Cloning and Characterization of the Promoter Region of Human Telomerase Reverse Transcriptase Gene

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Abstract

Activation of telomerase is one of the rate-limiting steps in human cell immortalization and carcinogenesis. Human telomerase is composed of at least two protein subunits and an RNA component. Regulation of expression of the catalytic subunit, human telomerase reverse transcriptase (hTERT), is suggested as the major determinant of the enzymatic activity. We report here the cloning and characterization of the 5′-regulatory region of the hTERT gene. The highly GC-rich content of the 5′ end of the hTERT cDNA spans to the 5′-flanking region and intron 1, making a CpG island. A 1.7-kb DNA fragment encompassing the hTERT gene promoter was placed upstream of the luciferase reporter gene and transiently transfected into human cell lines of fibroblastic and epithelial origins that differed in their expression of the endogenous hTERT gene. Endogenous hTERT-expressing cells, but not nonexpressing cells, showed high levels of luciferase activity, suggesting that the regulation of hTERT gene expression occurs mainly at the transcriptional level. Additional luciferase assays using a series of constructs containing unidirectionally deleted fragments revealed that a 59-bp region (−208 to −150) is required for the maximal promoter activity. The region contains a potential Myc oncoprotein binding site (E-box), and cotransfection of a c-myc expression plasmid markedly enhanced the promoter activity, suggesting a role of the Myc protein in telomerase activation. Identification of the regulatory regions of the hTERT promoter sequence will be essential in understanding the molecular mechanisms of positive and negative regulation of telomerase.

Introduction

Telomeres are specialized structures at chromosome ends, which consist of tandemly repeated DNA sequences and associated proteins 1, 2. In normal human somatic cells, which show no or little telomerase activity to synthesize new telomeres, the telomeric DNAs progressively shorten with each cell division. Critically short telomeres are suggested to cause irreversible cell growth arrest and cellular senescence 3, 4. In contrast, most cancer cells have mechanisms that compensate for telomere shortening, most commonly through the activation of telomerase 5, allowing them to stably maintain their telomeres and grow indefinitely 3, 4, 6. Thus, activation of telomerase is a rate-limiting step in human carcinogenesis, and telomerase repression in normal human somatic cells can act as a tumor-suppressive mechanism. Three components of the human telomerase enzyme are thus far identified: the RNA component (hTERC), which acts as an intrinsic template for telomeric repeat synthesis 7; a telomerase-associated protein (TEP1) with similarity to the Tetrahymena telomerase protein p80, 8; and a telomerase catalytic subunit, hTERT,3 which shares several motifs with other known reverse transcriptases 9, 10. Recent reconstitution experiments both in vitro and in vivo strongly suggest that hTERT is the major determinant of human telomerase activity 12, 13. Concomitant up-regulation or down-regulation of the hTERT mRNA expression and telomerase activity during cell immortalization or differentiation is observed 10, suggesting that control of the hTERT expression at the mRNA level mainly contributes to the regulation of telomerase enzymatic activity 14. We found that a putative senescence-inducing gene with a telomerase repressor activity on human chromosome 3p also acts through down-regulation of the hTERT mRNA 15. How the hTERT mRNA expression is controlled by factors that could play a role in cellular senescence, immortalization, and carcinogenesis (e.g., oncogene products, tumor suppressor gene products, and the telomerase repressor on chromosome 3p) is of great interest. Identification of cis-elements and trans-acting factors that regulate the hTERT gene transcription will help to answer this question. As a first step toward the better understanding of molecular mechanisms of the hTERT gene and telomerase expression, we describe here the cloning and characterization of the promoter region of the hTERT gene.

Materials and Methods

Isolation and Sequence Analysis of the hTERT Genomic Clones. Two independent methods were applied to obtain genomic DNA clones containing the 5′-flanking region of the hTERT gene: PCR-based genomic walking and BAC library screening. For the PCR-based method, we used the Human Genome Walker kit (Clontech Labs., Inc., Palo Alto, CA) according to the supplier’s protocol. The gene-specific primers in the 5′-region of hTERT cDNA were 5′-AGC ACT CGT GCC ACC ACC AGC TCT T-3′ (primer GW1) for the initial PCR and 5′-AAC GTG GCC ACC AGC AGC ACC TCT T-3′ (primer GW2, Fig. 1) for the nested PCR. The use of Advantage-GC Genomic PCR kit (Clontech Labs, Inc.) designed for PCR of highly GC-rich regions was critical to our successful amplification. The final PCR product (−1.8 kb in length) was cloned into pCR2.1 vector (Invitrogen Corp., San Diego, CA) via the TA cloning method and sequenced in both strands by the dRhodamine terminator cycle sequencing kit (PE Applied Biosystems, Foster City, CA). The RPCI-11 human BAC library4 was screened using a 430-bp hTERT cDNA fragment (nucleotides 18–447 in GenBank AF015950) as a hybridization probe at Research Genetics, Inc. (Huntsville, AL). Two resultant positive BAC clones were sequenced by the BigDye Terminator cycle sequencing kit (PE Applied Biosystems) using the primers that were designed based on the sequences from the PCR-based clones described above. A DNA homology search was performed at the National Center for Biotechnology Information using the basic local alignment search tool (BLAST) network service. Potential transcription factor binding sites were predicted by TESS (Transcription Element Search Software)5 search program. A search for the CpG island was carried out using

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3 The abbreviations used are: hTERT, human telomerase reverse transcriptase; BAC, bacterial artificial chromosome; HBV, hepatitis B virus; bHLHZ, basic helix-loop-helix zipper.

4 http://bacpac.med.buffalo.edu.

5 http://www.cshl.edu/tess.

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The assay was carried out to examine the transcription initiation sites of the hTERT (accession number AF098956). The hTERT promoter sequence shown in Fig. 1 has been submitted to GenBank though the downstream end of the insertion is not characterized by a 190-bp fragment that was reproducibly amplified (−211 to 40) was PCR amplified and cloned into the pCR2.1 vector (Promega Corp., Madison, WI) to allow transcription of firefly luciferase gene under the transcriptional control of SV40 enhancer/promoter. To investigate a role of c-Myc protein in the hTERT gene transcription (data shown in Fig. 4), a human c-myc cDNA expression plasmid, RSVMycSVpA (a kind gift from Dr. Chi V. Dang, Johns Hopkins University, Baltimore, MD), or an empty vector (0.5 μg/well; Promega) containing the Renilla reniformis luciferase gene under the transcriptional control of SV40 enhancer/promoter, was cotransfected with the hTERT promoter-luciferase constructs (0.5 μg/well) and the pRL-SV40 (1 ng/well; Promega) containing the Renilla reniformis luciferase gene under the transcriptional control of SV40 enhancer/promoter, was cotransfected with the hTERT promoter-luciferase constructs (1 μg/well, as described above). The level of firefly luciferase activity was normalized to that of Renilla reniformis luciferase activity for each transfection. For all experiments, cells were cultured for 45–48 h after transfection, and cell lysates were prepared and examined by using the Dual luciferase reporter assay system (Promega) and the MLX microtiter plate luminometer (Dynex Technologies, Chantilly, VA). All of the data shown in this study were obtained from at least three independent experiments.

Results

A 1.8-kb fragment of the 5′ region of the hTERT gene was amplified by the PCR-based genomic walking from the library 1 (EcoRV-digested library) of the Human GenomeWalker kit (Clontech; see “Materials and Methods”), cloned in the pCR2.1 vector, and confirmed to have the expected structure by nucleotide sequencing. We also isolated two BAC clones carrying the hTERT gene, and their sequences corresponding to the 5′-flanking region, exon 1 and intron 1, were determined (Fig. 1). The nucleotide sequences from the PCR-based clones and the two BAC clones were identical except for a few possible polymorphisms. The transcription initiation sites were examined by the RNase protection assay with an RNA probe containing the 390-base sequence (135 to −255 in Fig. 1). Multiple protected fragments ranging from 120 to 190 bases were reproducibly observed in the hTERT mRNA-expressing CMV-Mj-HEL-1, RCC23, hU-H-4 (hepatocellular carcinoma, Ref. 19; see below) and SiHa cells, but not in hTERT mRNA-negative SUSM-1, normal human fibroblasts, and RCC23+3 cells (Fig. 2 and data not shown), suggesting the presence of multiple transcription initiation sites. The most abundant fragment was 135 bases in length. This suggests that a G nucleotide, which lies 55 bp upstream of the transcriptional initiation site.
Table 1  hTERT gene promoter activity in endogenous hTERT mRNA-positive and -negative human cells

<table>
<thead>
<tr>
<th>Cells</th>
<th>Endogenous hTERT mRNA</th>
<th>pGL3-Basic (no promoter)</th>
<th>pGL3B-TRTP (hTERT promoter − 1665 to 5)</th>
<th>pGL3-Control (SV40 promoter/enhancer)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fibroblastic origins</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CMV-Mj-HEL-1</td>
<td>+</td>
<td>2.7 ± 0.2 (0.5%)</td>
<td>171.1 ± 17.2 (30.9%)</td>
<td>554.3 ± 63.1 (100%)</td>
</tr>
<tr>
<td>SUSM-1</td>
<td>−</td>
<td>14.0 ± 0.1 (0.1%)</td>
<td>3.4 ± 0.6 (0.2%)</td>
<td>1637.0 ± 292.6 (100%)</td>
</tr>
<tr>
<td>Normal human fibroblasts</td>
<td>−</td>
<td>0.3 ± 0.1 (0.7%)</td>
<td>0.4 ± 0.1 (1.0%)</td>
<td>41.0 ± 5.7 (100%)</td>
</tr>
<tr>
<td>Epithelial origins</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SiHa (uterine cervical carcinoma)</td>
<td>+</td>
<td>0.4 ± 0.1 (0.4%)</td>
<td>20.1 ± 3.1 (18.5%)</td>
<td>109.6 ± 16.5 (100%)</td>
</tr>
<tr>
<td>RCC23 (renal cell carcinoma)</td>
<td>+</td>
<td>1.5 ± 0.7 (0.1%)</td>
<td>104.3 ± 15.9 (6.0%)</td>
<td>1743.1 ± 210.9 (100%)</td>
</tr>
<tr>
<td>RCC23 + 3′</td>
<td>−</td>
<td>0.3 ± 0.1 (0.1%)</td>
<td>0.8 ± 0.1 (0.3%)</td>
<td>254.2 ± 27.0 (100%)</td>
</tr>
</tbody>
</table>

* Average light units and SD are shown. Luciferase activities of pGL3-Basic and pGL3B-TRTP were normalized with that of pGL3-Control for each cell line and are shown as a percentage in the parentheses.

† Examined by reverse transcription PCR.

‡ RCC23 cells with a transferred, normal human chromosome 3.

codon, is a major transcription initiation site, which matches the 5′-end of the hTERT cDNA sequence reported by Nakamura et al. 11. We thus refer to this G as +1 in this manuscript. A 390-base fragment was protected only in the hepatocellular carcinoma cell line, huH-4, which suggests an alternate transcription initiation upstream of −255.

The most striking feature of the region is a highly GC-rich content. Search by GRAIL identified a CpG island of 1138 bp in length (−808 to 330 in Fig. 1), with a GC content of 71.3% and a ratio of observed versus expected CpGs of 0.79. A DNA homology search by BLAST of known sequences in GenBank showed that the 65-bp sequence (−371 to −307) is identical to a cellular sequence of the integration site of the HBV in the huH-4 cell line (GenBank X51995, Ref. 20), implying a genomic rearrangement of the hTERT gene promoter and possibly, taken together with the RNase protection assay described above, a transcription initiation from a viral gene promoter in this cell line. We indeed confirmed the genomic rearrangement by Southern blot analysis (data not shown).

Although the hTERT gene promoter lacks a typical TATA box or a typical CCAAT box, as seen with many GC-rich promoters, the TESS search program predicts a number of potential transcription factor binding sites near or upstream of the major transcription initiation site, including potential binding sites for Sp1, MAZ (Myc-associated zinc finger protein), a bHLHZ class of transcription factors such as the c-Myc oncprotein and the upstream stimulatory factor 21. There is another typical E-box downstream of the major transcription initiation site (22

![Fig. 2. RNase protection assay to examine the transcription initiation sites of the hTERT gene. A 460-bp RNA probe complementary to the 390-bp sequence of the hTERT gene (from −255 to 135 in Fig. 1) was hybridized to the following RNA samples: Lane 1, CMV-Mj-HEL-1; Lane 2, SUSM-1; Lane 3, RCC23; Lane 4, RCC23+3; Lane 5, huH-4; Lane 6, yeast RNA. Left, undigested probe. Size markers were transcribed in vitro from the Century marker template (Ambion). A 135-base major protected fragment and a 390-base fragment specific to huH-4 are indicated by an arrow and an asterisk, respectively. Signals near the bottom of the figure were common to both the hTERT mRNA-positive and -negative cell lines and thus appear to be nonspecific.](image-url)
The expression of telomerase activity is strongly associated with human cell immortalization and carcinogenesis [3, 4]. Recent studies have suggested that the expression of the telomerase catalytic subunit gene, \( hTERT \), mainly regulates the expression of human telomerase enzymatic activity [10, 15]. Thus, investigation of the molecular mechanisms that regulate the \( hTERT \) gene expression could lead to a better understanding of telomerase regulation, cellular senescence and immortalization, and human carcinogenesis. The cloning and characterization of the \( hTERT \) gene promoter in this study is an essential step toward this goal. Our luciferase assays with \( hTERT \) mRNA-positive versus negative human cell lines of fibroblastic origin (CMV-Mj-HEL-1 versus SUSM-1 and normal human fibroblasts) or epithelial origin (SiHa and RCC23 versus RCC23+3) indicate that the \( hTERT \) gene expression is controlled mainly at the transcriptional level. Thus, identification of the cis-elements and trans-acting factors that regulate the \( hTERT \) gene transcription is important to understand the regulation of this gene.

By using a series of unidirectionally deleted fragments derived from the \( hTERT \) gene promoter, we identified a 59-bp region (−208 to −150 in Fig. 1) that is responsible for the maximal promoter activity in human immortal cells of both fibroblastic and epithelial origins. Among the potential transcription factor binding sites within this 59-bp region, a typical E-box (CACGTG, −187 to −182), to which the bHLH family of transcription factors bind 21, is likely to play an important role for the \( hTERT \) gene transcription. We showed that the expression of a member of this family, c-Myc oncoprotein, markedly induces the transcriptional activity of the E-box-containing \( hTERT \) gene promoter in the endogenous \( hTERT \)-negative SUSM-1 cells (Fig. 4). We also observed a 3–7-fold increase of the promoter activity by the c-Myc expression in the endogenous \( hTERT \)-positive cell lines (data not shown). These results suggest an important role of c-Myc in positive regulation of the \( hTERT \) gene expression and telomerase activation. This is consistent with the finding by Wang et al. [22] that retroviral expression of c-Myc increases the amount of \( hTERT \) mRNA.
mRNA and activates telomerase in human mammary epithelial cells and fibroblasts, although their work did not include transcriptional regulation of the hTERT gene. Considering that activation of c-Myc is a common target of several oncogenic signals, e.g., mutant p53 proteins 23, viral oncoproteins 24, and defects in the adenomatous polyposis coli/β-catenin pathway 25, an attractive hypothesis is that these oncogenic signals converge on the transactivation of the hTERT gene promoter through c-Myc activation as a part of their oncogenic functions. Involvement of other factors is also possible, including other bHLH transcription factors such as upstream stimulatory factor 21, members of the Ets family of oncoproteins, which are known to cooperate with the bHLH proteins 26, 27, and the AP-2 family of transcription factors. We are presently investigating direct bindings of these factors, as well as c-Myc protein, to potential binding sites and their functional significance. Although the second typical E-box downstream of the major transcription initiation site appeared to contribute little to the hTERT gene promoter activity in the presence of the upstream E-box (see p2XEB in Fig. 3), there is a possibility that the downstream E-box also acts as a positive regulatory element but is functionally redundant with the upstream one. Additional experiments will be needed to address this issue. It should also be noted that the constructs without either E-box (pBdTdl-149 and pBdTdl-130) still showed low, but significant, promoter activity. Multiple potential binding sites for the Sp1 and MAZ proteins, which function cooperatively at some promoters 28, 29, are likely to be responsible for this basal activity of the hTERT gene promoter. Indeed, the Sp1 binding was confirmed in the hTERT mRNA-positive cell lines by a supershift on gel mobility shift assay using a 20-bp probe (117 to 98, data not shown).

Although in this study we focused our attention on the elements that positively regulate the hTERT gene transcription, the mechanisms involved in the transcriptional repression of the hTERT gene in normal human somatic cells are also of great interest. Although positive regulatory factors, e.g., c-Myc protein, may explain enhanced transcriptional activity, negative regulatory factors that function in telomerase-negative cells may play a role in the transcriptional repression. The hTERT gene promoter sequence and a series of constructs generated in this study may help to identify DNA elements and protein factors that negatively regulate the hTERT gene transcription. It has also been suggested that chromatin structure is a major determinant of gene activity 30. In this respect, the highly GC-rich content, forming a CpG island, of the hTERT gene promoter is notable. Increased DNA methylation and associated histone deacetylation could turn off the hTERT gene expression by establishing and maintaining an inactive state of chromatin structure.

Finally, we found a genomic rearrangement at the hTERT promoter region in a hepatocellular carcinoma cell line huH-4. The rearrangement probably resulted from the integration of the viral (HBV) genome into the promoter region, which is reminiscent of the activation of some oncogenes by insertion of viral genomes 31, 32. Determination of the precise structure of the HBV integration and examination of the transcriptional activity of the rearranged promoter will be needed to clarify functional significance of this rearrangement.

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12. Wang, J., Xie, L. Y., Allan, S., Beach, D., and Hannon, G. J. Myc activates oncogene transcription, the mechanisms involved in the transcriptional repression of the hTERT gene in normal human somatic cells are also of great interest. Although positive regulatory factors, e.g., c-Myc protein, may explain enhanced transcriptional activity, negative regulatory factors that function in telomerase-negative cells may play a role in the transcriptional repression. The hTERT gene promoter sequence and a series of constructs generated in this study may help to identify DNA elements and protein factors that negatively regulate the hTERT gene transcription. It has also been suggested that chromatin structure is a major determinant of gene activity. In this respect, the highly GC-rich content, forming a CpG island, of the hTERT gene promoter is notable. Increased DNA methylation and associated histone deacetylation could turn off the hTERT gene expression by establishing and maintaining an inactive state of chromatin structure.

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