Origin-dependent initiation of DNA replication within telomeric sequences

Isabel Kurth and Jean Gautier*

Institute for Cancer Genetics, Department of Genetics and Development and Herbert Irving Comprehensive Cancer Center, Columbia University Medical Center, New York, NY, 10032, USA

Received March 15, 2009; Revised October 7, 2009; Accepted October 8, 2009

ABSTRACT

Replication of telomeres requires the action of telomerase, the semi-conservative replication machinery and the stabilization of the replication fork during passage through telomeric DNA. Whether vertebrate telomeres support initiation of replication has not been experimentally addressed. Using Xenopus cell free extracts we established a system to study replication initiation within linear telomeric DNA substrates. We show binding of TRF2 to telomeric DNA, indicating that exogenous DNA exclusively composed of telomeric repeats is recognized by shelterin components. Interaction with telomere binding proteins is not sufficient to prevent a DNA damage response. Notably, we observe regulated assembly of the pre-replicative complex proteins ORC2, MCM6 and Cdc6 to telomeric DNA. Most importantly, we detect origin-dependent replication of telomeric substrates under conditions that inhibit checkpoint activation. These results indicate that pre-replicative complexes assemble within telomeric DNA and can be converted into functional origins.

INTRODUCTION

In vertebrates, telomeric DNA is composed of 5–50 kb of repetitive arrays of TTAGGG. These sequences are recognized by a protein complex called ‘shelterin’, which is essential for telomere end-protection and length regulation (1). Loss of telomeric proteins or shortening of telomeres beyond a critical length triggers a DNA damage response characterized by the recruitment of DNA damage response proteins to telomeric ends and the activation of checkpoints, which lead to senescence or apoptosis (1). Complete and faithful replication of telomeric DNA is essential to maintain chromosome stability and for cell cycle progression. However, little is known about the molecular mechanisms that underlie replication initiation and progression of the semi-conservative replication machinery through telomeric DNA. Telomeres are challenging structures to replicate due to their repetitive sequences and the structures they can adopt including G-quadruplexes and heterochromatin (2). In yeast and human cells, replication forks naturally stall at telomeric DNA (3,4), indicating that telomeric DNA is replicated slowly. TRF1 and TRF2 inhibit replication fork progression in an in vitro replication system of SV40 DNA, (5), whereas in fission yeast, absence of Taz1 induces replication fork stalling and entanglement of telomeres (4). In Saccharomyces cerevisiae, replication is initiated within autonomously replicating sequences (ARS), which are bound by the origin recognition complex (ORC) in a sequence specific manner (6). The origins used to replicate telomeric DNA lie in the subtelomeric region and origins are not fired within telomeric sequences (7,8). In contrast, initiation of DNA replication in humans, Drosophila and Xenopus, is mostly sequence independent and multiple factors including sequence bias, chromatin structure, DNA methylation patterns, transcriptional activities and protein chaperones participate in the selection of replication origins (9). Notably, binding of transcription factors increase site-specific origin firing, indicating that the local chromatin structure significantly affects origin selection (12). A number of DNA substrates containing random DNA sequences injected in Xenopus leavis eggs initiates replication efficiently at random locations (10,11). However, it has not been shown that DNA templates adopting a non-canonical chromatin structure including centromeric or telomeric DNA replicate in Xenopus eggs. Recent findings from studies in mammalian cells show that pre-replicative complex (pre-RC) proteins localize to telomeres through interaction to TRF2 (13,14). Whether these pre-RCs represent functional origins is not known.

Cell-free extracts from X. laevis unfertilized eggs contain nuclear and cytoplasmic proteins to support 12 cell divisions in the absence of transcription and have been instrumental to the study of DNA transactions...
including DNA damage response and DNA replication (15,16). When supplemented with sperm chromatin, cytosolic extracts support nuclear assembly followed by one round of cell cycle regulated, semi-conservative DNA replication (17). Origin assembly starts with binding of ORC proteins followed by Cdc6- and Cdt1-dependent loading of MCM helicase. Geminin, a protein that sequesters Cdt1 prevents origin assembly and origin-dependent DNA replication (18). Protein kinases activate this pre-RC to permit Cdc45, MCM10, GINS and polymerases to load.

*Xenopus* embryonic cells replicate their genome in less than 20 min and a replication fork should not travel more than 12 kb at a synthesis rate of 10 nt/s (19,20). *Xenopus* telomeres range from 10 kb to over 50 kb (21), making their replication originating uniquely from subtelomeric origins problematic. Given their length and inherent difficulty, it would be beneficial to establish active origins within telomeric DNA.

To test this possibility, we used *X. laevis* cell-free extracts supplemented with exogenous linear DNA substrates containing exclusively telomeric repeats. We show that these substrates are specifically bound by TRF2, support the regulated assembly of pre-RC components and undergo origin-dependent DNA replication. Binding of shelterin components, however, is not sufficient to prevent a DNA damage response induced by the relatively short telomeric substrates. We establish that telomeric DNA supports the assembly and activation of functional origins.

**MATERIALS AND METHODS**

**Cell free extracts**

Cell-free extracts from unfertilized *Xenopus* eggs were prepared as described (28).

**Cloning of non-telomeric substrate**

A non-telomeric (NT) control plasmid pRST5_NT was generated by PCR amplification of positions 666–1254 of *Xenopus* XLX gene and cloned into the HindIII and BamHI restriction sites of pRST5.

**Preparation of biotinylated substrates**

One microgram of telomeric or NT DNA fragment (gel extracted from BsmBI and HindIII digested pRST5 or pRST5_NT, respectively) was end-labeled with 1 U T4 polymerase in the presence of 33 μM each of dATP, dGTP, dTTP and biotin-dCTP for 15 min at 12°C. Reactions were stopped by addition of 50 mM EDTA and incubated at 76°C. Labelled DNA was purified using PCR purification kit (Qiagen) and quantified by photospectrometry.

**Pull-down experiments**

Three hundred nanograms of end-labeled 0.6 kb linear NT or exclusively telomeric DNA was bound to 10 μl Streptavidin-bound magnetic beads according to the supplier (Dynal). Washed beads were resuspended in 11 μl dH2O. One microliter was analyzed on gel electrophoresis using SYBR-gold to visualize bound DNA to quantify binding efficiency. In total, 5–10 μl beads were incubated with 90 μl egg cytosol (LSS) at a final concentration of 3 x 10^6 double strand breaks (DSB)/μl for 20 min at 22°C. Beads were pelleted in a table top centrifuge for 10 sec at 1500 rpm prior to separation from the supernatant on a magnet. Beads were washed four times with 200 μl ELB, 0.2% Triton-X and resuspended in 10 μl Laemmli buffer for SDS-PAGE analysis. Pull-down experiments in the NPE system were performed by incubating 2 μl membrane-free egg cytosol (HSS) supplemented with energy mix (10 mM Creatin phosphate, 10 μg/ml Creatin kinase, 2 mM ATP, 2 mM MgCl2, 5 mM HEPES, pH 7.5, 1 mM DTT) for 30 min in the presence of 150 ng bead-bound 0.6 kb linear DNA and either buffer control or 100 ng/μl geminin. Two-fold volumes of NPE extract supplemented with energy mix was added and incubation continued for 25 min prior to processing as described above.

**Western blot analysis**

One microliter of extract was diluted in loading buffer, electrophoresed, transferred to nitrocellulose and probed with polyclonal antibodies specific for *Xenopus* TRF2 (a generous gift from Dr Ishikawa), Cdc6, Orc2, MCM6 (48), Mre11 (25), ATM (26), Nbs1 (a generous gift of Dr H. Lindsay) and human Ku70 (MMS-263R, Covance) and P-Chk1 (Ser345 polyclonal, Cell Signaling). Bead bound substrates were directly dissolved in 10 μl loading buffer.

**Preparation of NHEJ substrates**

In total, 0.6 kb of telomeric substrate was excised from pRST5 by Ddel and BsmBI digestion. NT fragment was excised by HindIII and BsmBI. Digested products were gel extracted.

**NHEJ assays**

A typical NHEJ reaction consisted of 9 μl egg cytosol (LSS) and 1 μl DNA substrate. Samples were incubated at 17°C for 2.5 h. Reactions were stopped by the addition of 200 μl stop solution (10 mM Tris, pH 7.5, 5 mM EDTA and 1% SDS) and digested with 1 mg/ml proteinase K (Roche) at 50°C for 1 h. DNA was Phenol-Chloroform extracted and Ethanol precipitated. DNA pellets were resuspended in 10 μl TE, pH 7.5. 2–5 μl of extracted DNA was separated on a 0.7% native agarose gel.

**Southern blot analysis**

Agarose gels were depurinated in 0.2 M HCl for 10 min and washed briefly with dH2O. DNA was denatured by incubating the gel in 100 ml 1.5 M NaCl, 0.5 M NaOH for twice 15 min and neutralized in 1.5 M NaCl, 1 M Tris, pH 7.4 for twice for 15 min. DNA was transferred on Nylon membranes (Hybond-XL, Amersham) by capillary blotting in 10 x SSC and membranes were UV-crosslinked. NT probes were prepared by random labeling.
of 10 ng of pRST5_NT in the presence of 50 μCi ($\gamma$-32P)dCTP and hybridized in Hybridisation buffer at 60°C overnight. Telomeric probes were generated by 5'-end-labelling of 100 pmol of a (C3TA2)$_6$ oligonucleotide with 5U of PNK in the presence of 50 μCi of ($\gamma$-32P)dATP. Hybridisation was for 3 h at 50°C. Membranes were rinsed with 2× SSC, 0.1% SDS and washed twice with 0.5× SSC, 0.1% SDS for 20 min and once with 0.1× SSC, 0.1% SDS. Membranes were exposed to a phosphorimager and signals quantified using ImageQuant. For quantification, the mean value from three independent experiments of the ratio between LD and LM was calculated from dilutions 3 × 10$^5$, 10$^6$ and 3 × 10$^9$ DSB/μl.

Replication assays

Caffeine (Sigma) was dissolved in 10 mM PIPES. Five nanograms of pRST5_NT linearized with BsmBI or 5 ng of a 0.6 kb NT or telomeric fragment excised with HindIII and BsmBI from pRST5 or pRST5_NT, respectively, was incubated with membrane-free egg cytosol (HSS) supplemented with energy mix for 30 min in the presence of either buffer control, 5 mM caffeine, 100 ng/μl geminin or caffeine and geminin together at 22°C. Two-fold volumes of NPE extract supplemented with energy mix and 0.1 μl ($\gamma$-32P)dCTP was added and incubation continued for 1 h. Reactions were stopped by addition of 200 μl stop solution (10 mM Tris, pH 7.5, 5 mM EDTA and 1% SDS) and incubated with 1 mg/ml proteinaseK at 50°C for 1 h. Samples were phenol-chloroform extracted and ammonium acetate precipitated in the presence of 5 μg Glycogen. Precipitated DNA was resuspended in 10 μl TE and half of the reaction was separated on a 1% native agarose gel and fixed in 50% TCA for 30 min before squeezing the gel and drying under vacuum. Gels were exposed to a phosphorimager screen and signals were quantified using a phosphorimager and ImageQuant software.
We therefore turned to a two-step cell-free extract system that uses concentrated nuclear extract (NPE), which contains high kinase activities to support conversion of a pre-RC into a functional initiation complex on plasmid DNA templates (28). Previous studies showed that MCM3 and ORC2 load on linear dsDNA templates as short as 100 bp in length and addition of NPE converts DNA templates into functional pre-initiation complexes as seen by binding of Cdc45 (29). This suggests that the relatively short length of our substrates (600 bp) should allow us to assess DNA replication initiation. We monitored TRF2 binding following incubation of immobilized DNA substrates in NPE (Figure 2B). Consistent with the results obtained with cytosolic extracts (Figures 1B and 2A), TRF2 was enriched on telomeric substrates and similar levels of ORC2 and MCM6 assembled on both templates (Figure 2B, lanes 4 and 5) A non specific protein signal from the Ponceau stain was used to normalize the signals for quantification (Figure 2C). Importantly, treatment with geminin, which prevents the assembly of MCM proteins through sequestering Cdt1 (18), abolished MCM but not ORC loading, as anticipated (Figure 2B, lanes 7 and 8). Our observations establish that the presence of TRF2 on DNA does not interfere with assembly of a pre-RC and suggest that cell cycle regulated loading of MCMs to telomeric DNA and to bona fide origins are regulated by similar mechanisms. It further indicates that pre-RC assembly to telomeric DNA is not due to non-specific binding to telomeric chromatin. We consistently observe increased ORC2 loading in geminin treated extracts, with a more pronounced ORC2 association on NT DNA substrates (Figure 2C). It is possible that TRF2 or other shelterin components are modulating some of the steps during pre-RC assembly. Overall, our data are consistent with in vivo studies showing cell cycle regulated assembly of pre-RC proteins to telomeres (13) and with the recent report of active origins within telomeres in mouse embryo fibroblasts (30).

A number of components of the DNA damage response including ATM, Nbs1/Mre11/Rad50 or PARP1 harbor a conserved FxLxP motif and bind TRF2 via its TRFH protein docking site (31). To assess a potential role for these DNA damage response proteins in pre-RC assembly, we immunodepleted Mre11 and ATM from cytosolic extracts and monitored binding of MCM6, ORC2 and Cdc6 to immobilized substrates. ATM or Mre11 depletion did not affect the assembly of pre-RC components (Supplementary Figure S1). Due to the lack of antibodies to quantitatively deplete TRF2 from extracts, we were not able to test whether TRF2 is involved in assembly of a pre-RC.
Linear DNA substrates can replicate in *Xenopus* extracts

To assess the functional significance of pre-RC assembly we sought to establish conditions that support initiation-dependent DNA replication of linear DNA substrates in *Xenopus* extracts. Small circular plasmids can be replicated in the two-step cell-free NPE extract system but it has not been reported whether this system also supports replication of linear DNA substrates. We anticipated that the ends of linear DNA templates would be sensed as DSBs. Broken DNA triggers a DNA damage response that interferes with origin firing due to activation of ATM/ATR checkpoint kinases, which inhibit the S-phase kinase Cdk2 (32). When a 3.5 kb linear NT DNA substrate was incubated in NPE in the presence of $^{32}$P-dCTP, we detected incorporation of radiolabelled nucleotides (Figure 3A, lane 1). Treatment with caffeine, an inhibitor of the ATM/ATR protein kinases, significantly enhanced the signal as predicted (Figure 3A, lane 2 and Figure 3B). This strongly suggests that nucleotide incorporation was restricted by checkpoint activation and that the caffeine-sensitive signal is the result of origin-dependent DNA replication. Geminin, which specifically inhibits origin assembly and firing but does not affect DNA repair, abolished the caffeine-sensitive DNA synthesis (Figure 3A, lanes 3 and 4 and Figure 3B). The high molecular weight molecules that appeared in addition to the linear plasmid suggest that DNA ligation, most likely through NHEJ, was taking place in extracts (25). Electrophoresis of the replication products on denaturing gels partially resolves the labeled products (Figure 3A, bracket on the left) into discrete bands, similar to products detected in NHEJ reactions (see below and data not shown), indicating that repair through end-joining contributes to formation of the high molecular weight products. Quantification of replicated DNA substrates revealed that 23% of input linear DNA substrate was replicated, compared to 50% of input circular plasmids (data not shown). Nucleotide incorporation was inhibited by treatment with the Cdk2 inhibitor Roscovitine, confirming that nucleotide synthesis resulted from origin-dependent DNA replication (Supplementary Figure S2, lanes 3 and 4). DNA replication was strictly dependent on exogenous DNA templates (Supplementary Figure S2, lane 5). Taken together, our results show that linear DNA substrates can replicate in this *Xenopus* extract system.

Origin-dependent replication of telomeric DNA

Next, we performed replication assays using untagged linear 0.6 kb NT or telomeric DNA templates. Both substrates incorporated radiolabelled nucleotides (Figure 4A, lanes 1 and 5) and caffeine treatment reproducibly enhanced the signal significantly (Figure 4A, lanes 2 and 6; 4B), suggesting that DNA synthesis was restricted by checkpoint activation, as observed in Figure 3. Next, we wanted to confirm that a caffeine-sensitive checkpoint...
affecting origin-dependent DNA replication was limiting DNA synthesis. Indeed, addition of geminin largely abolishes incorporation of 32P-dCTP (Figure 4A, lanes 4 and 8; Figure 4B). This strongly suggests that active origins assemble and fire within DNA composed exclusively of telomeric repeats and that, under our experimental conditions, their activity is limited by a caffeine sensitive DNA damage checkpoint. We observed that the caffeine-insensitive nucleotide incorporation (Figure 4A, lanes 1 and 5) was not decreased by geminin treatment (Figure 4A, lanes 3 and 7). We propose that this origin-independent DNA synthesis could be due to processing events at DNA termini. Quantification of the replication efficiency reveals that 5% (NT) and 7% (T) of the 0.6 kb substrates replicated, compared to 23% for the linear 3.5 kb substrates. Thus, origin-driven DNA replication is less efficient for small than for long linear templates and the geminin-resistant signal represents a larger fraction of nucleotide incorporation for short templates. End processing and ligation of the linear substrates by NHEJ could also account for the more complex pattern of nucleotide incorporation of short substrates (compare Figures 3A and 4A and also see Figure 5A). We also observe ~1.4 fold higher efficiency of replication of telomeric versus NT short substrates. The reason for this difference is not entirely clear but could indicate a role of shelterin components in stabilization of the replication fork on passage through telomeric DNA.

**Short telomeric DNA substrates are repaired by NHEJ and induce a DNA damage response**

To test the possibility that initiation-independent DNA synthesis was coupled to repair by non-homologous end-joining (NHEJ), we monitored the formation of repair products by Southern blot analysis. Linear DNA templates are efficiently repaired by NHEJ in *Xenopus* extracts (33). End-joining is very robust and independent of the nature of the end termini (25). Upon incubation of
the linear 0.6 kb unlabelled DNA substrates in cytosolic extracts, we observed formation of linear dimer (LD) and multimer (M) products with similar efficiency for NT and telomeric DNA (Figure 5A). Dilution of the DNA did not affect the repair patterns, suggesting that depletion of telomere binding proteins is not the explanation for the failure to protect telomeres. Quantification of the ratios between linear dimers (LD) and linear monomers (LM) indicated that ligation was at least as efficient for telomeric as for NT substrates (Figure 5A). These findings differ from recent experiments in mammalian cell extracts where stretches of 12 telomeric repeats at the ends of linear plasmid DNA were sufficient to protect linear substrates from NHEJ (34). Next, we performed NHEJ assays with 3.5 kb DNA substrates that harbor a stretch of 75 TTAGGG repeats at one end only (Supplementary Figure S3). We observed efficient intra- and intermolecular end-joining, regardless of the sequence of the substrate. The difference between our observations and previously described results could reflect the fact that Xenopus cytosolic extracts support efficient NHEJ regardless of end termini unlike mammalian cell-free extracts that repair primarily compatible ends with lower efficiency (35). In addition, it has been shown that intra-molecular end-joining in Xenopus extracts is dependent on Ku70 (25,36), whereas inter-molecular end-joining in Xenopus is not (25) and might reflect non-canonical (i.e. alternative) NHEJ pathways.

Telomeric substrates generated less sharp repair products possibly due to processing events occurring specifically at telomeric DNA and is consistent with the appearance of higher molecular bands appearing in the replication gels in Figure 4A. These events could include microhomology-directed end-joining (MMEJ) favored by the high degree of homology along the telomeric DNA templates (37). Priming events on a single stranded overhang generated by telomerase (23) could also contribute to the extension of telomeric substrates (Figure 5A) and geminin-insensitive nucleotide incorporation (Figure 4). Our observation that telomeric DNA could be repaired by NHEJ prompted us to determine whether these telomeric substrates could trigger a DNA damage response. As predicted, NT DNA substrates induced phosphorylation of Nbs1 and Mre11 at concentrations higher than $10^8$ ends/µl (Figure 5B, lanes 1–4). Notably, we observed a similar response induced from telomeric ends (Figure 5B, lanes 5–8). We also observed caffeine sensitive phosphorylation of Chk1 (Figure 5C), suggesting that ATM/ATR kinases are involved in the signal transduction. Overall, our data indicate that assembly of telomeric proteins on a 0.6 kb telomeric DNA-only fragment is not sufficient to establish telomere protection in Xenopus cell extracts. This suggests that other processing events such as the generation of a single stranded overhang are required to establish a protective end-structure. We propose that the short substrates used here might reflect a deprotected state as it is often linked to critically short telomeres (38,39). The induction of a DNA damage response however, does not interfere with the assembly of a pre-RC (Figure 2).

**DISCUSSION**

Xenopus cell-free extracts can support assembly and replication of at least 10 000 nuclei/µl. Given a telomere length of 50 kb, this represents $4 \times 10^7$ kb telomeric sequences/µl and would correspond to $8 \times 10^7$ DNA molecules/µl for a...
600 bp long DNA substrate. Here, we have developed a system to study proteins assembled on telomeric DNA substrates independent from other sources of DNA and at concentrations close to these physiological levels of telomeric DNA (Figure 5). Exogenous telomeric DNA fragments can be added to *X. laevis* cell-free extracts and are specifically bound by TRF2 (Figures 1 and 2), an aspect of telomere biology that is fully recapitulated. Furthermore, *Xenopus* extracts support origin-dependent DNA replication of linear DNA substrates (Figures 3 and 4). Therefore, this system represents a powerful tool to study various aspects of telomere biology by allowing to use physiological amounts of telomeric DNA substrates in a soluble environment that contains nucleoplasmic proteins.

Using this approach we investigated whether telomeric DNA supports replication initiation. Our data show that DNA templates containing uniquely telomeric sequences and bound by TRF2 support origin-dependent initiation of DNA replication in *Xenopus* cell-free extracts under conditions close to physiological levels of natural telomeres. We also show that ATM and Mre11, two shelterin accessory factors, are not involved in the regulation of pre-RC assembly. These novel observations suggest that in *Xenopus* and possibly in other organisms harboring long telomeres, origins of DNA replication can assemble and could fire within telomeric DNA (Figures 2 and 4). Indeed, origin firing within telomeres was recently reported in mouse embryo fibroblasts by single molecule analysis of replicated telomeres. The fraction of telomeres that displayed active origins was small (3%), suggesting that in mouse embryo fibroblasts the majority of replication forks travel from subtelomeric origins into telomeric DNA (30).

It has been proposed that the localization of a pre-RC to telomeres is cell cycle regulated and could be influenced by telomere structure (14). We find that localization of pre-RC components to telomeric DNA does not require a native telomere structure, e.g. the presence of a single stranded overhang or the formation of a T loop. This would permit assembly of pre-RCs away from the ends of natural telomeres that represent only a minor fraction of total telomeric DNA. Indeed, within a native 5–50 kb long vertebrate telomere, the 3’ overhang and/or the formation of a D-loop only accounts for a small portion of the total telomeric complex.

The exact functional relationships between TRF2 or other shelterin components and pre-RC assembly and activation are not fully understood. TRF2 is associated to telomeres throughout the cell cycle (23,40). Here, we show that pre-RC assembly on telomeric DNA is inhibited by geminin and therefore regulated in a cell cycle dependent manner, as in human cells (13). Human ORC1 physically interacts with the amino terminal domain of TRF2 and down-regulation of either TRF2 or ORC1 results in lower levels of pre-RC assembly within telomeric DNA (13,14). The former suggests that pre-RC assembly is influenced by the formation of proper telomeric chromatin. Conversely, ORC2 depletion by siRNA or hypomorphistic cell lines for ORC2 display loss of telomere repeat DNA (14), indicating that pre-RC components are involved in telomere length homeostasis. Telomere instability in the absence of ORC could also be explained by collapsed replication forks within telomeres, which cannot be rescued by a neighboring origin. While our results demonstrate cell cycle regulated assembly of a pre-RC, we cannot exclude that shelterin components are involved in some of the steps of pre-RC assembly or the stabilization of a replication fork that travels through telomeric DNA. In fact, recent data in mammalian cells demonstrate that TRF1 is required for efficient replication through telomeric DNA and prevents replication fork arrest (30).

The genome in *Xenopus* eggs replicates within 20 min, which requires a very efficient and fast duplication of the 5–50 kb long *Xenopus* telomeres. Mammalian telomeres, in contrast, replicate their telomeres throughout S phase in an average of 6–8 h (41). Therefore, *Xenopus* chromosomes must have the ability to complete faithful replication of their telomeres in a short amount of time. This task is complicated by the fact that the repetitive G-rich regions within telomeric DNA are difficult stretches to replicate and result in higher frequencies of stalled replication forks (3,4). Consequently, additional factors including DNA helicases that stabilize passage of a replication fork and prevent secondary structure formation are required for telomere replication (4,42). *In vivo* studies in other eukaryotes showed that one single short telomere induces cell cycle arrest (43), which indicates a tight requirement for complete replication of telomeric DNA. Stalled replication forks within chromosomal DNA can be repaired by several pathways including break-induced replication or homologous recombination. However, the recombinogenic potential within the repetitive sequence of telomeres is repressed by the action of shelterin components (44) in order to prevent recombination events that could yield short telomeres, which can affect the proliferative life span of cells. Furthermore, unlike other chromosomal regions, where DNA synthesis from a collapsed polymerase can be completed by adjacent replication forks, a stalled polymerase traveling from subtelomeric regions towards the end of the telomeres could not. Therefore, restoring of stalled replication forks is likely to occur through a different mechanism. In a NT DNA context, replication fork stalling triggers the activation of surrounding dormant origins (45,46), a mechanism that could apply to telomeres to solve the ‘random completion’ problem there (47). Our data demonstrate that the levels of pre-RC components recruited to telomeric DNA and the efficiency of replication is comparable to substrates containing a random DNA sequence. Thus, in *Xenopus*, origin firing within telomeric DNA may occur at least as efficient as in NT DNA. The presence of multiple origins within telomeric DNA may provide a mechanism to replicate telomeres more rapidly and/or to compensate for failing replication forks originating in sub-telomeric regions.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.
ACKNOWLEDGEMENTS

The authors thank Dr H. Lindsay for XNbs1 antiserum, Dr F. Ishikawa for XTRF2 antibody and Dr J. Griffith for pRST5 plasmid. They are grateful to Dr M. Ben-Yehoyada for providing extracts and to Dr J. Lingeer and Dr T. Teixeira for comments on their manuscript. They also thank Dr M. O’Donnell and members of the Gautier laboratory for helpful discussions during this work.

FUNDING

Swiss National Research Foundation post-doctoral fellowship (to I.K.); National Cancer Institute grants RO1 (CA092245 and GM077495 to J.G.). Funding for open access charge: National Institutes of Health grants RO1 (CA092245 and GM077495).

Conflict of interest statement. None declared.

REFERENCES