Conserved N-terminal Motifs of Telomerase Reverse Transcriptase Required for Ribonucleoprotein Assembly in Vivo*

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Telomerase is a ribonucleoprotein (RNP) reverse transcriptase responsible for the maintenance of one strand of the telomere terminal repeats. The key protein subunit of the telomerase complex, known as TERT, possesses reverse transcriptase (RT)-like motifs that directly mediate nucleotide addition. The RT motifs are located in the C-terminal region of the polypeptide. Sequence alignments also revealed the existence of four conserved motifs (named GQ, CP, QFP, and T) in the N-terminal region of TERT. The GQ motif of yeast TERT has been demonstrated previously to be essential for telomerase catalysis and may participate in RNP formation. In this report, we show that substitution of conserved residues in the CP, QFP, and T motifs of yeast TERT also impairs both telomere maintenance and telomerase activity, thus confirming the validity of the sequence alignment. The extent of telomere shortening correlates with the extent of reduction in the level of telomerase activity, TERT protein, and TERT-associated TLC1 RNA. Overexpression of the mutant proteins does not result in telomere shortening, implying that assembly rather than catalytic function was affected. This notion was further supported by comparing the efficiency of RNP formation in the wild type and the overexpression strains. Taken together, our results show that three of the four N-terminal motifs are required for efficient telomerase RNP formation in vitro but not for the enzymatic function of telomerase. We also show that the majority of telomerase-associated TLC1 RNA has a more upstream 3′ end than previously reported, consistent with additional processing events during RNP maturation.

Telomerase activity has been characterized from a wide range of organisms and genes encoding both the RNA and protein components of the enzyme complex identified (for reviews see Refs. 3 and 4). Telomerase RNAs found in ciliated protozoa, in addition to having a short templating region, share a common secondary structure. Telomerase RNAs from yeast and mammals are considerably larger, and within each group conserved structural elements can be identified based on phylogenetic and mutational analysis (5, 6). The catalytic reverse transcriptase protein subunit (TERT), first purified from Euplotes aediculatus as p123, was found to be homologous to Est2p, a protein from Saccharomyces cerevisiae required for telomere maintenance (7–9). Both proteins possess reverse transcriptase (RT)-like motifs, alterations in which render telomerase inactive both in vitro and in vivo. Subsequently, homologues of TERT were identified in a phylogenetically diverse group of organisms (10–17). Because co-expression of TERT and telomerase RNA in rabbit reticulocyte lysates suffices to reconstitute enzyme activity (18, 19), these two subunits probably constitute the core of the enzyme complex. Quite a few telomerase-associated polypeptides have been identified using either biochemical or genetic tools. Studies from several laboratories (20–24) suggest that these factors may participate in telomerase assembly, catalytic function, or regulation.

The RT-like motifs are located in the C-terminal region of cloned TERTs. Extensive mutational analysis of these motifs in TERTs supports an overall conservation of basic catalytic mechanisms between telomerase and conventional RTs. For example, the TERT analogues of RT residues essential for catalysis are absolutely required for telomerase activity and telomere maintenance (9, 18, 25–27). Conserved residues shown previously (28–30) to modulate RT processivity have been found to be important determinants of telomerase processivity as well. In addition, the same tyrosine residue in conserved motif A allows both TERTs and RTs to discriminate against incorporating ribonucleotides (31). However, some other crucial RT residues (e.g. a Gln in motif B) appear to be less important or even dispensable for telomerase catalysis (9). Taken together, these results suggest that despite the high degree of sequence divergence (<20% sequence identity), the RT domains in both classes of proteins are mechanistically quite similar.

Detailed sequence analysis of nine cloned TERTs revealed, in addition to the RT motifs, four telomerase-specific motifs (named GQ, CP, QFP, and T) positioned N-terminal to the RT region (32). The functions of selected TERT N-terminal residues have been analyzed by reconstituting mutated TERT protein with telomerase RNA either in vitro (Tetrahymena and human) or in vivo (S. cerevisiae, Schizosaccharomyces pombe, and human) (18, 27, 31–33). In addition to confirming the functional importance of many of the conserved residues, the
results from *Tetrahymena* indicate that the CP and T motifs may be required for TERT binding to telomerase RNA *in vitro* (33, 34).

We have initiated a detailed structure-function analysis of the N-terminal region of *S. cerevisiae* TERT (Est2p). In an earlier report (32), we showed that the most N-terminal GQ motif is required for telomere maintenance and, in some cases, for telomerase activity *in vitro*. Overexpression of some of the mutants resulted in telomere shortening, implying that telomerase catalytic function, rather than RNP formation, was impaired by the mutations. We now report an analysis of the remaining three N-terminal motifs using an extensive panel of mutations. Our results confirm the functional importance of the CP, QFP, and T motifs in both telomere maintenance and telomerase activity. In addition, for mutations in these motifs, the extent of telomerase activity loss correlates with the extent of reduction in the amount of TERT protein and TERT-associated TLC1 RNA. Overexpression of the mutant proteins does not result in telomere shortening, implying that assembly rather than catalytic function was affected. This notion was further supported by a comparison between the efficiency of RNP formation in the wild type and the overexpression strains. Taken together, our results imply that three of the four N-terminal motifs in TERTs are required for efficient RNP formation *in vivo* but not for the telomere extension function of telomerase. We also show that the majority of telomerase-associated TLC1 RNA has a more upstream 3′ end than reported previously, consistent with additional processing events during RNP maturation.

**MATERIALS AND METHODS**

**Yeast Strains and Plasmids**—The construction of an est2Δ strain harboring the pSE-Est2-C874 plasmid (containing a protein A-tagged EST2 gene) has been described (32). This fully functional Est2p is designated wild type telomerase throughout the text. The construction of the protein A-tagged C745 mutant has also been described (29). All substitution mutations in the CP, QFP, and T motifs of EST2 were generated by using the Quick-Change protocol (Stratagene), appropriate primer oligonucleotides, and pSE-Est2-C874 as template. All point mutations were confirmed by sequencing. The oligodeoxynucleotide primers used for mutagenesis were purchased from Sigma-Genosys and purified by denaturing gel electrophoresis prior to use. For overexpression of TERT mutants, a vector containing the triose-phosphate isomerase promoter (pRX292, Ingenous Inc.) was utilized. The NcoI site within the polylinker of pRX292 was converted to an NdeI site, and the NdeI-SalI fragments from the pSE-Est2-C874 series of plasmids were inserted between the NdeI and SalI site of the resulting vector (32).

**Comparative Sequence Analysis**—All sequences used in comparative analysis were obtained from NCBI website at www.ncbi.nlm.nih.gov. The final alignment was based on manual adjustment of a hidden Markov model as described previously (32).

**Analysis of Telomere Length**—The construction of an est2Δ and W303 strain were transformed with the pSE and pYX series of plasmids, respectively. Independent clones were re-streaked twice on plates. Chromosomal DNAs were then isolated using the “Smash and Grab” protocol, digested with PstI, and electrophoretically separated on a 0.9% agarose gel. Southern blots were hybridized with a 32P-labeled poly(dG-dT) probe (32).

**Purification of and Assay for Yeast Telomerase**—Whole cell extracts, DEAE fractions, and IgG-Sepharose-purified telomerase were prepared as described previously (29, 32, 35, 36). Each primer extension assay was carried out using 20 μl of IgG-Sepharose-purified telomerase containing 4 μg of protein extract and was initiated by the addition of a 15-μl mixture containing 100 mM Tris-HCl, pH 8.0, 4 mM magnesium chloride, 2 mM dithiothreitol, 2 mM spermine, primer oligodeoxynucleotides, and varying combinations of labeled and unlabeled dGTP and dTTP. Primer extension products were processed and analyzed by gel electrophoresis as described previously (36, 37). The critical nucleotides primer used for telomerase assays were purchased from Sigma-Genosys and purified by denaturing gel electrophoresis prior to use. The primers have the following sequences: TEL15, TGTGTGGTGTGTGGG; TEL66, TAGGTAAGTAGTGGG.

**Protein and RNA Analysis**—The levels of protein A-tagged yeast TERT in cell extracts were determined by Western blotting as described previously (30). RNase protection studies were carried out as follows. A PCR fragment that spans nucleotide 1–1301 of the TLC1 gene (38) was generated and cloned between the BamHI and EcoRI site of pBluescript II KS+ to give pBS-TLC1. For the synthesis of labeled antisense probe, pBS-TLC1 was linearized by digestion with HindIII and transcribed with T7 RNA polymerase in the presence of 12 μM [α-32P]GTP as described (39). For the synthesis of the 1–1300 and 1–1917 sense transcripts, the same plasmid was digested with XhoI and AflIII, respectively, and transcribed with T7 RNA polymerase. For the protection assay, total RNAs from DEAE fractions or from *in vitro* transcription reactions were hybridized with the probe (100,000 cpm), and the mixtures were precipitated with ethanol. The RNAs were then hybridized in 80% formamide, digested successively with RNase T1, RNase A, and proteinase K, and analyzed with gel electrophoresis as described (40).

**High Resolution Mapping of the TLC1 RNA 3′ End**—Total RNAs from DEAE fractions or from *in vitro* transcription reactions were isolated by proteinase K digestion, phenol/chloroform/soyamol alcohol extraction, and ethanol precipitation. The RNAs were then polyadenylated using yeast poly(A) polymerase and reverse transcribed using a poly(dT)-containing primer (CCCGAATCTTTTTTTTTTTTTTTTTTTTTTT) (41). cDNAs spanning the 3′ end of TLC1 RNA were amplified by PCR using a TLC1 internal primer (CCGGATCCGATGTAAGAACTTGATGAC) and the same poly(dT) primer. Following gel purification and restriction enzyme cleavage, the fragments were cloned between the EcoRI and BamHI site of pBluescript II KS+, and the TLC1-poly(A) junctions were determined by sequencing.

**RESULTS**

**Previously Identified N-terminal Motifs of TERT Are Conserved in Newly Discovered Homologues**—Through the use of a hidden Markov model, we had earlier reported the identification of four conserved motifs in the N-terminal extension of TERTs from ciliates, fungi, mammals, and a plant (32). Subsequently, sequences for 11 additional TERTs were reported, including those from *Cryptosporidium parvum*, *Eucephalitozoon cuniculi*, *Giardia lamblia*, *Mesocricetus auratus*, *M. upolotes crassus*, *Oryza sativa*, *Plasmodium caudatum*, *Plasmodium yoelii*, *Plasmodium falciaparum*, *Xenopus laevis*, and *Caenorhabditis elegans* (42–50). Some of the newly discovered homologues manifest a surprising degree of evolutionary divergence. For example, the TERTs from *P. falciparum* and *P. yoelii* are more than twice the size of many other proteins of this family. Nevertheless, a realignment of the N-terminal extension suggests that, with the exception of CeTERT, the four N-terminal motifs are universally conserved (Fig. 1). Close inspection of the new alignment revealed the following two interesting features. First, even though there are very few absolutely conserved residues, many positions appear to tolerate only conservative substitutions. A great majority of these conserved positions favor hydrophobic or aromatic residues, which may correspond to key positions in the core of a domain or surface locations crucial for interactions with other domains or molecules. Second, the proposed linker region between the GQ and CP motif is even more variable in length than previously suspected, ranging in size from 19 residues to more than twice the size of many other proteins of this family. Nevertheless, a realignment of the N-terminal extension suggests that, with the exception of CeTERT, the four N-terminal motifs are universally conserved (Fig. 1). Close inspection of the new alignment revealed the following two interesting features. First, even though there are very few absolutely conserved residues, many positions appear to tolerate only conservative substitutions. A great majority of these conserved positions favor hydrophobic or aromatic residues, which may correspond to key positions in the core of a domain or surface locations crucial for interactions with other domains or molecules. Second, the proposed linker region between the GQ and CP motif is even more variable in length than previously suspected, ranging in size from 19 residues to more than twice the size of many other proteins of this family. Nevertheless, a realignment of the N-terminal extension suggests that, with the exception of CeTERT, the four N-terminal motifs are universally conserved (Fig. 1). Close inspection of the new alignment revealed the following two interesting features. First, even though there are very few absolutely conserved residues, many positions appear to tolerate only conservative substitutions. A great majority of these conserved positions favor hydrophobic or aromatic residues, which may correspond to key positions in the core of a domain or surface locations crucial for interactions with other domains or molecules. Second, the proposed linker region between the GQ and CP motif is even more variable in length than previously suspected, ranging in size from 19 residues to more than twice the size of many other proteins of this family. Nevertheless, a realignment of the N-terminal extension suggests that, with the exception of CeTERT, the four N-terminal motifs are universally conserved (Fig. 1). Close inspection of the new alignment revealed the following two interesting features. First, even though there are very few absolutely conserved residues, many positions appear to tolerate only conservative substitutions. A great majority of these conserved positions favor hydrophobic or aromatic residues, which may correspond to key positions in the core of a domain or surface locations crucial for interactions with other domains or molecules. Second, the proposed linker region between the GQ and CP motif is even more variable in length than previously suspected, ranging in size from 19 residues to more than twice the size of many other proteins of this family. Nevertheless, a realignment of the N-terminal extension suggests that, with the exception of CeTERT, the four N-terminal motifs are universally conserved (Fig. 1).

**The CP, QFP, and T Motifs of Yeast TERT Are Required for Telomere Maintenance and Telomerase Enzyme Activity**—To extend our earlier functional analysis of the GQ motif, we created a series of substitution mutants of yeast TERT with alterations in the CP, QFP, and T motifs, and we tested their abilities to support telomere maintenance. A total of 18 mutants with substitution in conserved residues (SCR mutants) were generated, each with one or two residues (and in one case, three residues) changed to alanines: IL256, CP261, LE264, F286, IL290, LLP294, MP299, LL316, LL330, DF338, WL341, W367, IL372, IL376, FF380, TS384, Y394, and W400. Each mutant is designated by the identity and location of the altered
**Fig. 1.** Hidden Markov model-generated multiple sequence alignment for the N-terminal region of known and predicted telomerase reverse transcriptases (TERT). Conserved residues are highlighted, and hydrophobic positions are boxed. Triangles indicate the locations of the *S. cerevisiae* mutations examined in this work. Numbers indicate the number of residues not depicted explicitly. The sequences and their

| GQ | CP | QFP |
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| TERT | GQ | TERT |
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Fig. 2. Mutations in the CP, QFP, and T motifs impair telomere maintenance. Telomere lengths were determined for strains bearing wild type or mutated TERT. The identities of the mutants are indicated at the top of the panel. The location of Y' type telomeres is indicated by brackets. The amplified Y' fragment that are often observed in senescent strains are marked by filled circles.

Mutations in the CP, QFP, and T motifs caused a reduction in the amount of TERT protein and TERT-associated TLC1 RNA. To determine the basis for the activity loss manifested by the SCR mutants, we estimated the levels of TERT protein in wild type and mutant strains using antibodies directed against the protein A tag. The levels of TERT protein in the majority of SCR mutants exhibited varying degrees of telomere shortening. Based on the degree of shortening, the mutant phenotypes were classified as mild (CP261, LE264, GK307, W367, T384, and W400; less than 50 bp shorter than wild type), intermediate (F286, IL290, MF299, LL316, DF338, WL341, LI372, and Y394; 50–200 bp shorter than wild type), or severe (LLP294, LL330, I1376, and FF380; more than 200 bp shorter than wild type). The four strains with severe telomere shortening (LLP294, LL330, I1376, and FF380) also exhibited reduced growth on agar plates as evidenced by reduced colony size (data not shown). In addition, these strains display evidence for amplification of the subtelomeric Y' fragment (indicated by filled circles in Fig. 2), which has been shown previously (51) to correlate with senescence and the generation of type I survivors. As predicted, the single non-SCR mutant (GK307) exhibited no defect in telomere maintenance. Surprisingly, five of the SCR mutants (CP261, LE264, W367, T384, and W400) showed either normal telomeres or very mild shortening. However, where it has been tested in other systems, the equivalent residues appear to be relatively unimportant for telomerase enzyme activity or telomere maintenance (18, 33). We conclude that sequence alignment in the CP, QFP, and T region is useful for identifying functionally important TERT residues.

To determine whether the telomere maintenance defects can be explained by telomerase activity loss or alteration, we precipitated protein A-tagged telomerase from the wild type and mutant strains by adsorption to IgG-Sepharose, and we subjected the Sepharose beads to primer extension analysis. All of the mutant enzymes were tested side-by-side with wild type telomerase using a 16-mer oligonucleotide with non-canonical telomere repeats (TEL66) as the primer substrate (Fig. 3, A and B). In most cases, comparisons were also made using a 15-nt primer with canonical repeats (TEL15), which yielded very similar results (Fig. 3B, and data not shown). As shown in representative assays and the summary plot (Fig. 3C), there is an excellent correlation between the extent of telomere shortening and telomerase activity reduction. Mutant strains with the most severe telomere length defect contain essentially no telomerase activity (LLP294, LL330, I1376, and FF380). For mutants with intermediate telomere defects, the reduction in telomerase activity ranges from ~65% for F286 (which exhibits the least telomere length defect among the intermediate group) to ~95% for DF338, WL341, LI372, and Y394 (which have the most length defect in this group). Mutant strains with mild or no defect had close to or more than 50% of the wild type level of telomerase activity (CP261, LE264, GK307, W367, T384, and W400). None of the mutants with detectable telomerase exhibited an obvious processivity defect (Fig. 3, A and B, and data not shown). Taken together, our results indicate that mutations in the CP, QFP, and T motif impair simultaneously telomere maintenance and telomerase activity but not telomerase processivity.
RNase protection analysis (Fig. 5). In most experiments, a single protected species can be detected (Fig. 5A). However, in some experiments, an additional smaller band can be visualized, presumably arising from excessive degradation of the hybrid by RNases (Fig. 5B). Because both bands are due to TLC1 RNA protection, both are included in the calculation of the amount of this RNA. Comparison of the summary plots in Figs. 5C and 3C revealed an excellent correlation between the extent of activity loss and the degree of reduction in the level of TERT-associated TLC1 RNA. Mutants with close to wild type telomerase activity had high levels of TERT-associated RNA (CP261, LE264, GK307, W367, T384, and W400), whereas those with severe defects had little or no associated RNA (LLP294, LL330, II376, and FF380). These results indicate that the loss of telomerase activity in the mutant strains may be accounted for by the loss of TERT and TERT-associated TLC1 RNA. Furthermore, analysis of mutants with appreciable activities suggests that the telomerase complexes containing mutant proteins have specific activities that are comparable with those containing wild type TERT. For example, although the DF338, WL341, LI372, and Y394 mutant each suffered a 90–95% reduction in activity, each also suffered a 90–95% reduction in TERT-associated RNA (Figs. 3C and 5C). The mutant proteins therefore appear to be catalytically competent once associated with RNA.

Overexpression of the Mutant Proteins Does Not Result in Telomere Shortening—The concomitant reduction in the level of telomerase activity, TERT protein, and TERT-associated TLC1 RNA suggests that mutations in the CP, QFP, and T motifs affected RNP assembly rather than the in vivo and in vitro activity of telomerase. To explore this possibility, we overexpressed various mutant proteins in a wild type strain background, and we analyzed the lengths of telomers in the resulting strains. If the mutant proteins are defective in assembly, then they should not compete with endogenous TERT for association with TLC1 RNA and should not act in a dominant-negative fashion even when overexpressed. This was indeed found to be the case. Five SCR mutants of TERT (LLP294, MF299, LL330, II376, and FF380) were cloned downstream of the strong and constitutive triose-phosphate isomerase promoter, and the resulting plasmids were introduced into a reference strain containing a native TERT gene (W303). Following two re-streaks (−5 generations), chromosomal DNAs were isolated from the clones and analyzed for telomere length alteration (Fig. 6). As a control, a C-terminal truncation mutant (C745), previously shown to be defective in telomerase activity and processivity but not assembly, was tested in parallel (29). As expected, the C745 mutant, when overexpressed, caused dramatic telomere shortening, by ∼200 bp. In contrast, none of the SCR mutants (with alterations in the QFP and T motif) was able to act in a dominant-negative fashion with regard to telomere maintenance. We are led to conclude that the major deficiency engendered by the mutations is in telomerase assembly rather than enzyme function.

The Efficiency of RNP Formation Is Reduced by the Mutations—In the non-overexpression strains analyzed in Figs. 2–5, the concurrent loss of TERT and TERT-associated RNA can be explained as either a direct or indirect consequence of mutations on protein stability. In the former scenario, the mutations might have caused protein misfolding, leading to accelerated degradation. Fewer TERT molecules would then be available for association with TLC1 RNA. In the latter scenario, the
Mutations in the CP, QFP, and T motifs lead to reductions in the level of TERT protein. A, levels of protein A-tagged TERT in the mutant strains were determined by Western blotting using antibodies directed against protein A and compared with that of the wild type strain. The identities of the mutants are indicated at the top, and the relative amounts of extracts loaded indicated at the bottom. The amount 1X denotes 400 μg of total protein. B, the levels of protein A-tagged TERT in the mutant strains were estimated visually based on assays such as those presented in A and the results summarized. The levels are scored as follows: -, < 12.5% of wild type; +, 12.5–25% of wild type; ++, 25–50% of wild type; +++, >50% of wild type. Most of the assays (specifically, the CP and QFP mutants) were performed twice, with very similar results.

Mutations disrupted protein-RNA interaction, resulting in less RNP formation. The unincorporated protein molecules were then preferentially degraded. To distinguish between these possibilities, we examined the efficiency of RNP formation in our overexpression strains. As described earlier, these strains contain, in addition to the native TERT gene, a mutated TERT (tagged with protein A) that is under the control of the strong triose-phosphate isomerase promoter. For comparison, a yeast strain with a tagged wild type gene driven by the native promoter was tested in parallel. As judged by the Western analysis shown in Fig. 7 (top panel), all of the overexpressed mutant proteins accumulated to higher levels than the non-overexpressed wild type protein, which was undetectable in this particular experiment. (The non-overexpressed wild type protein can be detected when the developing time for the blot in the color substrates is increased, as seen in Fig. 4A.) Interestingly, the steady-state level of the LL330 mutant protein is lower than the other mutant proteins, implying some additional defect in protein stability. The levels of TLC1 RNA associated with mutant proteins were measured by IgG-Sepharose adsorption of tagged telomerase followed by RNase protection analysis. Of the mutant proteins, only C745 co-precipitated an increased amount of TLC1 RNA (Fig. 7, middle panel, compare lanes 1 and 7). The other mutants, despite their increased expression, associated with either comparable or reduced levels of RNA in comparison with the non-overexpressed native protein (Fig. 7, middle panel, compare lanes 2–6 with lane 7). Furthermore, the efficiency of RNA association correlates with the extent of functional loss in vivo. For example, of the five overexpressed SCR mutants, MF299 was able to associate with the highest amount of TLC1 RNA when overexpressed. This mutant was also the least impaired in terms of its ability to maintain telomeres in the absence of wild type protein (Fig. 2). These results suggest that the major defect of the mutant proteins is their reduced ability to associate with telomerase RNA.

Mapping of the 3’ End of TLC1 RNA in Telomerase RNP—In the process of quantifying the amount of TERT-associated TLC1 RNA, we noticed that the length of the probe protected by the RNA appears to be shorter than that predicted by previous analysis. According to a published report (41), the de-adenylated, mature RNA is thought to have 3’ ends that cluster near position 1250. If this were true, then the RNase protection assay should yield a protected fragment of ~150 nt. (See Fig. 8A for a schematic illustration of the RNase protection assay.) However, our analysis of telomerase-associated TLC1 RNA in both IgG-Sepharose precipitates and DEAE fractions consistently yielded a shorter fragment of ~70 nt (Figs. 5, 7B, and 8B). To determine whether the short fragment was due to an
unstable hybrid that can be cleaved internally by the RNases, we subjected an in vitro transcript that encompasses residues 1–1301 of the TLC1 RNA to the same assay. As shown in Fig. 8B, with this RNA, only a 200-nt fragment can be detected. Moreover, the use of a 1–917 transcript, missing the region of TLC1 complementary to the probe, completely abolished the signal. Taken together, our results indicate that the RNase protection assay correctly maps the 3′/H11032 end of the in vivo and in vitro RNA.

To further refine the mapping analysis, we sequenced the 3′/H11032 end of the in vivo RNA using a protocol developed previously (41). The RNAs in the fraction were extended by poly(A) polymerase and reverse-transcribed into cDNA using an oligo(dT)-containing primer. The 3′/H11032 region of TLC1 cDNA was then specifically amplified by PCR, cloned into a plasmid vector, and sequenced. As a control for the reliability of the pro-
cEDURE, we analyzed the 3’ end of the 1–1301 transcript in parallel. As shown in Fig. 6C, The PCR fragments for the in vivo and in vitro RNA differ in size by −130 bp, again consistent with the RNase protection study. Sequence analysis of independent clones indicate that the in vivo RNA terminates at either position 1167 or 1168, whereas the in vitro RNA terminates in a partial XhoI site after position 1301, precisely as predicted (Fig. 6D). We conclude that the major 3’ end for telomerase-associated TLC1 RNA is considerably more upstream of the major polyadenylation sites (~1250), suggesting that during telomerase maturation, the RNA undergoes both de-adenylation and nucleolytic cleavage.

**DISCUSSION**

The Functions of the CP, QFP, and T Motifs—We have shown in this study that three of the four conserved N-terminal motifs of yeast TERT are required for efficient telomerase ribonucleoprotein assembly but not for enzyme function. Evidence in favor of this proposition includes the following: 1) the simultaneous loss of telomerase activity, TERT protein, and TERT-associated RNA in the mutant strains; 2) the inability of the mutant proteins to act in a dominant-negative fashion when overexpressed in the presence of wild type protein; and 3) the failure of the overexpressed mutant proteins to associate with telomerase RNA efficiently; and 4) the close quantitative correlation between telomerase activity and telomerase-associated RNA in the mutant and overexpression strains. Friedman and Cech (52) have shown earlier that two 10-amino acid substitutions in region III of yeast TERT (corresponding to the QFP motif) impair association with TLC1 RNA. Our results are in agreement and highlight the importance of conserved TERT residues in mediating telomerase assembly.

The mechanistic basis for the observed assembly defect is not clear from the present analysis; telomerase biogenesis entails multiple steps, several of which can potentially be disrupted by the mutations. Based on earlier analysis from several systems, two plausible hypotheses may be considered. First, direct physical interaction between yeast TERT and TLC1 RNA may be impaired by the mutations. Consistent with this idea, the CP, QFP, and T motifs of Tetrahymena and human TERT have been demonstrated previously (33, 53-55) to be required for binding telomerase RNA in vitro. Second, relevant intracellular localization of yeast TERT may be impaired by the mutations, leading to reduced assembly. Consistent with this latter possibility, residues in the CP and T motifs of human TERT are believed to mediate nuclear localization, and nuclear localization has been proposed to be an important step in telomerase biogenesis (55-57). Further studies will be necessary to distinguish between these (non-mutually exclusive) hypotheses.

The phenotypic consequences of mutations in the CP, QFP, and T motifs contrast sharply with those of the GQ motif. For instance, some of the mutations in the GQ region adversely affect telomere maintenance without affecting telomerase activity (32, 52, 58). In addition, alteration of conserved residues in the GQ motif can result in mutants that act in a dominant-negative fashion when overexpressed in the presence of wild type protein, indicative of some defect in enzyme function rather than assembly (32). Finally, in complementation experiments in vitro, telomerase activity can be reconstituted by mixing an active-site mutant of human TERT with one that bears mutations in the GQ motif (but not in the other three motifs) (59). Taken together, these results strongly implicate a separate function(s) for the most N-terminal GQ motif, which apparently resides in a distinct physical domain (32).

**Evolutionary Conservation of the TERT N-terminal Motifs—** The evolutionary conservation of TERT N-terminal motifs is remarkable and is consistent with crucial function(s) for these motifs in telomerase assembly and/or catalysis. As described earlier, an interesting feature of these motifs is the preponderance of hydrophobic/aromatic residues at conserved positions. If the CP, QFP, and T motifs are indeed involved in direct RNA-protein binding, as suggested earlier, then it is tempting to speculate that this binding may occur primarily through base-stacking interactions. It is also tempting to speculate that common features of the telomerase RNAs may be recognized by these motifs. Conversely, the apparent lack of these motifs in C. elegans TERT suggests that the nature of RNA-protein interaction may be quite distinct for this telomerase.

**The Processing of Telomerase RNA—** The synthesis and maturation of telomerase RNA appears to be a poorly conserved process. For example, in ciliates, telomerase RNA is evidently transcribed by RNA polymerase III, whereas in yeast and mammals, the same function is mediated by RNA polymerase II (41, 60–62). Human telomerase RNA appears to be processed by the same factors that process small nuclear RNAs with the box H/ACA motif (62, 63). In contrast, the Saccharomyces TLC1 RNA is bound by Sm proteins and requires the same proteins for accumulation (64). Understanding the precise pathways of RNA maturation is clearly an important aspect of understanding telomerase biogenesis. An earlier study of TLC1 RNA processing indicates that this RNA is transcribed by RNA polymerase II and initially polyadenylated (41). The majority of RNA then becomes de-adenylated, and this appears to be the predominant form that is present in telomerase RNP. With the exception of the poly(A) tail, the two RNA populations are believed to have the same 3’ ends, clustering around position 1250. However, our current study suggests that the majority of telomerase-associated TLC1 RNA has a more upstream 3’ end, around position 1167. TLC1 RNA may therefore be subjected to additional cleavage events during maturation and RNP assembly. Curiously, the newly discovered 3’ end is only a few nucleotides downstream of the Sm protein-binding site (Fig. 8D), suggesting that the cleavage activity may be regulated by the Sm protein complex (64). Such a cleavage step appears to be common to small nuclear RNAs that associate with Sm proteins, implying a further parallel between the processing of these RNAs and TLC1 (65).

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