

# Cloning and characterization of the genomic DNA of the human *MSSP* genes

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## ABSTRACT

**MSSP proteins have been identified by their binding to an upstream element of *c-myc*. Independently, two different approaches yielded two cDNA clones highly homologous to the MSSP cDNAs, suggesting an involvement of MSSP in the regulation of the cell cycle (*scr2*) and in the repression of HIV-1 and ILR2  $\alpha$ -promoter transcription (human YC1). Screening human genomic libraries, we have isolated clones belonging to two different gene loci. Whereas the human *MSSP* gene 1 turned out to be intronless, the organization of the coding sequence within gene 2 is more complex. It spans more than 60 kb and contains 16 exons (including two alternative first exons), ranging from 48 to 287 bp, respectively. The intron sizes vary from 0.1 to more than 13 kb. Gene 1 has been completely sequenced. A deletion series of its upstream region was conjugated to the luciferase gene, but the transfection of the constructs did not display any promoter activity. Moreover, compared with gene 2 and the cDNA sequences known so far, about 20 point mutations as well as flanking direct repeats have been detected in the *MSSP* gene 1, showing that it possesses all the characteristics of processed retropseudogenes. Sequence analysis of a 1.7 kb fragment of the 5' flanking region of the *MSSP* gene 2 revealed that the promoter of gene 2 lacks consensus sequences for TATA and CCAAT boxes, is GC-rich, and contains numerous potential transcription factor binding elements including an Sp1 binding site. DNase I footprinting experiments showed that the putative Sp1 site was bound by proteins. The results of primer extension and S1 mapping analyses suggested the transcription of the gene starts at multiple positions upstream from the initiator methionine codon. Luciferase assays employing progressive deletions of the 1.7 kb promoter region allowed us to define the minimal promoter region of 428 bp (–488/+) and revealed a complex pattern of the transcriptional regulation the human *MSSP* gene 2. Furthermore, it can be concluded that the *MSSP* gene 2 encodes both *MSSP*-1 and *MSSP*-2, and moreover *scr2* and human YC1.**

## INTRODUCTION

The involvement of the proto-oncogene *c-myc* in crucial functions such as cell proliferation and differentiation requires a careful control in every cell type. Its delicately regulated expression and the elements involved therein have been the subject of numerous studies (1–3). A sequence of 21 bp about 2 kb upstream of the human *c-myc* gene has been shown to be essential for replication and transcription and to constitute both a putative DNA replication origin and a transcriptional enhancer (4,5). Its stimulation of SV40 DNA replication (6) and the functional substitution of its core sequence for the AT-stretch of the SV40 origin (7), in addition to the binding of a *c-myc* protein complex to it, suggested the role of the 21 bp sequence as a target for DNA–protein interaction (8). Indeed, several proteins showing direct binding to either of its strands could be identified and were named MSSP (*c-myc* single-strand binding proteins). Two cDNA clones coding for members of this protein family (*MSSP*-1 and *MSSP*-2) were characterized in respect to their DNA binding specificity as well as their promoting activity on DNA replication (9,10). Independently, the phenotypic complementation of *cdc2* and *cdc13* mutants of *Schizosaccharomyces pombe* yielded a third cDNA clone almost identical to *MSSP*-1 and *MSSP*-2, although containing a longer open reading frame, as well as a closely related one (*scr2* and *scr3*, respectively) (11), suggesting an involvement of MSSP in the regulation of the cell cycle (12,13), especially at the G<sub>1</sub> to S transition, when its expression level rapidly increases (9). The sequence of a fourth highly homologous clone, termed human YC1, was submitted to GenBank as a potential human repressor of HIV-1 and ILR2 alpha promoter transcription (L11289). Though the predicted sequences of these homologous proteins display some discrepancies, they share as a common feature a novel RNA binding motif, RNP-1 (14,15), which in addition to other RNP consensus sequences is required for DNA binding (10).

To shed full light upon this complex matter, the knowledge of the gene structure and mode of expression of MSSP is a prerequisite. In the present report, human genomic clones representing two gene loci have been isolated and characterized in order to gain insight into the regulation of the *MSSP* gene(s). Whereas *MSSP* gene 1 shares all the characteristics of processed pseudogenes, *MSSP* gene 2 codes for all *MSSP* cDNAs, as well

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as scr2 and YC1. Besides the description of the detailed structure of *MSSP* gene 2, we have also investigated its 5'-flanking region to identify *cis* elements important to drive transcription by deletion analysis.

## MATERIALS AND METHODS

### Screening of human genomic libraries

A human placental genomic library in EMBL3-SP6/T7 and a human leukocyte genomic library in EMBL3 were purchased from Clontech. The phages were propagated in host bacteria NM538 and LE392. The infection and plating procedures were according to the recommendations of the manufacturer. Plaques were screened under stringent conditions with [ $\alpha$ - $^{32}$ P]dCTP-labelled gel-purified DNA fragments ( $10^5$ – $10^6$  c.p.m./ml of hybridization solution) as probes. Human *MSSP*-1 was labelled with [ $\alpha$ - $^{32}$ P]dCTP using a random primer labelling kit from Boehringer Mannheim. *MSSP*-2 cDNA and genomic DNA fragments (Fig. 1) were labelled with [ $\alpha$ - $^{32}$ P]dCTP by nick translation (16). Prehybridization and hybridization were performed in 50% formamide at 42°C (16). Membranes were washed twice in 3 $\times$  SSC/0.1% SDS at 37°C and twice in 0.1 $\times$  SSC/0.1% SDS at 50–68°C (depending on the background of the respective probe) for 30 min. The filters were then autoradiographed and analyzed with a bioimaging analyzer (BAS 2000, Fuji Film Co.) and/or placed in contact with a Fuji X-ray film and an intensifying screen and exposed at –70°C for 1–3 days. Selected recombinants that hybridized to the screening probes were rescreened and purified. Phage DNA from the purified positive plaques was prepared by the bacteriophage lysate method (16). Inserts were excised and subcloned into pUC19 and pBluescript (Stratagene). Subcloned fragments were analyzed and intron lengths were determined by a combination of restriction endonuclease digestion, Southern blotting, PCR analysis, and nucleotide sequencing. PAC clones were obtained from Genome Systems [St. Louis, MO; clone addresses PAC-85-H1 (*MSSP* gene 2), PAC-280-C14 (*MSSP* gene 1) and PAC-320-C24 (*MSSP* gene 1)] after screening with a probe spanning exons II–IV, which was produced by PCR with exon-specific primers and *MSSP*-2 cDNA as a template. With these clones PCR and sequence analysis were performed.

### Nucleotide sequence analysis

Nucleotide sequencing was performed both manually using the chain termination method of Sanger *et al.* (17) with a Sequenase 2.0 kit (US Biochemical Corp.) and *BcaBest* kit (Takara Shuzo Co., Ltd.) and automatically on a model 373A DNA sequence (Applied Biosystems) using a fluorescent dideoxy terminator kit. In the case of the *MSSP* gene 1, nested deletions were performed on appropriately double-digested subclones with *ExoIII* for different time points, mung bean nuclease-treated, ligated and transformed in *Escherichia coli* strains DH5 $\alpha$  or C600. The resultant plasmids were sequenced with universal primers. To determine the sequence of each exon and adjacent sequence of the *MSSP* gene 2, synthetic oligonucleotides corresponding to known cDNA and genomic sequences were used besides universal primers (M4, RV, SP6, T3, and T7).

### Preparation of total RNA

HeLa cells were washed with phosphate-buffered saline (PBS) and lysed with ISOGEN (Nippon Gene) according to the instructions of the manufacturer. After purification by an additional phenol extraction and ethanol precipitation, RNA was resuspended in sterile water.

### Primer extension analysis

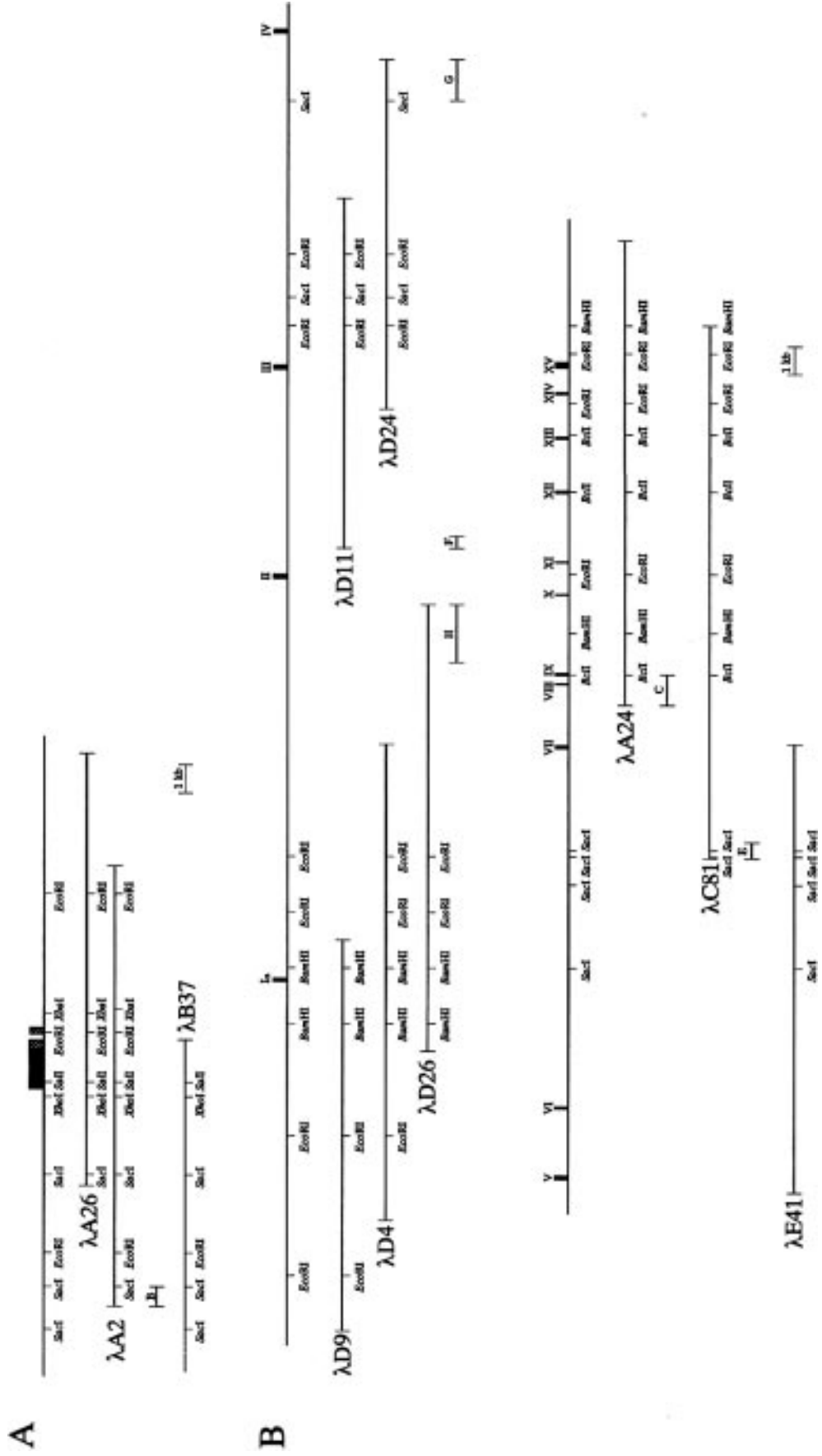
Primer extension analysis was performed using a 20mer oligonucleotide complementary to position +39 to +20 of the *MSSP* gene 2 (GCCGTGCAGGGTCGCGGACA). The primer was labelled at the 5' end with [ $\gamma$ - $^{32}$ P]ATP and T4 polynucleotide kinase. The labelled nucleotide was purified on a Sephadex G-50 spin column. A quantity of  $6 \times 10^5$  c.p.m. of the primer nucleotide was co-precipitated with 120  $\mu$ g of HeLa total RNA and resuspended in 30  $\mu$ l hybridization buffer (40 mM PIPES, pH 6.4, 0.4 M NaCl, 1 mM EDTA, and 0.2% SDS). The mixture was heated to 55°C during 10 min and annealed at 37°C for more than 3 h. The RNA and the annealed oligonucleotide were precipitated with isopropanol and rinsed with 70% ethanol. The pellet was resuspended in reverse transcriptase buffer with 1 mM dNTP, 130 U of RNase inhibitor, and 25 U Moloney Murine Leukemia virus reverse transcriptase. Elongation was carried out for 2 h at 37°C. The reaction products were phenol/chloroform-extracted, ethanol-precipitated, and resuspended in formamide loading buffer. One third was electrophoresed on an 8% polyacrylamide–8 M urea sequencing gel along with a sequencing ladder using the same primer for the dideoxy sequencing of a 5'-genomic clone.

### S1 mapping

p*MSSP*-Luc was digested with *HindIII* and treated with bacterial alkaline phosphatase before digestion with *SmaI*. The *SmaI*–*HindIII* fragment of 545 bp containing *MSSP*-1 promoter was end-labelled with [ $\gamma$ - $^{32}$ P]ATP and T4 polynucleotide kinase and was used for a probe. Cytoplasmic RNA (100  $\mu$ g) and the labelled DNA probe ( $10^5$  c.p.m.) were co-precipitated with ethanol, suspended with 50  $\mu$ l of hybridization buffer containing 80% formamide, 40 mM PIPES (pH 6.4), 400 mM NaCl and 1 mM EDTA, heated at 100°C for 8 min, and hybridized overnight at 42°C. The RNA mixtures were then mixed with 400  $\mu$ l of ice-cold S1 nuclease buffer containing 0.25 M NaCl and 300 mM sodium acetate, 3 mM ZnSO $_4$ , 100  $\mu$ g/ml of salmon sperm DNA, and 10 U S1 nuclease (Takara), and incubated 25°C for 30–60 min. The S1-resistant DNA hybrids were precipitated and electrophoresed on a 10% polyacrylamide denaturing gel.

### Reporter plasmids construction

The promoterless plasmid pGV-B (PicaGene<sup>TM</sup>, TOYO INK) served as the vector backbone for all the luciferase expression constructs. p*MSSP*-Luc: Nucleotide sequences of the PCR primers used were 5'-GCTCGAGGTCTAAACCATAGAAC-3' for *MSSP*-N and 5'-GAAGCTTCATGAAGCTGGAAGGG-3' for *MSSP*-C. After the PCR reaction with the above primers on the  $\lambda$  clone containing the upstream region of *MSSP* gene 2 as a template, the product was digested with *XhoI* and *HindIII* and was inserted to the *XhoI*–*HindIII* sites of pGV-B. p $\Delta$ X-Luc: The *XbaI*–*HindIII* fragment of p*MSSP*-Luc was first inserted to the *XbaI*–*HindIII* site of pBluescript SK(–). The *SacI*–*HindIII* fragment from the construct was then inserted to the *SacI*–*HindIII* sites of pGV-B. p $\Delta$ B-Luc: The



**Figure 1.** Organization of the human *MSSP* genes. Physical maps of the human *MSSP* gene 1 (A) and gene 2 (B) are shown. Exons (or homologous sequences, respectively) are represented as black boxes. Regions in gene 1 homologous to sequences downstream of the putative polyadenylation signal in gene 2 are shown as shaded boxes. Numbers above the boxes indicate exon numbers for the *MSSP* gene 2 transcripts.  $\lambda$  clones used in determining gene structure are shown below the genomic map. The fragments B, C, E, F, G and H were used for genomic library screenings. Partial restriction maps of the two loci are presented for restriction enzymes used in subclonings.

*Bam*HI–*Hind*III fragment of pMSSP-Luc was inserted to the *Bam*HI–*Hind*III site of pBluescript SK(–). The *Sac*I–*Hind*III fragment from the construct was then inserted to the *Sac*I–*Hind*III sites of pGV-B. p $\Delta$ S-Luc: pMSSP-Luc was digested with *Sma*I and the larger fragment yielded was self-annealed. p $\Delta$ P-Luc: pMSSP-Luc was digested with *Xho*I and *Pst*I and the larger fragment yielded was treated with Klenow fragment prior to self-ligation.

### Cell culture and transient transfection

Human HeLa cells were cultured in Dulbecco's modified Eagle's Medium (DMEM) supplemented with 10% calf serum. Five  $\mu$ g of the respective reporter plasmid and 2  $\mu$ g of the  $\beta$ -galactosidase expression vector (pCMV- $\beta$ -gal), carrying the cytomegalovirus (CMV) promoter, were co-transfected to the cells (60% confluent) by the calcium phosphate co-precipitation method (18). Four to five hours after transfection, the cells were boosted with 20% glycerol for 2–3 min at room temperature, then incubated for 48 h.

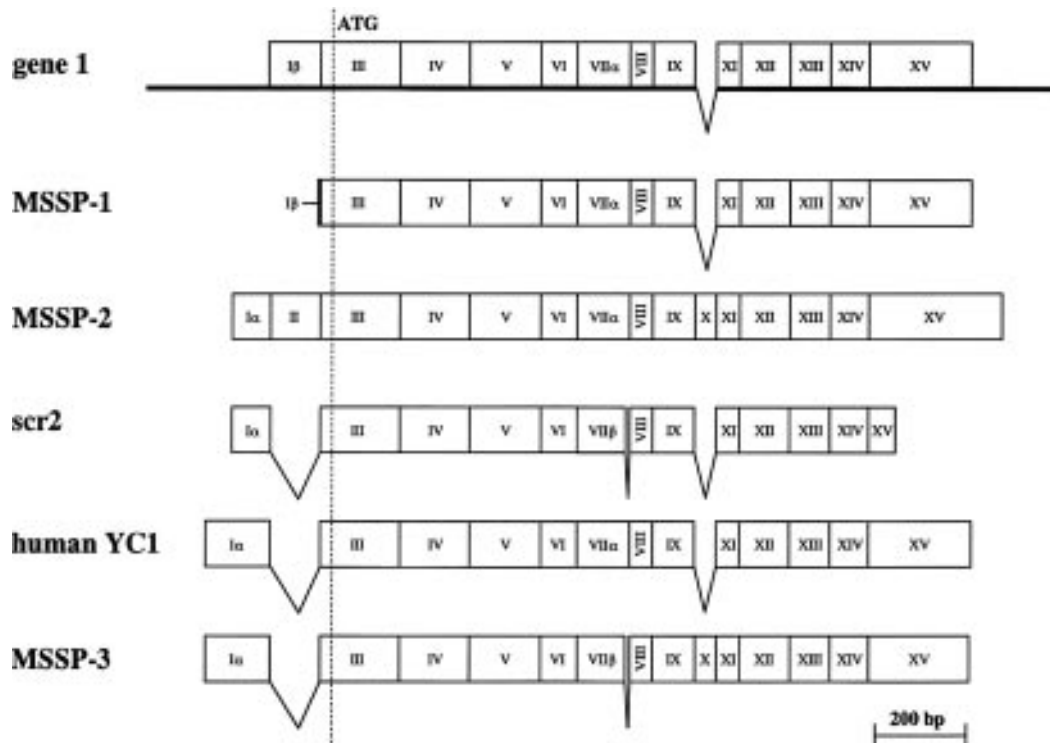
### Luciferase and $\beta$ -galactosidase assays

The transfected cells were washed with PBS and lysed in the plates using 200  $\mu$ l of a detergent solution (lysis buffer PicaGene<sup>TM</sup>, TOYO INK). The cell extract was then centrifuged for 5 s in an Eppendorf microcentrifuge and the supernatant was collected. The transfection efficiency was normalized by a  $\beta$ -galactosidase assay, set up in 300  $\mu$ l according to the standard

procedure (16), by incubation at 37°C until a yellow colour developed. The absorbance of the solution was then measured on a double beam spectrophotometer at 420 nm. The luciferase activity of the extract was determined by mixing standardized aliquots in a total of 20  $\mu$ l lysis buffer with 100  $\mu$ l of luciferase substrate (PicaGene<sup>TM</sup>, TOYO INK) in a vial. Immediately after mixing, the light intensities emitted by the samples were measured on a luminometer (lumiscouter ATP-300, Advantec Toyo Ltd.). Background luciferase activity was assessed in assays from parallel cultures transfected with the promoterless plasmid pGV-B.

### DNase I footprinting

The 259 bp fragment from –547 to –289 in the *MSSP* gene 2 promoter was used as a probe for DNase I protection assays. To create restriction enzyme sites at both ends, PCR was carried out on pMSSP-Luc as a template using primers of FtC (5'-AGGATC-CTTGGTGCCAGGCGGCA-3') and FtN (5'-GCTCGAG-CAACCGCGAGCCTGGG-3'). The PCR product was digested with *Xho*I and *Bam*HI, and inserted to the *Xho*I–*Bam*HI sites of pBluescript SK(–). The fragment was excised and labelled at either end with T4 polynucleotide kinase and [ $\gamma$ -<sup>32</sup>P]ATP. The labelled probe ( $\sim 3 \times 10^4$  c.p.m.) was mixed with HeLa nuclear extract (5, 10 or 15  $\mu$ g) in a buffer containing 10 mM HEPES (pH 7.9), 150 mM KCl, 1 mM DTT, 10 mM MgCl<sub>2</sub>, 1 mM EDTA and 2 mM poly(dI-dC). After incubation at 25°C for 30 min, DNase I was added to finally 10 ng/ $\mu$ l in the reaction. The reaction



**Figure 2.** Comparison of the exon compositions of the known *MSSP*-related cDNAs and the structure of the *MSSP* gene 1. ATG indicates the position of the start codon in the *MSSP*-1 and *MSSP*-2 cDNAs.



mixtures were kept at 0°C for 80 s, then denatured and separated in an 8% polyacrylamide denaturing gel.

## RESULTS

### Isolation of human *MSSP* genomic DNA clones

A human placental genomic library in EMBL3 SP6/T7 was screened with labelled full-length *MSSP*-1 cDNA (9) using the plaque hybridization method. Three intense clones (A2, A24, and A26) were isolated, subcloned and subjected to further analysis. The restriction analysis and the sequencing of the ends of the subclones revealed that these clones represented two different genomic loci, termed *MSSP* gene 1 (A2 and A26) and *MSSP* gene 2 (A24) (Fig. 1). Partial sequence analysis of the 5'-end of the genomic clone A26 down to the unique *SalI* site (223 bp downstream from the putative translation start in *MSSP*-1 cDNA) (Fig. 1A) revealed an intronless region identical to the 5'-end of the *MSSP*-1 cDNA (except for three mismatches) and indicated that this genomic clone extends about 3.5 kb upstream of the start of the cDNA. Attempts to screen for a sequence homologous to the head sequence of *scr2* (11) (exon I $\alpha$  in Fig. 2) in the far distal 5'-region of gene 1 with the genomic fragment B (Fig. 1A) and by genomic PCR did not yield the expected result. Following genomic Southern experiments showed the uniqueness of this sequence in the human genome as well as the uniqueness of another short region specific for *MSSP*-2 cDNA (10) (exon X in Fig. 2), missing in both *MSSP*-1 cDNA and gene 1 (data not shown). The discovery of the co-occurrence of these two stretches in one cDNA clone (*MSSP*-2) theoretically excluded the possibility of the existence of a sequence homologous to the *scr2* head upstream of gene 1 (Fig. 2).

Since A24 encompassed only the last eight exons of the human *MSSP* gene 2 (Fig. 1B), further screenings with genomic fragments (C and E) and a fragment, containing ~500 bp of the 5'-end of the *MSSP*-2 cDNA down to the unique *PstI* site (10) (D series), were

performed and yielded clones falling into three non-overlapping regions. As neither the screening of the placental genomic library and of a human leukocyte genomic library with other genomic fragments (F, G, and H) nor PCR amplification across the gaps using genomic DNA as template proved a successful strategy for obtaining the missing sections, a PAC library was screened with a probe spanning exons II–IV. PCR and sequence analysis revealed that two of these clones belong to gene 1 (clone addresses PAC-280-C14 and PAC-320-C24) and one to gene 2 (clone address PAC-85-H1). Using exonic, intronic and I $\alpha$  5'-flanking primers, it could be demonstrated that this clone encompasses at least the region from the second *EcoRI* restriction site upstream of exon I $\alpha$  (Fig. 1B) down to exon VII, and the existence of the exons I $\beta$ , II and IV therein was confirmed. These exons had not been covered by the bacteriophage clones. Thus, a contig spanning the whole genomic locus of *MSSP* gene 2 was finally established with the overlapping bacteriophage and PAC clones.

### Characterization of the human *MSSP* genes

The sequences in and around the exons of the *MSSP* gene 2 and those of the junctions of bacteriophage and plasmid subclones were determined. The comparison of the sequence of the human *MSSP* gene 2 (Fig. 3) with those of the cDNAs published so far shows that the human *MSSP* gene 2 is organized into 16 exons (including two alternative first exons, two optional ones and one with an internal splice site) (Fig. 2) and 15 intervening sequences, spanning a total of more than 60 kb. The exons are distributed sparsely at the 5'-end of the gene but rather densely at the 3'-end (Fig. 1B). Their sizes are rather small (Table 1). All the exon–intron junction sequences conform to the GT/AG rule (19) (Table 2). The sequence of the known exons coincides with those of all the known cDNAs, except for some mismatches most probably introduced by cloning procedures or sequence misreadings.

**Table 1.** The sizes of exons and introns in the human *MSSP* gene 2

Exon	Length (bp)	Amino acid position <sup>a</sup>	Intron	Type <sup>b</sup>	Length (kb)
I $\alpha$	132	–33 to –9	1	0	>13
I $\beta$	≥103	–31 to –9	1/2 $\beta$	0	>5
II	110		2	–	>5
III	176	(–8) 1 to 51	3	2	>12
IV	151	51 to 101	4	0	>0.5
V	158	102 to 154	5	2	3
VI	80	154 to 181	6	1	13
VII $\alpha$ ( $\beta$ )	116 (107) <sup>c</sup>	181 to 219 (216) <sup>c</sup>	7	0 (0)	2.0
VIII	50	220 to 236	8	2	0.125
IX	94	236 to 267	9	0	2.8
X	48	268 to 283	10	0	0.892
XI	51	284 to 300	11	0	2.9
XII	111	301 to 337	12	0	1.4
XIII	81	338 to 364	13	0	1.7
XIV	85	365 to 389	14	–	0.865
XV	287				

<sup>a</sup>Based upon the human *MSSP* gene 2 sequence in Figure 3.

<sup>b</sup>Intervening sequence type is defined where type 0 indicates placement between codons, type 1 interrupts a codon between the first and second nucleotide, and type 2 occurs between the second and third nucleotide of a codon (39).

<sup>c</sup>Alternative splicing sites (Table 2)



**Table 2.** Exon-intron boundaries of the human *MSSP* gene 2

5'							3'
exon I $\alpha$	CAA GCC	<sup>-9/-135</sup> AAG:gtaaaggggcccggggaga	intron 1	gtttcttttatttccctggag:	<sup>-/-134</sup> TPT GGA AGG	exon II	
exon I $\beta$	CGC AAG	<sup>-9/-25</sup> CAG:gtgaggcggcgnggggaan	intron 1/2 $\beta$	tcttgatctttgtttccag:	<sup>-8/-24</sup> CAG TCT CTG	exon III	
exon II	CAG AAA	<sup>-/-25</sup> AAT:gtatgtataaatcttccctg	intron 2	tcttgatctttgtttccag:	<sup>-8/-24</sup> CAG TCT CTG	exon III	
exon III	TGT CAA	<sup>51/152</sup> CC :gtaagtagtagttgttccta	intron 3/4	aacactctcttctgtttccag:	<sup>102/304</sup> CAA CAG GAA	exon V	
exon V	TPT GCT	<sup>154/461</sup> AG :gtaagccttctgcccagctct	intron 5	tctatttttattataaatag:	<sup>154/462</sup> G ATG GAA	exon VI	
exon VI	GPT TCT	<sup>181/541</sup> G :gtatgttgtttgtctgaaac	intron 6	atthttctctgtttacttag:	<sup>181/542</sup> CC CCC ACA	exon VII $\alpha/\beta$	
exon VII $\alpha$	GTF AGA	<sup>219/657</sup> CTT:gttaagtcccttcttgaact	intron 7 $\alpha$	tttctttctctttcccctag:	<sup>220/658</sup> GCT GGA ATG	exon VIII	
exon VII $\beta$	(GAA GGA	<sup>216/648</sup> GAG:gtggagactgttaagtccctt	intron 7 $\beta$	tttctttctctttcccctag:	<sup>220/658</sup> GCT GGA ATG)	exon VIII	
exon VIII	CAG AAC	<sup>236/707</sup> GG :gtatgtcgtttaaataaatc	intron 8	ggcttttgtttgtttctag:	<sup>236/708</sup> A TTT TAT	exon IX	
exon IX	GCC TAC	<sup>267/801</sup> CAG:gtttgtacctttaggattcg	intron 9	ttaactttggtctgccttag:	<sup>268/802</sup> GTG GCA AAG	exon X	
exon X	GCT ATC	<sup>283/849</sup> AAG:gtaaatcgcaataactctt	intron 10	caaaatcctcccttttctag:	<sup>284/850</sup> GTG CAA AGT	exon XI	
exon XI	CAG CAC	<sup>300/900</sup> CCT:gttaagttttttatcttaatg	intron 11	tcttgctcccaactcccag:	<sup>301/901</sup> GCT GCC GTG	exon XII	
exon XII	ACC GGA	<sup>337/1011</sup> ACA:gttagtggtgcaataattatc	intron 12	gacctcattctctttctag:	<sup>338/1012</sup> TAC ATG CCT	exon XIII	
exon XIII	CCT GTT	<sup>364/1092</sup> GAG:gtttggtagagaccatccagt	intron 13	ttctgctttgtttgtttag:	<sup>365/1093</sup> GAG GCA AGT	exon XIV	
exon XIV	ACT GTG	<sup>-/1177</sup> AG :gtatgagggaaaggtcttca	intron 14	cttttatttttctctccag:	<sup>-/1178</sup> A TGT ACA	exon XV	

Exon sequence is presented in upper case letters and intron sequence in lower case. The numbers identify codons within the coding sequence or the nucleotides of the *MSSP* gene 2 in Figure 3, respectively. The less common type intron 7 $\beta$ , which only occurs in scr2 and MSSP-3, is in parentheses.

**Table 3.** Amino acid exchanges in the human *MSSP* gene 1

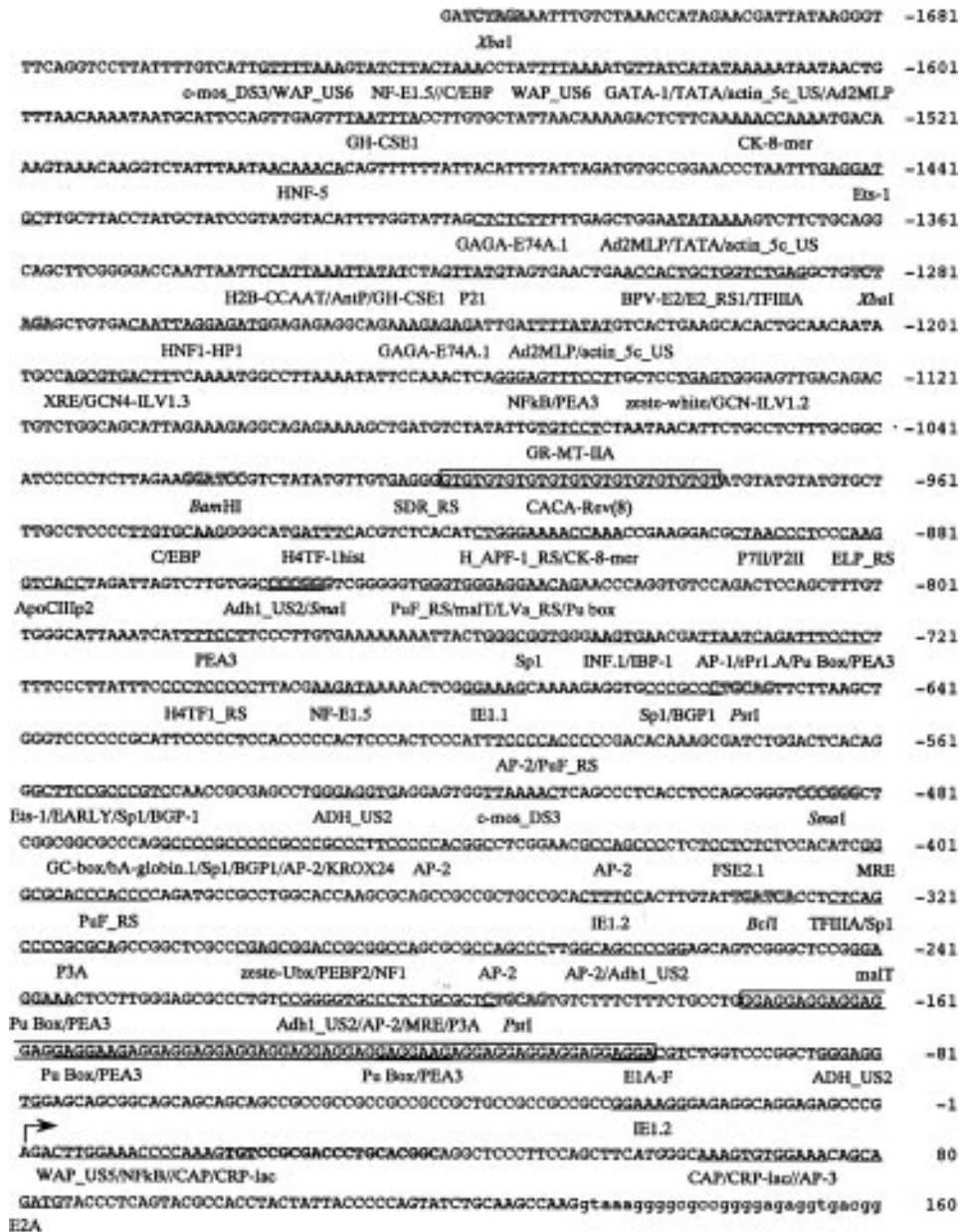
Number	Position	Nucleotide exchange	Amino acid number	Amino acid exchange
1	-73	AGT→AGC	-25	no
2	54	AGT→AGC	18	no
3	177	AAG→AAC	59	Lys→Asn
4	187	GAT→CAT	63	Asp→His
5	361	GAG→AAG	121	Glu→Lys
6	427	TCC→GCC	143	Ser→Ala
7	464	ATG→ACG	155	Met→Thr
8	494	ATT→ACT	165	Ile→Thr
9	571	GCT→TCT	191	Ala→Ser
10	658	GCT→ACT	220	Ala→Thr
11	702	CAG→CAA	234	no
12	779	GCA→GTA	260	Ala→Val
13	864 (816)	TCG→TCT	288 (272)	no
14	869 (821)	ATG→ACG	290 (274)	Met→Thr
15	900 (852)	CCT→CCC	300 (284)	no
16	1061 (1013)	GCA→GAA	354 (338)	Ala→Glu
17	1082 (1034)	GTT→GCT	361 (345)	Val→Ala

Nucleotides subject to exchanges are indicated in bold type.

The amino acid number and position identify codons within the coding sequence or nucleotides of the *MSSP* gene 2 (Fig. 3B), respectively. Differing values for the *MSSP* gene 1 are shown in parentheses.

The completion of the sequencing of the coding region of the *MSSP* gene 1 and its 3'-flanking region down to the first *Xba*I site (Fig. 1A) revealed that gene 1 is intronless. Figure 3B shows a sequence comparison of the human *MSSP* genes at the nucleotide level. The *MSSP* gene 1 harbours five nucleotide exchanges with

no effect on the amino acid composition of a possible gene product, whereas 12 nucleotide exchanges would lead to amino acid exchanges (Table 3), one of which would destroy an RNP consensus (Met<sup>155</sup>→Thr<sup>155</sup>). While there are neither insertions nor deletions in the coding sequence, added or missing nucleo-



**Figure 4.** The 5'-regulatory region of the human *MSSP* gene 2. Nucleotides are numbered in the right margin relative to the transcription start site determined by primer extension, 57 bp upstream from the translation start codon in exon I $\alpha$  (italicized). Consensus sequences for selected putative transcription factors are underlined, with abbreviations of the corresponding transcription factors shown below the sequences. Restriction enzyme sites are denoted in outlined letters and labelled. The sequence complementary to the oligonucleotide used in the primer extension analysis is represented in bold letters. The start site of transcription is marked by a hooked arrow. TG and GGA repeats are boxed. Intronic sequences are shown in lower case.

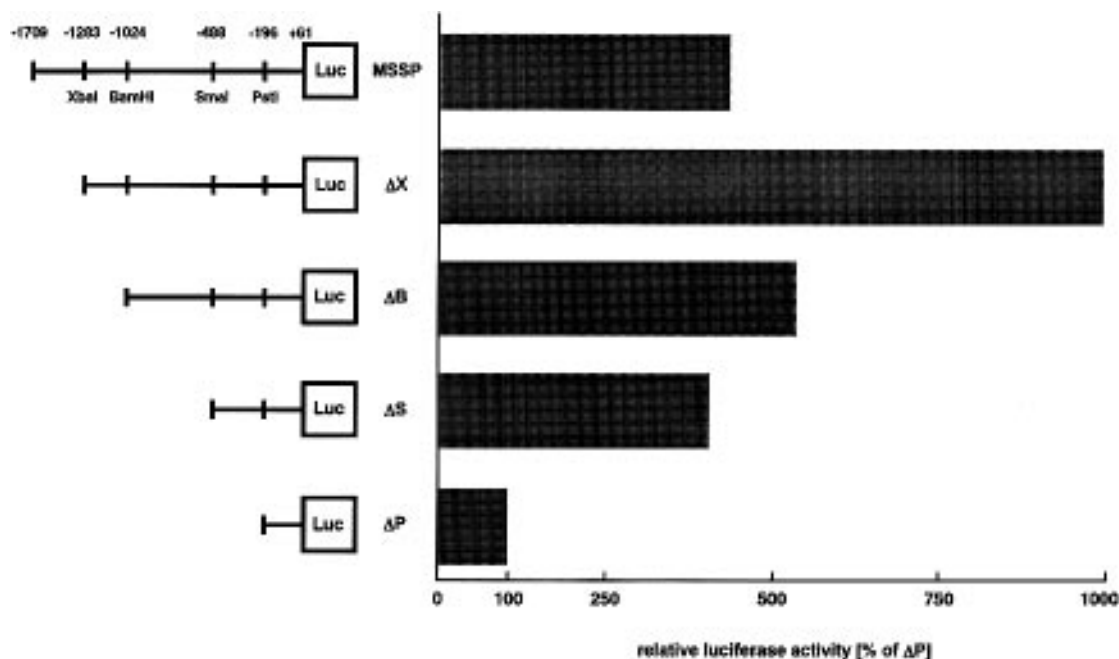
tides can be observed at the end of the region homologous to the longest cDNAs (region 1402–1470 in Fig. 3B). The theoretical length of 404 or 373 amino acids corresponds exactly to the size of the coding sequence of the correspondingly spliced product of gene 2 or the *MSSP*-1 cDNA, respectively. Although consensus sequences for transcriptional factors were discovered in the 5'-flanking region of gene 1, deletion studies with luciferase constructs did not display any promoter activity, neither were specific bands detected by nuclease S1 mapping analysis (data not shown). The discovery of the existence of flanking 11 bp direct repeats definitely confirmed that the human *MSSP* gene 1 shares all the characteristics of processed pseudogenes (20–22).

**Sequence of the 5'-flanking region of the *MSSP* gene 2**

Nucleotide sequence analysis of the 5' end of D26, containing ~1.7 kb of the 5'-flanking region, exon I $\alpha$  and part of intron 1 (down to the first *EcoRI* site) (Fig. 1B) of the *MSSP* gene 2, shows that this region is GC-rich and does not contain TATA and CAAT boxes at their characteristic positions in relation to the transcription initiation site (Fig. 4). However, it contains several consensus sequences for transcription factor binding sites such as Sp1 and AP-2. Two series of GGA repeats with sequence homology to the Epstein-Barr virus IR3 and a stretch of the Herpes simplex virus 2 genome were noted from -173 to -102, surrounding two





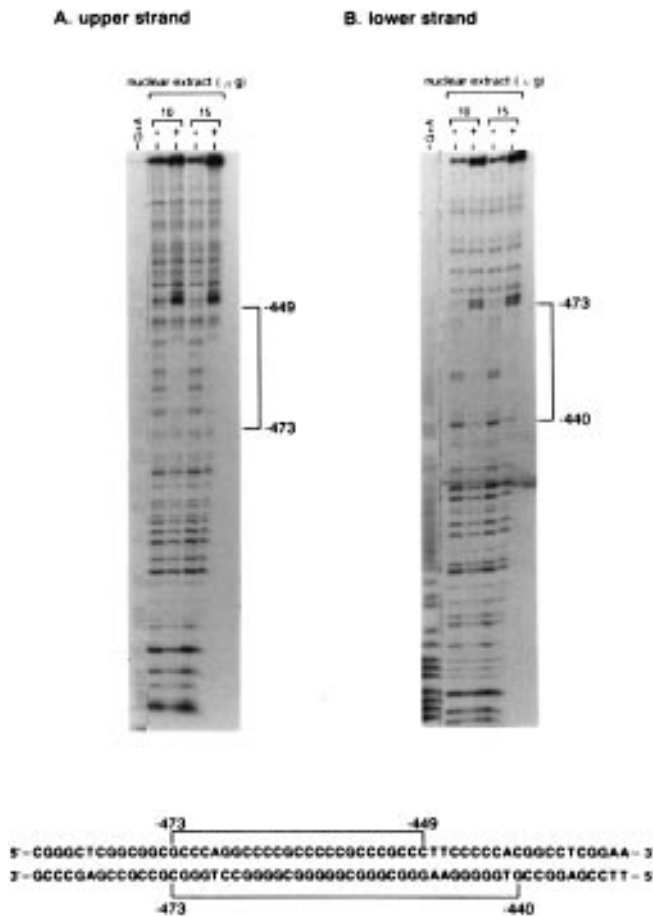


**Figure 6.** Promoter activities of upstream regions of the *MSSP* gene 2. The schematic diagram represents the human *MSSP* gene 2 promoter from -1709 to +61. The numbers refer to the position of the ends of the construct inserts relative to the transcription initiation site. Restriction sites used for subcloning are also indicated. HeLa cells were co-transfected with the indicated luciferase plasmids and pCMV- $\beta$ -gal. Luciferase activity is expressed as the average percentage of the chemiluminescence count for each construct standardized by that of p $\Delta$ P-Luc (set at 100) after correction of transfection efficiency. Data represent the mean from at least three independent transfection experiments.

exon I $\beta$ . The situation of the sequence around the 3' direct repeat is more complex. The homology between gene 1 and gene 2 in the 3'-flanking region continues beyond the putative polyadenylation signal, spanning about 470 bp interrupted after ~250 bp by a 299 bp insert, which comprises the downstream direct repeat sequence. The lack of this tract in gene 2 could be interpreted by its deletion in gene 2 rather than by its insertion in gene 1 after the formation of gene 1. Interestingly, the bounding sequences of the gap show a high degree of homology. As long as no sequence data of exon I $\beta$  upstream of -200 in Figure 3B are available, further homology in the 5'-flanking region cannot be excluded, either. The lack of a poly-A stretch before the 3' direct repeat might be due to reverse transcription before its addition to the fully spliced RNA. Negative Northern data, no hybridization of the homologous 3'-flanking sequences to HeLa RNA, would support this hypothesis. The percentage identity to the mRNA at the nucleotide level is 98.6% considering only the coding sequences, a typical value for a processed retrogene, suggesting that the *MSSP* gene 1 has arisen relatively recently in evolution. Commonly, the analysis of retrogenes does not go beyond a sequence comparison. Experiments to demonstrate the lack of promoter activities or transcription sites are hardly performed. In view of the absence of deletions, insertions or mutations to stop codons in the reading frame of gene 1, these approaches were considered necessary to provide further evidence for a final conclusion. Deletion series (from the 5' and the 3' end) of its upstream region were cloned upstream of the luciferase gene into vectors with and without the SV40 promoter, but never was any significant activity above background level obtained with constructs of the SV40-promoterless series. An S1 mapping was started at a very early stage, before the knowledge of the structure of gene 2, assuming the uniqueness of the 5' sequence of gene 1. We primarily obtained numerous non-specific bands due to S1

nuclease-sensitive sites. After the discovery of a second copy of this region in the human genome (exon I $\beta$ ) it was realized that an independent analysis of this region is impossible and that an optimal choice of the probe and an accurate interpretation of the results has to await the determination of the precise 5' end of the homology between the two genes and the functional analysis of the I $\beta$ 5'-flanking region. Since only the fortuitous placement of a retrosequence next to an active promoter could theoretically result in transcription, the absence of deletions, insertions or mutations to stop codons within the reading frame is only of secondary importance. In the case of gene 1, even on the assumption that it may be transcribed at a very low level, which cannot be ruled out completely, the mutation Met<sup>155</sup>→Thr<sup>155</sup> disrupts an RNP consensus and most probably precludes translation of the putative transcript into a functional polypeptide. In conclusion, although the precise reconstruction of its formation may be difficult to accomplish, the *MSSP* gene 1 arguably shares all the hallmarks of retropseudogenes.

A set of recombinant DNA clones that contain the entire *MSSP* gene 2 were isolated, and the gene 2 was shown to span more than 60 kb and to contain a total of 16 exons (including two alternative first exons), ranging from 48 to 287 bp. The intron sizes vary from 0.1 to more than 13 kb. The 5'-flanking region of the *MSSP* gene 2 contains a functional promoter: A relatively high promoter activity was observed in the region from -488 to +61 (relative to the transcription site), which can be divided into a sequence essential for transcription (the region up to -196) and the other sequence necessary for maintenance of a high expression level (-488 to -196). The complex patterns of transcriptional activity of the 5' deletion mutants suggests that both positive and negative elements are involved in the regulation of *MSSP* gene 2 transcription. The presence of consensus binding sites for various transcription factors implies, but does not prove, their involve-



**Figure 7.** DNase I footprinting analysis of the region from -547 to -289 in MSSP gene 2. The *XhoI* (upper strand) or the *BamHI* (lower strand) site at either end was labelled. Approximately  $3 \times 10^4$  c.p.m. of either labelled probe was incubated with the nuclear extract of HeLa cells, partially digested with DNase I and separated on a 10% denaturing polyacrylamide gel. A+G and G indicate the positions of A and G residues of the fragment analyzed as determined by Maxam-Gilbert chemical cleavages. + or - shows the presence or absence of the nuclear extract of HeLa cells in DNase reactions. The sequences bound by proteins are indicated by lines beside the gel and in the lower panel of the figure.

ment in the regulation of the promoter activity. The presence of overlapping binding sites (e. g. Sp1, AP-2, GC-box etc. at -460) suggests a balance activity of these transcription factors in different physiological conditions. Among the putative binding sites, at least the Sp1 binding site was protected from DNase I digestion by the nuclear proteins from HeLa cells, suggesting the involvement of Sp1 in the MSSP gene 2 transcription. Other notable features of the nucleotide sequence in the 5'-flanking region of the MSSP gene 2 are the presence of a 26 bp TG repeat (TG-element) at position -1001 to -976 and two series of GGA repeats from -173 to -102. Tandem repeat sequences of 2-5 reiterated nucleotides are frequently found in eukaryote genomes. The most common type is the dinucleotide CA repeat which can appear in up to  $10^5$  different locations, each of which contains up to 60 bp (31). Their varying length provides a useful system for the generation of genetic markers which can be used for mapping and linkage analysis (32). These elements can induce a conformational change from right-handed B-DNA to left-handed Z-DNA and negative supercoiling (33). It is not clear whether these

conformational changes play a role in transcriptional regulation, either as part of an enhancer or as part of a silencer. Additional investigations by deletion analysis and site-directed mutagenesis will be required to define more precisely the *cis*-acting elements and *trans*-acting factors important in the cell cycle-regulated expression of the human MSSP gene 2.

Potential polyadenylation sequences (AACAAA and AAGAAA) in the 3' end of the human MSSP genes differ from the putative poly(A) signal AAUAAA. However, polyadenylation sites different from the canonical poly(A) signal have been reported (34,35), suggesting that a perfect hexanucleotide AAUAAA is not an absolutely essential element in the efficient polyadenylation of MSSP transcripts.

The divergence of the cDNA sequences at the point where the 5' exons splice onto exon III (or also onto exon II in the case of exon I $\alpha$ ) suggested that gene 2 might have an additional 5' exon located somewhere upstream of exon III. The 12 bp head sequence in the MSSP-1 cDNA (corresponds to the region -25 to -36 in Fig. 3B), which is only slightly different from the 3' end of exon I $\alpha$  (-135 to -149 in Fig. 3A), also exists in gene 1. Assuming that the homology between the two genes continues farther towards the 5' end, an 18 bp primer homologous to the 12 bp and 6 additional bp in gene 1 (-25 to -42 in Fig. 3B) was designed and used for sequencing the PAC clone containing gene 2. Gratifyingly, this approach finally resulted in the discovery of exon I $\beta$  and extended the known scope of homology between the two MSSP genes up to -200 in Fig. 3B. All cDNAs cloned so far are consequently not transcripts of different genes but alternatively spliced products of the same gene. In other words, gene 2 encodes MSSP-1, MSSP-2 and MSSP-3, as well as scr2 and YC1.

Further studies will be necessary to pinpoint exon I $\beta$ , to perform functional analysis of its 5'-flanking region and to map its transcription start site(s), although we could not detect any transcript in the region upstream of exon III under the conditions used in this experiment. These should also include: a comparison of the expression patterns of I $\alpha$  and I $\beta$  transcripts; their relative abundance at different developmental stages and/or in different tissues; the identification of the set or combination of transcription factors for each promoter; and a comparison of their secondary structures. Thus, the meaning and importance of the differential promoter usage could be determined. The differential utilization of two alternative promoter sequences may even provide a mechanism for translational regulation of the MSSP gene 2. Due to the non-excludable possibly non-coding nature of exon I $\alpha$  and I $\beta$  (all fusion proteins of MSSP used in *in vitro* studies lacked the scr2 head sequence and started at +1 in Fig. 3B), transcription initiation from both promoters might even result in identical protein products. Thus, the transcription under the control of multiple promoters would result in an alternative splicing of sequences within the 5' UTR, which might regulate the expression of the MSSP gene 2 at the translational level. Lastly, determining the sequence of the alternate candidate promoter in the I $\beta$  5'-flanking region should reveal the precise range of homology between the two MSSP genes and should eventually allow the development of more specific probes to prove or disprove the possibility of a transcription of gene 1.

Along with the knowledge of the gene structure, the dissection of the structure and transcriptional activity of the MSSP gene 2 promoter region reported herein will facilitate further study on its regulation, thus contributing to a better understanding of the

physiological and cellular roles of MSSP, e.g. its involvement in the modulation of the biological functions of *c-myc*.

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