**Arabidopsis thaliana** telomeric DNA-binding protein 1 is required for telomere length homeostasis and its Myb-extension domain stabilizes plant telomeric DNA binding

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**ABSTRACT**

Telomeres are specific protein–DNA complexes that protect the ends of eukaryotic chromosomes from fusion and degradation and are maintained by a specialized mechanism exerted by telomerase and telomere-binding proteins (TBPs), which are evolutionarily conserved. **AtTBP1** is an *Arabidopsis thaliana* protein that binds plant telomeric DNA in vitro. Here, we demonstrated that lack of **AtTBP1** results in a deregulation of telomere length control, with mutant telomeres expanding steadily by the fourth generation. DNA-binding studies with mutant **AtTBP1** proteins showed that the Myb-extension domain of **AtTBP1** is required for binding to plant telomeric DNA. Our results suggest that **AtTBP1** is involved in the telomere length mechanism in *A. thaliana* and that the Myb-extension domain of **AtTBP1** may stabilize plant telomeric DNA binding.

**INTRODUCTION**

Eukaryotic telomeres are maintained by several telomeric factors, including telomerase, shelterin subunits (TRF1, TRF2, TIN2, Rap1, TPP1 and POT1) and non-shelterin proteins (Mre11/Rad50/Nbs1, ERCC1/XPF, WRN, BLM, DNA-PK, Tankyrases and Rad51D) (1). The typical shelterin components, TRF1 and TRF2, recognize telomeric DNA, have the capacity to regulate t-loop structures, and can be involved in the canonical DNA damage response (1,2). The in vivo dominant inhibition studies suggest that the main function of TRF1 is to negatively regulate telomere length (3) and that of TRF2 is to protect chromosome ends (4). In mouse embryonic cells, a conditional null mutation in TRF1 induces growth defects and chromosomal instability (5). Deletion of TRF2 results in extensive telomere fusions and activates the DNA damage response machinery without detectable degradation of the telomeric DNA (6).

In contrast to mammals, *Arabidopsis thaliana* displays a remarkable tolerance to telomere dysfunction and chromosome instability (7,8). This makes *A. thaliana* a useful system to investigate the roles of shelterin genes in telomere biology by studying lines containing multiple mutations. For example, the disruption of **AtTERT** gene leads to telomere shortening and the symptom of developmental defects in the sixth generation of the mutant (9). **AtRad50** mutant cells present a dramatic loss of telomeric DNA and cell death (10). In contrast, *A. thaliana* mutants lacking **Ku70**, **Ku80** and **MRE11** display increased telomere length (11–13). Using activation-tagged line screening method, Ren et al. characterized a novel zinc-finger protein, telomerase activator 1, which induces telomerase in leaves (14). However, this activity does not increase telomere length. This result implies that access to the telomeres by telomerase is regulated by shelterin proteins. Thus shelterin is more critical regulator in telomere homeostasis.

Although several non-shelterin proteins from plants have been characterized, the physiological functions of the *A. thaliana* double-stranded TBPs have not previously been assessed. Several *A. thaliana* **AtTBP** genes have been identified, and these genes encode proteins that specifically bind to plant telomeric DNA in vitro (15,16). These proteins are similar in structure to the mammalian TRFs as they harbor a single Myb telomeric DNA-binding domain in their C-terminus (16). Here, we investigate the role of *A. thaliana* telomeric DNA-binding protein 1 (**AtTBP1**) in telomere maintenance and describe the consequences of an **AtTBP1** deficiency in *A. thaliana*.

In the mouse, inactivation of the shelterin (**mTRF1** or **mTIN2** genes) results in embryonic lethality, and this phenotype is not due to unregulated telomeric function (17,18). In contrast, we found that mutant **AtTBP1** plants were viable and that a lack of this gene resulted in a

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deregulation of telomere length control, with mutant telomerases expanding steadily by the fourth generation.

MATERIALS AND METHODS

Plant material and growth conditions

Arabidopsis thaliana plants (ecotype Wassilewskija) were cultivated at 22°C in a growth chamber under a 16/8 h light/dark photoperiod. Arabidopsis seeds were surface sterilized in 5% bleach solution and plated on solid 1X Murashige and Skoog (MS) medium or transferred to soil.

Mutant identification

We screened the Institut National de la Recherche Agronomique Versailles (INRAV) Arabidopsis T-DNA insertion database (19), and identified a putative mutant at the TBP1 gene. The progeny of plants heterozygous for a T-DNA insertion into the TBP1 gene were genotyped by PCR, using the primers TBP1-KO-F (5'-GGTCCTACCACCAAATTACAT-3') and L1 (T-DNA left border) (5'-CTACAAATTGCCCTTTTCTATCGAC-3'). A 997-bp product was generated from the wild-type allele and a 593-bp product from the disrupted allele. For segregation analysis and for the selection of plants with the T-DNA disruption, plants homozygous for the T-DNA disruption in the AtTBP1 gene were genotyped (as G1) and self-pollinated to obtain subsequent generations. For the DNA blots, 10 µg total DNA, isolated using a standard method (20), were digested overnight with EcoRI or HindIII. The probe used on the blot was a 1.5-kb GUS fragment, labeled with [α-32P]dCTP.

Expression analysis of AtTBP1 mRNA

Fifteen micrograms of total RNA was separated in a 1.2% formaldehyde gel and blotted onto a Hybond N+ membrane (Amersham). Hybridization with 32P-labeled cDNA probes, labeled by random priming, was carried out as described (20). Expression analysis of the regions flanking the T-DNA insertion in the AtTBP1 gene was performed, using 2 µg of total RNA and the M-MLV reverse transcriptase RT-PCR kit (Promega) (16). The following primer sets were used: F1 (5'-ATGGTGTTGCAAAAGGAGACATTGAATGTGAA-3'), R1 (5'-AAGAGGAGACATTGAATGTGAA-3'), R2 (5'-TTCCAGAACAAAGAAGGAGGAGCAAGGAA-3'), R3 (5'-GGTGGGAGTCCTCTACATC-3'), R4 (5'-GGTGGGAGTCCTCTACATC-3') (to visualize products on SDS-PAGE) or without labeled primers (10). PCR products were resolved by electrophoresis on 1% agarose gels.

Complementation analysis

For the complementation test of AtTBP1−/− plants, a 5.1-kb genomic DNA fragment of the AtTBP1 gene, containing 2.0 kb of putative promoter sequence, was amplified by PCR, using primers TBP1-Compl.-F (5'-GTACCTGAGTGTTGTCATGACATATCAG-3') and TBP1-Compl.-R (5'-GTACCGGAAACAGTCAGGCAATG-3'), cloned into a pGEM-T Easy vector (Promega) and then subcloned into a binary vector pFP100 (25). The complementation vector was introduced into the Agrobacterium tumefaciens strain, GV3101. Plants homozygous for the T-DNA disruption in AtTBP1 were transformed by the in planta method (26). Transformants were selected using a seed-expressed fluorescent marker (25) and then genotyped and analyzed for AtTBP1 mRNA expression and telomere length, as described above.

Protein expression

Expression of full-length AtTBP1 and AtTBP1ΔMyb mutant constructs was achieved by using a rabbit reticulocyte lysate TNT system (Promega) under reaction conditions described by the supplier. Briefly, 1.0 µg cloned plasmid DNA was used per 50 µl reaction, containing T7 RNA polymerase in the presence of [35S] methionine (to visualize products on SDS-PAGE) or without labeled amino acids (for EMSA). After the transcription–translation reaction, samples were diluted 1:3 with the addition of 100 µl of EMSA buffer. Of this mixture, ~2.0–8.0 µl was used in EMSA reactions.

To test telomeric DNA-binding activity of AtTBP1 mutants, the plant TBP-specific domain deletion mutants were cloned into the vector, pGEX-5X-2, between the EcoRI and XhoI sites, using PCR-generated fragments. GST-AtTBP1661-640, ΔC1 (461-592), ΔC2 (461-601), ΔC3 (461-609), ΔC4 (461-618), ΔC5 (461-622) and ΔS593-618 were expressed in E. coli BL21 (DE3)/RIL cells.
(Stratagene) and purified on a GSTrap™ column, as directed by the manufacturer (Amersham). Mutations R607G and R607I were introduced, using the QuickChange site-directed mutagenesis kit (Stratagene). The protein concentration was determined by Bradford assay and stored in aliquots at −80°C. Purified proteins were analyzed by SDS-PAGE.

Electrophoretic mobility shift assay (EMSA)

Electrophoretic mobility shift assay (EMSA) was performed, as described previously (16). Telomeric DNA probes and competitors were designed with double-stranded oligonucleotides. Oligonucleotides were labeled at the 5' end with T4 polynucleotide kinase, using [γ-32P]ATP and annealed in TNE buffer (10 mM Tris-HCl, pH 8.0, 100 mM NaCl, 1 mM EDTA) by boiling, followed by cooling to room temperature and purified in 8% polyacrylamide gels. To reduce non-specific DNA–protein binding, proteins were pre-incubated with 1.0 μg poly (dl-dC) in 20 μL EMSA buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA, 1 mM dithiothreitol, 50 mM NaCl and 5% glycerol) for 20 min on ice. The end-labeled DNA probe (10 fmol) was added to the reaction mixture. After incubation for 30 min on ice, the mixture was loaded on a 5% non-denaturing polyacrylamide gel (29:1, monomer:bis). Before loading, gels were pre-run at 16 mA for 30 min, and electrophoresis was performed at 16 mA in 1× TBE for 2.5 h; dried gels were analyzed using the Phosphorimagier (Fuji Photofilm). For competition experiments, varying amounts of cold competitors were pre-incubated with reaction samples before the addition of radiolabeled probe. Binding activity was quantified with an Image Gauge Version 2.53 (Fuji Photofilm).

RESULTS

Isolation and characterization of the AtTBP1 mutant

To study the biological function of AtTBP1 in planta, we screened the INRAV Arabidopsis T-DNA insertion collection (19) and identified a putative mutant plant (FST 072C05) with a T-DNA insertion into the AtTBP1 gene. In the INRAV database, the insertion was annotated (FST 072C05) with a T-DNA insertion into the AtTBP1 gene. The protein concentration was determined by Bradford assay and stored in aliquots at −80°C. Purified proteins were analyzed by SDS-PAGE.

Electrophoretic mobility shift assay (EMSA)

Electrophoretic mobility shift assay (EMSA) was performed, as described previously (16). Telomeric DNA probes and competitors were designed with double-stranded oligonucleotides. Oligonucleotides were labeled at the 5' end with T4 polynucleotide kinase, using [γ-32P]ATP and annealed in TNE buffer (10 mM Tris-HCl, pH 8.0, 100 mM NaCl, 1 mM EDTA) by boiling, followed by cooling to room temperature and purified in 8% polyacrylamide gels. To reduce non-specific DNA–protein binding, proteins were pre-incubated with 1.0 μg poly (dl-dC) in 20 μL EMSA buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA, 1 mM dithiothreitol, 50 mM NaCl and 5% glycerol) for 20 min on ice. The end-labeled DNA probe (10 fmol) was added to the reaction mixture. After incubation for 30 min on ice, the mixture was loaded on a 5% non-denaturing polyacrylamide gel (29:1, monomer:bis). Before loading, gels were pre-run at 16 mA for 30 min, and electrophoresis was performed at 16 mA in 1× TBE for 2.5 h; dried gels were analyzed using the Phosphorimagier (Fuji Photofilm). For competition experiments, varying amounts of cold competitors were pre-incubated with reaction samples before the addition of radiolabeled probe. Binding activity was quantified with an Image Gauge Version 2.53 (Fuji Photofilm).

Northern blot analysis of mutants homozygous for the T-DNA insertion failed to detect AtTBP1 mRNA, while mRNA of the predicted size, ~2.5 kb, was detected in wild-type plants (Figure 1B). We confirmed that expression of the full-length transcript was abolished by the T-DNA insertion by performing RT-PCR, using various primers. No product was obtained after 38 cycles of PCR amplification (data not shown). RT-PCR of the AtTBP1 5' and 3' coding regions flanking the T-DNA insertion, however, revealed the presence of low-abundance transcripts, undetectable by northern blotting (Figure 1C). Remarkably, the expression of an AtTBP1 mRNA downstream of the insertion was detected (Figure 1C, F2 + R4). As in other T-DNA mutants (11,27,28), these short transcripts are probably abnormal RNA forms that are fused with RNA produced from the T-DNA marker cassette, which is regulated by the 35S promoter and initiated within the T-DNA insert (Figure 1C, L1 + R4). It is unlikely that this unusual RT-PCR product is functional, because it contains only a very short coding region of the C-terminus of AtTBP1 (~30 a.a.). Sequence analysis of the cDNA species, amplified by RT-PCR with the 5' flanking region of T-DNA, predicts that the mutant produces a truncated protein, comprised of the first 451 a.a. of the 640 a.a. full-length AtTBP1 protein, because a TAA stop codon is encountered in the eighth exon (Figure 1D). These results suggest that the function of this truncated AtTBP1 protein is severely compromised if not null.

Selected heterozygous plants were self-pollinated to obtain homozygous mutants (G1 AtTBP1/−) and wild-type plants (G1 WT). Four homozygous lines, including two mutant G1 plants and two wild-type plants, were generated from the heterozygous line. These wild-type siblings were used for experimental controls. Individual lines were propagated through successive generations by self-pollination. Seeds from several plants within a single line were pooled each generation until G4. Plants with an AtTBP1 disruption, however, did not exhibit an obvious phenotypic difference from wild type in the first four generations under normal growth conditions.

Telomere status in AtTBP1-deficient Arabidopsis

As AtTBP1 mutant plants were visibly indistinguishable from wild-type plants, we next examined the role of AtTBP1 in telomere length homeostasis by determining telomere length in mutant plants with TRF analysis. A recent study suggested that the Ws ecotype of A. thaliana displays a bimodal size distribution, with one group bearing shorter telomeres (2–5 kb) and the other bearing longer telomeres (4–9 kb) (24). In our experiments, the wild-type telomeres ranged in size from 2.5 to 4.5 kb and were the same size as the telomeres in the short group (Figure 2A, lane 2). This short telomere size of wild-type plants was stably inherited for at least four successive generations (data not shown). In sharp contrast, TRF analysis of G2 to G4 mutant populations showed that telomeres in AtTBP1 homozygous mutants increased steadily to 10 kb after four generations (Figure 2A, lanes 3–5). Thus, telomeres in AtTBP1 mutants extended...
to over twice the size of those in wild-type plants in four generations.

To investigate telomere dynamics in individual plants, we examined TRFs from individual G2 to G4 mutant leaves. As expected, the telomeres in individual mutants increased steadily like those of pooled mutant seedlings (Figure 2B). The banding profile of TRFs in individuals was, however, displayed in a more discrete pattern than that of pooled samples. For analysis of individual chromosome ends, TRF analysis was performed with a probe specific to the Ch2R. As shown in Figure 2C, the Ch2R probe displayed a discrete band of 4–5 kb in wild-type plants, and one or two discrete bands of 4–7 kb in mutant plants. Individual telomere tracts at the same generation were distributed within a 1-kb range. These results indicate that the telomeres in individual mutant plants also increased continuously for each generation.

To verify that the telomere elongation phenotype was associated with the T-DNA insertion in the AtTBP1 gene, molecular complementation was performed. A wild-type genomic fragment, containing a putative promoter sequence, was introduced into the AtTBP1 mutant background via in planta transformation. Selected T3 transformants were analyzed for AtTBP1 mRNA expression and telomere length (Figure 3). The complemented mutants expressed wild-type AtTBP1 mRNA ectopically (Figure 3A). In each case, the ectopic expression of AtTBP1 prevented the telomere extension and restored the telomere length to that of the wild-type plants (Figure 3B, lanes 4 and 5). Therefore, we conclude that attbp1/C0 corresponds to a mutant allele of the AtTBP1 gene. These results also demonstrate that AtTBP1 is involved in the regulation of telomere length.

**Telomeric DNA-binding activity and the functional telomere-binding domain**

We previously reported that the isolated C-terminal segment of AtTBP1 is capable of sequence-specific binding
to plant telomeric repeats in vitro (15,16). The \textit{AtTBP1} mutant that we characterized here, carries a T-DNA insertion at the eighth exon, which encodes the putative DNA-binding domain of \textit{AtTBP1}. Although we could detect no full-length transcripts in \textit{AtTBP1} mutant plants, a transcript of very low abundance, containing the N-terminal sequence upstream of the T-DNA insertion, was detected by RT-PCR. It is unlikely that a truncated protein translated from this RNA would be functional in telomere maintenance. Therefore, we hypothesized that full-length \textit{AtTBP1} binds to plant telomeric DNA, whereas the C-terminal deletion mutant does not bind to plant telomeric DNA. Expression of full-length \textit{AtTBP1} and mutant \textit{AtTBP1} (\textit{AtTBP1}−/− Myb) was achieved by using an in vitro translation system. As expected, in vitro translation of the \textit{AtTBP1} and \textit{AtTBP1}−/− Myb cDNAs resulted in the synthesis of a polypeptide with an apparent molecular weight of ~70 and ~50 kDa, respectively (Figure 4A). In order to test whether full-length \textit{AtTBP1} binds to plant telomeric DNA, specifically, the in vitro translated protein was used in EMSAs with a radiolabeled DNA probe. The reticulocyte lysate, containing \textit{AtTBP1}, gave rise to a discrete complex, whereas the lysate devoid of \textit{AtTBP1} did not exhibit any DNA-binding activity under the same conditions (Figure 4B, lanes 2–8). However, the full-length \textit{AtTBP1} and telomeric DNA complexes failed to exit the well of the gel, as also noted from a previous study (29). Nevertheless, the intensities of discrete bands increased upon the addition of an increasing amount of the expressed \textit{AtTBP1} (Figure 4B, lanes 2–4). Competition binding experiments showed that a 5-fold excess of cold \textit{AtTR-4} is enough to displace the labeled probe, whereas higher molar amounts of unrelated non-specific cold competitor (commercial 1-kb DNA ladder marker or non-plant telomeric repeats, such as the human telomeric repeat, TTAGGG) did not compete (Figure 4B, lanes 5–7, data not shown). These results demonstrate that the telomeric DNA-binding activity of full-length \textit{AtTBP1} increased with increasing amounts of protein, and the binding activity was sequence specific to plant telomeric DNA. In contrast, the \textit{AtTBP1}−/− Myb mutant did not bind to plant telomeric DNA (Figure 4B, lanes 9 and 10). These results suggest that full-length \textit{AtTBP1} is sufficient for specific interaction with duplex telomeric DNA in vitro, and the C-terminus of this protein may be required for the telomeric function.
Thus, these results strongly suggest that the telomere length deregulation in the AtTBP1 mutant may be associated with the loss of the telomeric DNA-binding activity of AtTBP1.

Sequence analysis of plant TBPs has demonstrated that there are key features of specific, well-conserved domains (16). Interestingly, plant TBPs have an expanded and plant-specific Myb-domain, which is very highly conserved. We asked whether this domain would play an important role in binding to plant telomeric DNA. Recent results have shown that A. thaliana TBPs, TRFL1 (At3g12560) and AtTRP1 (At5g59430), have the Myb-extension domain and that this domain is required for binding plant telomeric DNA (29,30). However, these reports did not characterize the functional region of the Myb-extension domain in detail. Therefore, we characterized several mutant AtTBP1 proteins in order to define the minimal length for telomeric-DNA binding and also to examine the binding properties of the Myb-extension domain of AtTBP1. To examine the contribution of the expanded plant-specific Myb domain and to avoid the problem of protein aggregation associated with the full-length protein-binding assay, we performed EMSA with the various mutated forms, using either fragments or the entire GST-AtTBP1461–640 (Figure 4C). The results shown in Figure 4D demonstrate that the truncated mutants, C1 (461–592), C2 (461–601), and C3 (593–618), did not bind to plant telomeric DNA (lanes 4–7 and lanes 18–20). In contrast, the other mutant proteins, C3 (461–609), C4 (461–618) and C5 (461–622) were capable of binding to the telomeric DNA (lanes 8–13). Lanes 2 and 3 and lanes 12 and 13 showed that C5 (461–622) formed a complex with plant telomeric DNA which resembled that of the GST-AtTBP1 461–640 control. A noteworthy observation is that, when more of the Myb-extension domain of AtTBP1 was deleted, weaker DNA–protein complexes were observed (lanes 8 and 9 and lanes 10 and 11). The binding signal of the deletion mutants, C3 and C4, were 39 and 60%, respectively, of that of GST-AtTBP1 461–640 (Figure 4E). Additionally, in order to evaluate the importance of this putative α-helix portion of the Myb-extension domain, we constructed AtTBP1 point mutants, containing a glycine (R607G) or an isoleucine (R607I) at position 607. The single substitution of the 607 arginine residue reduced the capacity to bind telomeric DNA to 41% (R607G) and 23% (R607I), respectively, of that of GST-AtTBP1 461–640 (Figure 4D lanes 21–26 and Figure 4E). These results firmly support the idea that the region of the plant-specific Myb-extension domain between residues 593 and 622 is critical for optimal plant telomere binding of AtTBP1.

Figure 3. Molecular complementation of AtTBP1 deficiency using wild-type AtTBP1 gene. (A) Analysis of the complemented plants by semi-quantitative RT-PCR. RNAs of complemented transformants were extracted from seedlings of T3 homozygous and heterozygous plants. AtTBP1 transcripts were amplified by 35 cycles of PCR with specific sets of primers (F1 and R3). The 60S RP L27A gene was used to indicate the amount of template for quantitative comparison (bottom panel). (B) TRF assay of complemented plants. Tru9I-digested DNAs from wild-type, AtTBP1 mutant plants, complemented heterozygous plants (compl.+/0) and complemented homozygous plants (compl.+/+) were analyzed.

A recent study suggested that hTRF1 enters the nucleus through a nuclear import pathway mediated by Importin and that the concentration of nuclear hTRF1 is critical in regulating telomere length (31). Based on these observations, we concluded that understanding the NLS (Nuclear Localization Signal)-singular form of AtTBP1 should be important in understanding the biological function of AtTBP1. In order to confirm the nuclear localization of AtTBP1, we performed experiments involving green fluorescent protein fused to AtTBP1. Our
Figure 4. DNA-binding properties of full-length AtTBP1 and analysis of Myb-extension domain of AtTBP1. (A) SDS-PAGE gel showing \[^{35}\text{S}\] methionine-labeled products resulting from in vitro translation of the AtTBP1 derivatives. (B) EMSA with full-length AtTBP1 (lanes 2–7) and AtTBP1-ΔMyb (lanes 9 and 10). The shifted bands indicate DNA–protein complexes with end-labeled plant 4-repeat telomeric DNA (AtTR-4). Schematic diagrams on right-hand sides of figures show possible DNA–protein complexes. (C) Analysis of the Myb-extension domain contained in \(\text{AtTBP1}^{461-640}\). Domain D (16) is marked with underlined italic letters. The single Myb telomeric DNA-binding domain is indicated with a white box, and the Myb-extension domain is indicated with a black box. The putative \(\alpha\)-helix in Myb-extension domain is schematically indicated below. The asterisk indicates the amino acid that was altered by site-directed mutagenesis. (D) DNA-binding properties of Myb-extension domain mutant proteins. EMSA was performed with the various mutant proteins, as shown in (C). The shift bands indicate DNA–protein complexes with end-labeled AtTR-4 in the absence or presence of specific competitor DNAs. (E) Quantification of DNA-binding activities of mutant proteins. The data represent the means of three independent assays; bars denote standard deviation.
localization experiments indicate that AtTBP1 proteins accumulate in nucleus and the NLS for these proteins is present in the fourth basic cluster (287-KRETHKRRK-296) of the full-length protein (supplementary Figure S2). Thus, these results demonstrate that the functional NLS of AtTBP1 may play crucial roles in telomere functions, such as the localization to the nucleus, in Arabidopsis. Because onion cells, in which we transiently expressed GFP-AtTBP1, apparently lack Arabidopsis-type telomeric repeats (32), we could not show the sub-nuclear localization of AtTBP1. Therefore, further analysis will be required to determine whether this protein associates specifically with Arabidopsis-chromosome ends in vivo.

DISCUSSION

The telomeres of A. thaliana became much longer when the AtTBP1 gene was disrupted. One possible explanation for this phenomenon derives from the role that shelterins play in telomere length control. Shelterin determines the t-loop architecture of the telomere terminus and controls the synthesis of telomeric DNA by telomerase (1). Disturbing expression levels of shelterin components dramatically impacts on telomere length (1). As t-loops are also observed at plant telomeres (33), the telomere regulation mechanism in A. thaliana may be very similar to other eukaryotes. Therefore, the longer telomeres in AtTBP1 mutant plants could result from a disruption in higher order telomere structure that increases the access of telomerase.

Several mutational analyses revealed that A. thaliana telomeric factors are orthologous to human and yeast telomeric factors, but have some unique functions. For example, AtKu70 mutants have dramatically extended telomeres that reach to ~20–30 kb by the second generation (11,34). Additionally, in AtKu80/−/− cells, telomeres have reached their maximum length (ca. ~10 kb) after 27 weeks, and this length is stable for 34 weeks of growth (12). On the other hand, the telomeres of the AtTBP1 mutants shown in the present study are like those of AtMre11 mutants (13), which have telomeres extended to ~10 kb by the fourth generation (Figure 2). These findings demonstrate that these telomeric proteins may have different effects on telomere length. Based on these observations, we suggest that AtTBP1 may have a more subtle role in telomere length regulation, as compared to the double-strand break repair proteins, such as the Ku heterodimer. Recent data showed that A. thaliana contains multiple AtTBP1 members which can bind to plant telomeric DNA in vitro (16,29), whereas vertebrates have only two double-strand TBP's, TRF1 and TRF2. Thus, it is possible that the plant shelterin structure is more complex than that of human shelterin. Therefore, whether A. thaliana plants with mutations in multiple members of this gene family have any effect on telomere homeostasis needs to be investigated further. In addition, monitoring telomere status in subsequent generations of the AtTBP1 mutants studied in present study will be necessary to determine whether and when equilibrium is reached.

The telomeric-DNA-binding function of AtTBP1 is likely to be completely abolished in the AtTBP1 mutants, based on our in vitro results (Figure 4B). However, we cannot rule out the possibility that a polypeptide derived from the AtTBP1 N-terminus, which was detected at the transcript level by RT-PCR, interferes with the biological functions of the telomere machinery in planta. Human TRFs contain different N-terminal domains, such as an acidic domain in hTRF1 and a basic domain in hTRF2, as well as a conserved TRF homology domain, which can form homodimers and also mediate interactions with other telomeric proteins (1). These domains play important roles in protein modification, such as ADP-ribosylation, phosphorylation and ubiquitination, which may play a role in telomere maintenance (35–39). Like other well-known telomere-binding proteins (TBPs), such as hTRF1 and hTRF2, highly conserved domains are also located in the N-terminus of AtTBP1 family members (16,29). Therefore, whether the N-terminal conserved domains of AtTBP1 are involved in metabolism of this protein and/or the regulation of telomere length needs to be investigated further.

One of the most conspicuous differences between AtTBP1 and hTRF1 is the presence of a highly conserved Myb-extension domain in AtTBP1 (Figure 5). We found that the Myb-extension domain is necessary to allow the C-terminus of AtTBP1 to bind to plant telomeric DNA and to stabilize the DNA–protein complex (Figure 4D). The NMR structure of the C-terminus of AtTRP1, which is a member of A. thaliana TBPs, displays a novel four-helix tetrahedron rather than the three-helix bundle structure, found in hTRF1 families (30). However, similar to the hTRF1 Myb-domain, AtTRP1 uses a helix-turn-helix motif to bind to telomeric DNA, and the third helix plays a major role in sequence-specific recognition. Although there are structural similarities between plant and animal proteins, our present data showed that Myb-extension domain deletion mutants of AtTBP1, which have an intact, three-helix bundle motif, like hTRF1, were unable to bind either to plant telomeric DNA or to human telomeric DNA in vitro (Figure 4D lanes 18–20, data not shown). Therefore, we conclude that the C-terminus of AtTBP1 comprises a domain unique to plants that specifically recognizes plant telomeric DNA.

Taken together, our study provides the first insight into the role of AtTBP1 as a negative regulator of telomere homeostasis in A. thaliana. Our results also demonstrate that a plant-specific Myb-extension domain may be critical for recognition of plant telomeric DNA and in stabilization of AtTBP1 binding to plant telomeric DNA. In addition, further analysis of the genetic interactions of AtTBP1 and other telomeric components using previously isolated A. thaliana mutants, like attert, atku70, atku80, atmre11 and others, should help to clarify the contribution of these proteins to telomere maintenance.

SUPPLEMENTARY DATA

Supplementary Data is available at NAR Online.
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Conflict of interest statement. None declared.

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