenced except some parts of introns. The structure of MSE mRNA corresponding to that of MSE gene is shown below.

is separated into 12 exons by 11 introns, Fig. 2A shows the nucleotide sequence of 5'-flanking region, exon 1, intron 1 and exon 2 of MSE gene. The nucleotide sequence of the exon (1-12) regions completely corresponded to the cDNA sequence. The boundary sequences of the exon-intron junctional sequences in the gene were all referable to the typical 5'-GT-AG3' rule as shown in Fig. 2B [10]. The length of each exon varied from 59 bp (exon 11) to 223 bp (exon 7). The 3'-noncoding region is 151 bp long and is located in exon 12. The 5'-noncoding region is 63 bp long and is split into exons 1 and 2 as described later. The translation start codon ATG is located in exon 2 and the stop codon TAG in exon 12. The nucleotides for the putative substrate-binding site, arginin residue, are split into exon 11 and 12. The nucleotides for the Mg^{2+} -binding site, histidine residue, are located in exon 7.

3.2. Characterization of the transcription initiation site and 5'-flanking region of the MSE gene

For the determination of the 5'-terminus of the gene, we used S1 nuclease mapping analyses and the primer extension. The protected 5' end by S1 nuclease mapping analysis was nucleotide C as shown in Fig. 3. Primer extension gave a product corresponding to C at 63 bp upstream to the translation initiation site. The most extended broad major band of 136 bases was found by the primer extension analysis (data not shown). Maxam-Gilbert sequencing of DNA eluted from this major band gave the same nucleotide sequence to MSE cDNA extended to base C at -63 on the base of the translation initiation site. Sequence analysis of DNA from the upper minor band did not give any cDNA sequence. Nucleotide C was therefore assigned as the transcrip-

tion initiation site (+1). In the case of MSE gene, the transcription start site was single, different from those of NSE gene.

Fig. 2A also shows the nucleotide sequence of 5'-end of the MSE gene. The nucleotide sequence upstream from the MSE mRNA start point contains a TATA-box-like sequence at -26 to -22. CAAT and GC boxes are absent. About 1.8 kbp 5' flanking sequence was examined by the homology search. Ten MyoD-binding motifs (CANNTG) were found in this region. Further, CA-rich G box sequence (-227 to -238) was also found. The significance of these findings will be described in the section of general discussion.

3.3. The comparison of MSE gene with NSE gene

The structure of MSE gene in Fig. 1 was compared with that of NSE gene [4]. Both genes were similar in the exon-intron organization, indicating the presence of 12 exons. The total size of the MSE gene from the transcription start point to the poly(A) addition site was about 6 kbp and considerably smaller than that of NSE gene. The reason for this difference was due to smaller size of all introns except introns 6 and 9. Particularly the size of the introns 1 and 7 of MSE gene was much smaller than that of NSE gene introns. However, the intron 6 of MSE was longer than that of NSE. As we previously reported in the cDNA, 3' noncoding region in the exon 12 was much smaller than that of NSE gene. It is important that the transcriptional start site of MSE gene is single, indicating the difference from the multiple start sites in NSE gene. Furthermore, in the 5' flanking region MSE gene contains a TATA-box-like sequence, but NSE gene did not contain any typical TATA-box-like sequence.

A

-1781 -1761 -1731 -1701 -1671
 GGATCCCGCTCCAGCATCAGAGCCTCGCCCATGCCTGAACCTGACTACAGAGGTCACTTGAATAGGGCGCCACGGGGTGACAAGACGGGACTCATTTTTCAAGCGGAA
 -1641 -1611 -1581 -1551
 GAATACTAAAGTACCAAGAATGACAACCTTTTATAAGAAGAGGAAAGTTCCCTCTACTTTGGACCCATTGGGGCTTTCTTCTTTCCCGTAAAACCTTTGCTAAGTATTTGTGTGGATC
 -1521 -1491 -1461 -1431
 AGGTCACTTCCCGCGTGCAGGTCTAGGGGGAATGGCAGGCCAGTGAAGGTGGAGGAGTAAGGAATCACTCGACCCAGCTCCGAGGGGCTCGGCCGCTCCGGTCCCTCGGAGGAGG
 -1401 -1371 -1341 -1311
 GGGCGCGGGTATGCAGCCTCTCCCACTGGAGGATTTGGTTCGCTGCCTCTCTGGAGCGGGTTAGGCTCCCTGATGTTTCATCTCAAAATTTGGCTCCCCACGACCCCCCCCCCAGC
 -1281 -1251 -1221 -1191
 CCTAGTCTTCGACAGCGCGTGGCTGAGTCACGGCGGGCGCGCTGGGCACTGGCGGTCTGGCCCCGCATCCCTTGACCTCTGATCTGCGCGCTCCCGCCGGGGTGAAAAA
 -1161 -1131 -1101 -1071
 ATCTGCGGGAGTGGCAGGATGATAAGAGGGGAGGGCGGGACGGGACGGGAGCGGTGGGACCCCTAGGGTGGAGGCAAGAAGGGCCACCCCGAGGGTAGGGCGGAGGGGAAGGA
 -1041 -1011 -981 -951
 CGCTCGAGAGCCTCGCGTGCCTGAGTCACCGCTCCAGCGCCGCGAGTGAAAGCTGAGGGCGCCTGGAAAAAGAGCCGTCGGCCCGCCAGGCTTCGCGGAGCGCGGGGAGAGC
 -921 -891 -861 -831
 CCACACTAGCCCTGCCCTGCCAAGGAGCAGAGATTACCGAGGGCAGAGATTCATTTCTGCGGTGCTGCAATGGATGGACAGTCCACAGCGCTCCAAGAGCTTACAAAGGTCAT
 -801 -771 -741 -711
 CCCCTTGTCCTCCATTCATAGTTTTTTGTTTTTTTCCATTCTGCTGATATAATACCATCTTTGACAGGCAAGGGTTGAACCGTGAAGCGCCACAGTCGGTGGGAAAAAGG
 -681 -651 -621 -591
 ACTCCTCACCATTAGGCTTCACGAGGGACATAAATGCTGTCCAGCAGTATCTGTCAAGCGCCAGGCCAAAGCTCAGTGTGCTTATATTCGTCTCCTGCCTCTCATCGCTCATC
 -561 -531 -501 -471
 ACTGGCCAAGAGGATAGGGCGGAGTGGTCCGCAATGGCTGTTGTGAGGACCTGAGAGGTGAAAGCGCTGGCCCTCTTTGGTCGAGGGGTGCGACTTTAGACCACAGAGCTTGCTC
 -441 -411 -381 -351
 AGCATCACTGATGCCTTCCCCCACTGCGTGGCTGCACCGCTGCCTCCAAGTCGAGCACTGTACATGTCACTTTGACAGCCCTTTTCTAGGCCCTCCTCAGCCTGCCGGGTCA
 -321 -291 -261 -231
 GATTACCCCTGGCCTTTTAAAAAGGGCACTTGGTTTCTTTAACTTTTGAAGTGGGGAAGACCCCTTCCATCAGAAGCCTCTCTCTGCTTTCCCAAA
 -201 -171 -141 -111
 TAGTGAGCTTCAAGTAGAGACTTTTATTTGGGACAGAAAGAAATGCATGAGGGTACTCAACTTTTGAAGGGGATACATGCCCTTAGGCCAGAGTCTTCTCTCAGGCTGTAG
 -81 -51 -21 -1
 TGGGCACTTGGCTATCTGCCCCGTGTGAGGGGAGGAGTGAATGAGAGCGGGGCTGGCTGGGTACAGGATGGCTTGGAGATAATGCCAGCCTGAGAGGGGTGAGCTGACACTGT
 40 70 100 130
 CCCAAGCTGCTACCTAGGCACTCTACTCAAGGTTCCAAAGAAGCATTACAGGTTTGGAAAAAGCTCAGTACCGGGTGTGAGGTGCGGGCGGGGTGGTCTGCTTGGAAAAAGTGAAGG
 160 190 220 250
 GGGATTTTGGCTTTTTTCTTCTAGGACAGGGGTAAGAGAGAGAGGCTAGGTTGGAGGAAGCAGAAGTCAATACAGAAGGGTACTGACAGATATAAGAAAGACTCTGAAGAATGG
 280 310 340 370
 GGAAGGAGATAAGACACAATCGAGCTAGGCGAGAGAATCTGGGATCTGGGAGGATTGGGAATGAACAGTGAACAGATAGGTATAAGGTGTAGGAAGATGTGCAAGCAGATTACTTAA
 400 430 460 490
 TCATAAAGGTGCAAGGAGGCATAAACTTGGTGAAGTATCCAGGAGTGGTGTCTGCTGGGGAAATATAAGATTATGAGCCCTTGATTTTGAGATTGGAGGGGTGCAACAAGAGCTATTCCA
 520 550 580 610
 GTGTGGGGGGGGAGGGACCAAGCTGCCTTCTCTTTGGTCTGTGACCTTTTATAGGGTATTTTATAGCTCCAGCAGCTGCCTTCTCGGGTGGAGAAGACTCTTAAAGGGCAAGGGA
 640 670 700 730
 TTTCTAGTTCCTTAAGGATCAACTGTCCACTTGTCTCACTCACTCATCTCTTGTGGTGCACTCATGGCCATGCAAAAAATCTTTGCCCGAGAAATCCTGGAAGTCCAGGGGCAACCC
 760 790
 CACAGTGGAGGTGGACCTGCACACAGCCAAAGGTAACACAGGCCTGCTGAAATGGTTTGCCTCAGAAAA..... Intron 2

B

INTRON	EXON	INTRON
	61bp	
	CTGACACTGT-----GACATTACAG GTTTGGAAAA--- 614bp	
	87bp	
---TGTGGTGCAG	CCATGGCCAT-----ACAGCCAAGG GTAACACAGG--- 237bp	
	MetAlaMe ThrAlaLysG	
	96bp	
---TCCTGCCAG	GTCGATTCCG-----CTGGGGAAG GTGAGCAGAG--- 126bp	
	lyArgPheAr LeuGlyLysG	
	59bp	
---CTGGAATCAG	GAGTGGCGAA-----GCTGGAAGAG GTAAGTCGAG--- 146bp	
	lyValProLy uLeuGluLys	
	70bp	
---CCTCCTTAC	AAACTAAGTG-----GAGAATAAGT GTATAGTGAG--- 402bp	
	LysLeuSerV GluAsnLysS	
	134bp	
---CTCTCTTAG	CCAAGTTTGG-----TCCCGTGCCT GTGAGTGTGT--- 1475bp	
	erLysPheGl uProValPro	
	223bp	
---TGTGTCCAG	GCCTTCAATG-----AACAATGAGG GTCAGTGTGT--- 116bp	
	AlaPheAsnV AsnAsnGluA	
	198bp	
---TCCCTCCTAG	CCCTGGAAGT-----AACTATCCCG GTGTTTCTTC--- 196bp	
	laLeuGluLe AsnTyrProV	
	202bp	
---TCCCTATCAG	TGGTCTCCAT-----CCATCTTGGC GTGAGTGCCT--- 373bp	
	aiValSerIl erIleLeuAl	
	109bp	
---TCCACACAG	CTGTAACTG-----CACAGGACAG GTACTCAGGG--- 138bp	
	aCysLysLeu sThrGlyGln	
	59bp	
---CCCACCTCAG	ATCAAGACTG-----AGCTTATGAG GTACAGTTTG--- 96bp	
	lleLysThrG lnLeuMetAr	
	151bp	
---TGTATTGTAG	GATTGAGGAG-----CCAAACAAGA	
	gIleGluGlu	

Fig. 2. The nucleotide sequence of the 5'-end and the exon-intron junctional regions of MSE gene. (A) Nucleotide position +1 is assigned to the C of the transcriptional start site; negative numbers refer to the nucleotides on the 5' side of nucleotide 1. The TATA-box-like sequence and MyoD binding motifs are underlined and the CA-rich G-box sequence is double-underlined. The nucleotides in the exons are boxed. (B) Exon-intron junctional regions.

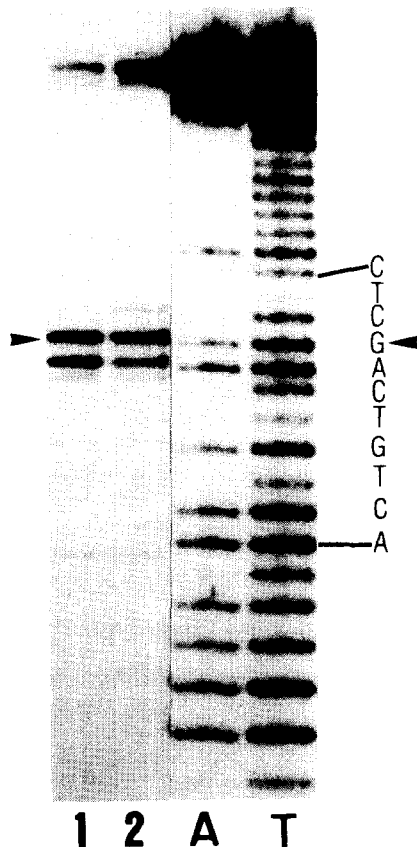


Fig. 3. S1 nuclease protection analysis. The arrow indicates the protected bands. The concentrations of S1 nuclease were 120 and 240 units/ml respectively in lanes 1 and 2. A and T show the sequence ladder of the same probe DNA.

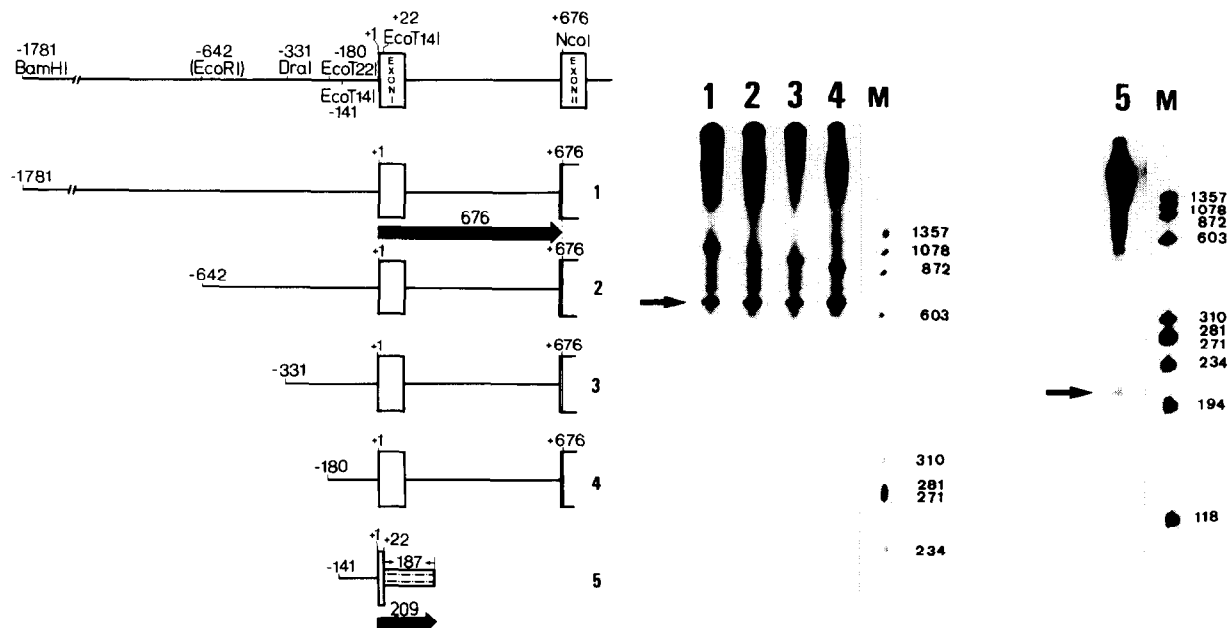


Fig. 4. Analysis of RNA transcripts synthesized in vitro. *NcoI*-truncated pMX1-4 DNAs contain 1781 bp, 642 bp, 331 bp or 180 bp of the 5'-flanking region, the first exon, intron 1 and exon 2 of MSE gene. Another plasmid, pMX5, contains 141 bp of the 5'-flanking region, a portion of exon 1 (22 bp) and a spacer (187 bp). These structures are shown on the left side. The putative cap site is marked with +1. The standard 12.5 μ l reaction mixture contained 12 mM Hepes, pH 7.9, 7 mM MgCl₂, 60 mM KCl, 0.2 mM EDTA, 1.3 mM DTT, 10% (v/v) glycerol, 10 mM creatine phosphate, 600 μ M GTP and CTP, 25 μ M ATP, 50 μ M UTP (10 μ Ci of [α -³²P]UTP), 5–7.5 μ l of HeLa cell extract and 0.5 μ g of cleaved plasmid DNA. The reaction mixtures were incubated at 30°C for 60 min. The transcripts were analyzed on the 5% polyacrylamide – 7 M urea gel. Lanes 1–5 indicate the transcripts from pMX1–5, and do not contain α -amanitin. The concentration of α -amanitin is 1 μ g/ml. Lane M shows the molecular markers. The arrows indicate the bands of the faithful transcripts (lanes 1–4, 676 bp; lane 5, 209 bp).

The boundary amino acids in the exon-intron junctional regions were almost similar between MSE and NSE except two: Lys \rightarrow Ser in the 3' end of the exon 4 and Lys \rightarrow Gly in the 5' side of the exon 5. Considering this similarity of the exon-intron organization in the MSE and NSE genes, it was evolutionally presumed that both enolase isozyme genes should come from the same ancestral gene.

3.4. In vitro cell-free transcription of the MSE gene

The MSE gene is predominantly expressed in the mature muscle and the regulation of its expression may take place at the level of transcription. To examine the potential activity of the putative promoter region for the transcription initiation of MSE gene and to look into the mechanism of its muscle-specific expression, we first attempted to study in vitro cell-free transcription of the truncated genomic DNA fragment as a template using HeLa cell extract.

Plasmid pMX1-4 containing 1781 bp, 642 bp, 331 bp or 180 bp of the 5'-flanking region, exon 1, intron 1 and exon 2 was truncated with *NcoI* and used as a template. Some α -amanitin sensitive transcripts were observed. A faithful major transcript (about 676 bp), which corresponded to the transcription start point, was obtained. Another plasmid, pMX5 containing 141 bp of the 5'-flanking region, a portion of exon 1 (22 bp) and a spacer (187 bp), was used as a template. In this case, a faithful transcript was also obtained (209 bp). These transcripts were all α -amanitin-sensitive (Fig. 4).

These data suggest that for the active transcription HeLa cell extract could recognize the putative promoter sequence (at least 141 bp) which contains a TATA-box-like sequence and the putative transcription start point is correct and single. This 141-bp region contains the promoter sequence enough for transcription of MSE gene.

3.5. General discussion

Recently, the *cis*-acting regulatory regions required for transcriptional regulation have been examined for several muscle-specific genes; quail troponin I [11,12], human cardiac actin [13], and mouse muscle creatine kinase genes [14,15]. Some studies have identified an enhancer element in the quail muscle troponin I [11,12] and mouse muscle creatine kinase genes [14,15]. Furthermore, some *trans*-acting factor proteins like MyoD and Myf-5 etc. were found in muscle creatine kinase [15] and myosin light chain genes [16]. The sequence homology search in 1.8 kbp of the 5' flanking region of MSE gene could clarify the presence of at least ten muscle-specific elements homologous to the sequence CANNTG motif to which a muscle-specific *trans*-acting factor, MyoD binds. A CA-rich G-box sequence was also found as previously described in actin gene by Minty and Kedes [13]. The regulatory function of these nucleotide sequences and a *trans*-acting factor from muscle nuclear extract should be examined in detail in future. Further, to study the molecular mechanism that controls the expression of MSE gene in the specific early developmental stages of the muscle cells, the gene structure of NNE should be clarified. Very recently the structure of human NNE gene was described [17]. Already we found a switching appearance and increase of MSE mRNA from NNE mRNA in the course of differentia-

tion from myoblast to myotubules (unpublished observation). The MSE gene will be used as a model system to examine the mechanism of muscle-specific gene expression.

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