RNA G-quadruplex folding is a multi-pathway process with a variety of short-lived intermediates

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ABSTRACT

The kinetics of folding is crucial for the function of many regulatory RNAs including RNA G-quadruplexes. Here, we characterize the folding pathways of a G-quadruplex from the telomeric repeat-containing RNA by combining all-atom molecular dynamics and coarse-grained simulations with circular dichroism experiments. The quadruplex fold is stabilized by cations and thus, the ion atmosphere forming a double layer surrounding the highly charged quadruplex guides the folding process. To capture the ionic double layer in implicit solvent coarse-grained simulations correctly, we develop a matching procedure based on all-atom simulations in explicit water. The procedure yields quantitative agreement between simulations and experiments as judged by the populations of folded and unfolded states at different salt concentrations and temperatures. Subsequently, we show that coarse-grained simulations with a resolution of three interaction sites per nucleotide are well suited to resolve the folding pathways and their intermediate states. The results reveal that the folding progresses from unpaired chain via hairpin, triplex and double-hairpin constellations to the final folded structure. The two- and three-strand intermediates are stabilized by transient Hoogsteen interactions. Each pathway passes through two transient, on-pathway intermediates. Since these intermediates are degenerate with two to four alternative conformations per state, RNA quadruplex folding is a multi-pathway process with high conformational entropy.

INTRODUCTION

RNA G-quadruplexes (rG4s) play a crucial role in a variety of physiological processes such as regulation of transcription and translation (1, 2) or pre-mRNA processing (3, 4). G4-forming sequences are abundant in the human genome and non-canonical structures of guanosine-rich sequences can be formed by DNA and RNA. While long debated (5), advances in the development of highly sensitive approaches provided further evidence for the existence of rG4s in vivo and revealed their dynamic nature in cells (6). However, to resolve how rG4 folding and unfolding affects its function, a detailed understanding at the molecular level is required.

The overall architecture of G4s is striking: Four non-neighboring guanosine nucleobases assemble in quartets and several quartets stack onto one another to form a central channel. For rG4s, this channel is typically flanked by propeller loops, while a large variety of different loop arrangements have been reported for DNA G-quadruplexes (dG4s) (7). The three-dimensional structures are stabilized by cations. In particular, K^+ and Na^+ are frequently observed in the channel and lead to the highest stabilization efficiency against denaturation among alkali and alkaline earth cations (8).

An important rG4 example is telomeric repeat-containing RNA (TERRA). Telomeres are specialized nucleoprotein structures that protect chromosomal DNA from progressive degradation. Transcription of the telomeric C-rich strand in the chromosomes produces TERRA, which has a canonical G-rich motif with sequence r(UUAGGG) (9, 10). TERRA is essential in maintaining genomic integrity by regulating telomerase activity and protecting the chromosome ends against degradation (11, 12). Telomere dysfunction is connected to cell aging and cancer (13, 14) and the design of small drug molecules targeting TERRA attracts therefore increasing scientific attention (15).

Despite the importance of rG4s, most scientific work has focused on dG4s so far (16). The scientific focus on dG4s can be rationalized by the fact that their existence in vivo has been demonstrated early on by different experimental techniques (17, 18). By contrast, the existence of rG4s in vivo and their biological relevance are just now starting to be established (2, 6, 19, 20). In addition, the investigation of rG4s requires much more sensitive experimental techniques since rG4s are more dynamic compared to their DNA counterparts (6).

Moreover, the folding intermediates of rG4s are transient, making their detection and resolution a major challenge (21). Consequently, the molecular details of folding have not been resolved so far and the intermediate states remain elusive.

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Insights into the atomistic structure of folded G4s are obtained from nuclear magnetic resonance (NMR) spectroscopy (22–25) and X-ray crystallography (26). In addition, time-resolved NMR spectroscopy yields information on possible folding intermediates (27–29). Such experiments recently revealed that the folding kinetics of TERRA is fundamentally different compared to a homologous DNA sequence (30, 31). The K^+ induced folding kinetics of TERRA is an order of magnitude faster ($k_1 = 1.45/\text{min}$) compared to the dG4 of identical nucleotide sequence ($k_1 = 0.41/\text{min}$) (21).

While some dG4 intermediates have been resolved at atomistic resolution by NMR (23, 32–34), the intermediate states of rG4s remain elusive due to their short lifetimes (27). Further information on the folding intermediates can be obtained from single-molecule techniques such as single-molecule Förster resonance energy transfer (smFRET). Based on the measured distance between strategically placed fluorophores, hairpin and triplex structures have been suggested as intermediates of two and three quartet rG4s and dG4s (35, 36).

To complement experiments, biomolecular simulations are powerful tools which provide molecular insights into the folding pathways and intermediate states of rG4s and dG4s (16, 37–41). At first sight, all-atom molecular dynamics (MD) simulations in explicit water seem to be the ideal computational method. For instance, atomistic simulations allow to resolve the conformational rearrangements in the folded state of G4s, their interactions with different cations, (42–44) or the stability of putative intermediates along the folding pathway (37, 38). Moreover, combining atomistic simulations and enhanced sampling techniques such as replica exchange can improve the sampling of rare folding events (37–40). Still, G4 folding is on the timescale of minutes. Simulating a single folding pathway, let alone the large variety of different pathways, is therefore out of reach for atomistic simulations.

The limitations of atomistic simulations can be overcome by coarse-grained (CG) simulations. CG models simplify the atomistic representation by reducing the number of particles to three to seven beads per nucleotide and employing implicit solvent thereby reducing the computational costs further. For instance, the HiRE-DNA model revealed the potential of CG model to investigate dG4 folding by resolving numerous intermediates of human telomeric dG4s (41). By now a variety of CG models for RNA are available such as SimRNA (45), HiRE-RNA (46), seRNA (47) and TIS model (48–53). TIS, the three-interaction site model developed by Thirumalai and coworkers, is a simple low-resolution model. Its efficiency and accuracy to describe folding has been demonstrated for a variety of RNA molecules ranging in size from larger molecules such as ribozyme (52) to smaller RNAs like riboswitch (54), pseudoknot (50), and hairpin (49).

By combining CG simulations using the TIS model and circular dichroism (CD) experiments, we resolve the folding pathways and intermediate states of the TERRA rG4 sequence consisting of a monomeric 25-mer human telomeric RNA repeat. In a first step, we validate the CG model by CD experiments and obtain close agreement as judged by the population of folded states as a function of temperature and salt concentration. Quantitative agreement is obtained by a newly developed concentration matching procedure, which takes the ionic double layer into account via additional all-atom MD simulations. Subsequently, we resolve the folding pathways from the CG simulations and identify hairpins, triplexes and double-hairpins as intermediate states.

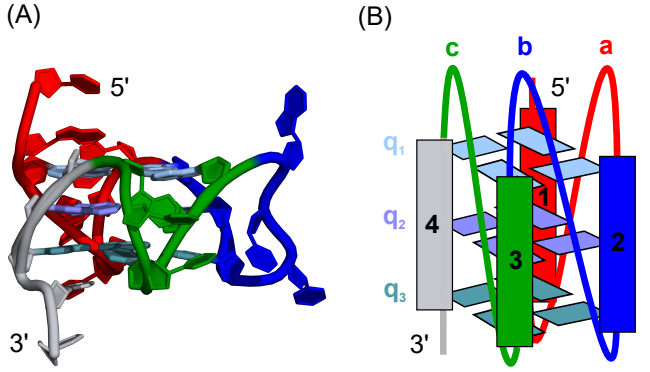

Figure 1. Monomeric 25-mer TERRA G4 with sequence 5'-UAGGGUUAGGGUUAGGGUUAGGGUU-3' in the simulations. Simulation snapshot from all-atom MD simulations (A) and schematic representation (B). Each of the four GGG-repeats is represented in a different color (from 5' to 3': red (1), blue (2), green (3), gray (4). The three G-quartets consist of four guanosines from different repeats and are labeled q_1, q_2, q_3 in (B). The three propeller loops are labeled a, b, c. The connecting loops all have the sequence UUA. The sequence has a UU-overhang at the 3' end and a UA-overhang at the 5' end.

METHODS

Coarse-grained and atomistic simulations

Simulation model:

We modeled the monomeric 25-mer G4 from human telomeric RNA (TERRA25). As starting point, we used the NMR resolved structure of a dimeric 24-mer TERRA G4 in K^+ solution (PDB-ID: 2KBP from ref. (55)) with sequence $(UAGGGUUAGGGU)_2$. In a first step, we used the ModeRNA homology modeling server (56) to connect the two strands of the RNA into a single strand through U12 and U13. We created an additional propeller loop and added a U25 to the 3' end of the strand. In a second step, we optimized the structure using the SimRNA server (45) and selected 10 minimum energy structures. We preformed MD simulations of the 10 structures for 100 ns and selected the one with lowest root mean square deviation (RMSD) with respect to the experimental structure (2KBP).

The equilibrated TERRA25 structure with sequence 5'-UAGGGUUAGGGUUAGGGUUAGGGUU-3' is shown in Figure 1A. It consists of four repeats. Each repeat is formed by three consecutive guanosines in anti-conformation (i.e. with a glycosidic torsion angle between 180° and 240°). The repeats are connected by propeller loops. The guanosines from the four repeats form 3 quartets that give the G4 its characteristic non-canonical structure.

All-atom MD simulations:

The MD simulations were performed with Gromacs version 2018.1 (57). Periodic boundary conditions were used with the particle mesh Ewald method (58) to calculate long range electrostatics, with cubic interpolation and a Fourier spacing of 0.12 nm. The cutoff for Coulomb and Lennard-Jones interactions was 1.2 nm and long-range dispersion corrections for energy and pressure were applied. Bond to hydrogens were constrained with the LINCS algorithm (59) with order of four for the matrix inversion correction and one iterative correction. Simulations were performed for 100 ns with a 2 fs time step. TERRA25 was simulated using parameters from Amber99sb - ildn* force field (60) with parambsc0 (61) and χ_{OL3} (62) corrections and TIP3P water model (63). Optimized parameters were used for K^+ and Cl^- ions, which correctly reproduce the thermodynamic and kinetic properties of the ions in TIP3P water (64).

In the first set of simulations, we simulated the 10 conformations obtained from simRNA for which the interatomic potential energy is lowest. 1 M KCl was used in each replica. The structures were initially placed in a triclinic box with dimensions 5.4 × 5.0 × 5.6 nm^3. From these simulations, the equilibrated structure with the lowest RMSD with respect to the experimental structure was selected for all further simulations. In the RMSD calculations only heavy atoms from the central pore were used.

In a second set of simulations, we calculated the ion distribution profiles to establish the relation between bulk salt concentration and the local concentration in the double layer. We performed simulations of TERRA25 at two concentrations of KCl, namely 190 mM and 1.19 M. The rG4 was placed in a cubic box with dimensions 9.0 × 9.0 × 9.0 nm^3. Each system was equilibrated in NVT and NPT simulations. During equilibration harmonic restraints with force constant 1000 kJ/(mol nm^2) were applied on the heavy atoms of TERRA25 to prevent large conformational changes. The NVT equilibration was done in two parts. During the first 1 ns restraints of 2000 kJ/(mol nm^2) were applied to ions to prevent ion pairing before a complete hydration shell is formed. In the subsequent 1 ns, the restraints on the ions were released. As thermostat the velocity rescaling algorithm with a stochastic term (65) and with a coupling constant of 0.1 ps was used. During the 2 ns NPT equilibration, pressure coupling was performed using the Berendsen barostat (66) with a 1 ps coupling constant. In the production runs, the velocity rescaling thermostat (65) and the Parrinello-Rahman barostat (67) with a 2 ps coupling constant were used. Position restraints on TERRA25 were released during the production run. The radial concentration profile was calculated as follows: First, a 2D number density profile of K^+ around the central pore of the G4 was calculated using Gromacs and an in-house code (68). The radial concentration profile was obtained by integration and normalization.

CG simulations using TIS:

The CG simulations were performed using the Three Interaction Sites (TIS) model developed by Thirumalai and coworkers (48–53). In the TIS model, each nucleotide is represented by three beads, located at the center of mass of the phosphate group, sugar and nucleobase. The parameters for the canonical interactions between the beads were taken from previous work (48). The intramolecular attractive interactions were defined based on the residues that appear in the native structure of TERRA25. This ensures that the native structure is the minimum energy structure (69). Native hydrogen bonds and tertiary stacks were defined based on the modelled monomeric TERRA25 structure described above.

In order to capture folding intermediates that are not stabilized by native interactions, non-native secondary structure interactions were included via the base-stacking interactions of consecutive nucleotides and hydrogen-bond interactions between all nucleobases as in previous work (53). A non-interacting uridine was added capping the structure at the 3' end. The RNA was placed in a cubic box with an edge length of 70 nm.

The solvent was modeled implicitly, and the electrostatic interactions were modeled by employing the Debye-Hückel approximation in combination with the concept of counterion condensation. Specifically, the interaction between two phosphate groups is calculated from

$$V_{\mathrm{ij}} = \frac{Q^2 e^2}{4\pi\epsilon_0\epsilon_r} \frac{e^{-r_{ij}/\lambda}}{r_{ij}} \tag{1}$$

where r_{ij} is the distance between the two phosphate groups i and j, Q is the charge of a phosphate group, e is an elementary charge, ϵ_0 the dielectric constant of vacuum, ϵ_r is the dielectric constant of water and λ is the Debye length. Hence, the ionic concentration is included in the CG model via the Debye length

$$\lambda = \sqrt{\frac{\epsilon_0\epsilon_r k_B T}{2e^2 N_{\mathrm{A}} c_{\mathrm{CG}}}} \tag{2}$$

where N_{A} is Avogadro's constant and c_{CG} is the uniform ion concentration of the CG model.

Numerical integration of the equations of motion was performed using the leap-frog algorithm with time step $h = 0.05\tau$, where $\tau = 50$ fs as in previous work with the TIS model (49). The simulations were performed in the low friction regime to increase the sampling efficiency by reducing the viscosity of water by a factor of 100 (70). The cut-off for electrostatic interactions was set to 3 nm.

To investigate the temperature dependence of the population of folded rG4 states, we performed simulations in the temperature range from 1-120°C. Each temperature was simulated at a concentration of $c_{\mathrm{CG}} = 150$ mM (corresponding to $c_{\mathrm{bulk}} = 9$ mM) for about 100 μs.

To investigate the concentration dependence of folding, we performed simulations at different concentrations in a range of from 10 μM to 1 M (corresponding to $c_{\mathrm{bulk}} = 0.01$ μM to $c_{\mathrm{bulk}} = 750$ mM) at two different temperatures, 25°C and 60°C. Each setup was simulated for about 100 μs. To provide sufficient statistics at T=25°C, additional simulations were performed at 0.1, 0.4 and 1 mM using 50 additional replicas of 20 μs.

The folding and unfolding pathways were simulated at room temperature (T=25°C) and at $c_{\mathrm{CG}} = 50$ mM (corresponding to $c_{\mathrm{bulk}} = 0.7$ mM). The salt concentration

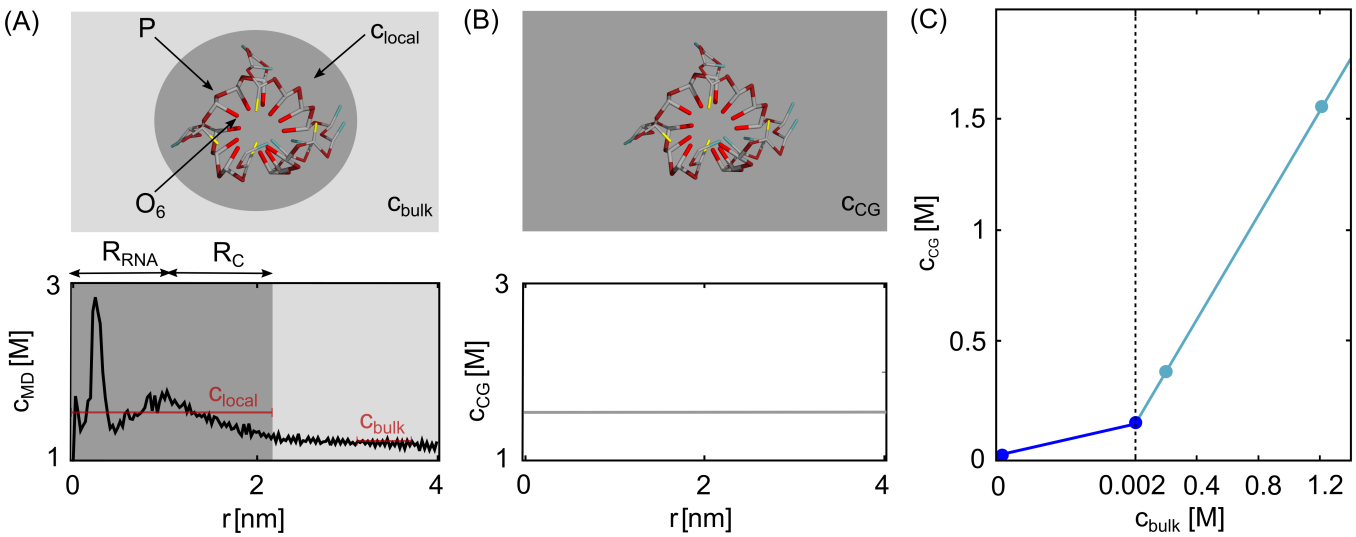

Figure 2. Concentration matching to mimic the effect of an ionic double layer in implicit solvent CG simulations. (A) Schematic representation of the ion atmosphere around the rG4 (top) and concentration profile $c_{\mathrm{MD}}(r)$ of K^+ ions as function of the distance from the central channel from all-atom MD simulations (bottom). c_{bulk} is the bulk salt concentration and c_{local} the averaged concentration in the double layer within $R_{\mathrm{RNA}}+R_{\mathrm{C}}$. (B) Uniform concentration profile of the CG model $c_{\mathrm{CG}}=c_{\mathrm{local}}$ after matching to the local concentration in the double layer obtained from the MD simulations. (C) Matching relation of the bulk concentration c_{bulk} and the CG concentration c_{CG}.

was chosen such that the probabilities of folded and unfolded structures are similar. For 23 replicas of the system, we performed 180 μs long simulations and for 77 replicas we performed 52.5 μs long simulations. In total, 8182.5 μs of simulation time was used.

Number of native contacts and radius of gyration:

To identify the transition between the folded and unfolded state, we calculated the radius of gyration r_g and the number of native contacts n_C between the guanosines in each quartet. $n_C=12$ corresponds to the fully folded, native state. n_C is calculated using the coordination function of PLUMED (71) with cutoff distance between guanosine base beads $r_0=0.75$ nm, offset parameter $d_0=0.08$ nm and parameters $n=35$ and $m=55$.

Order parameters:

To characterize the folding intermediates, we introduce two order parameters. The repeat order parameter counts the number of native contacts between repeats i and j (with $i\neq j$ and $i,j=1-4$). It is calculated from the indicator function

$$h=\begin{cases}1 & \text{for} \quad n_C>2c\\ 1/(1+e^{\kappa(n_C-\gamma c)}) & \quad\quad \text{otherwise}\end{cases} \tag{3}$$

where n_C is the number of native contacts between repeats i and j and the parameters $\kappa=-5$, $\gamma=1.3$, $c=1.4$. This choice provides a smooth function for the order parameter without fluctuations. The repeat order parameter $r_{ij}=h$ is one if all three native contacts have formed between the neighboring repeats i and j.

The quartet order parameter q_k counts the number of native contacts in each of the three quartets ($k=1-3$). q_k is calculated from equation **3** with $\kappa=-4$, $\gamma=1.9$, $c=1.93$, and n_C being the number of native contacts in quartet k. The quartet order parameter is one if all four native contacts have formed in a quartet.

Fraction of folded structures:

For the fraction of folded structures n_f, we calculated the total number of contacts between the guanosines and use equation **3** with $\kappa=-5$, $\gamma=2$ and $c=4.5$. n_f is one in the folded state. The fraction of folded structures was calculated from the time the molecule spends in the folded state relative to the total time. The error is calculated by block averaging over 2.5 μs blocks.

Lifetimes:

We used the repeat order parameter to discriminate between the 12 different conformations of the rG4 (folded, unfolded, four hairpins H1-H4, four triplexes T1-T4, two double-hairpins D1-D2). For each conformation, we calculated the average lifetime the systems spends in the respective conformation. A threshold of 500 steps (1.25 ns) was used to eliminate rapid fluctuations.

Concentration matching:

In the CG simulations, the solvent is modeled implicitly and the concentration of ions is homogeneous in the simulation box (Figure 2B). Due to the highly charged backbone of the rG4, cations are attracted to the phosphodiester backbone and form a pronounced electric double layer (Figure 2A). Since screening of ions in the vicinity of phosphodiester groups of RNA is a driving factor in RNA folding, the concentration in the CG model needs to be matched to the local concentration of ions in the electric double layer.

To achieve this, we developed the following matching procedure: Firstly, we derive the correlation between the

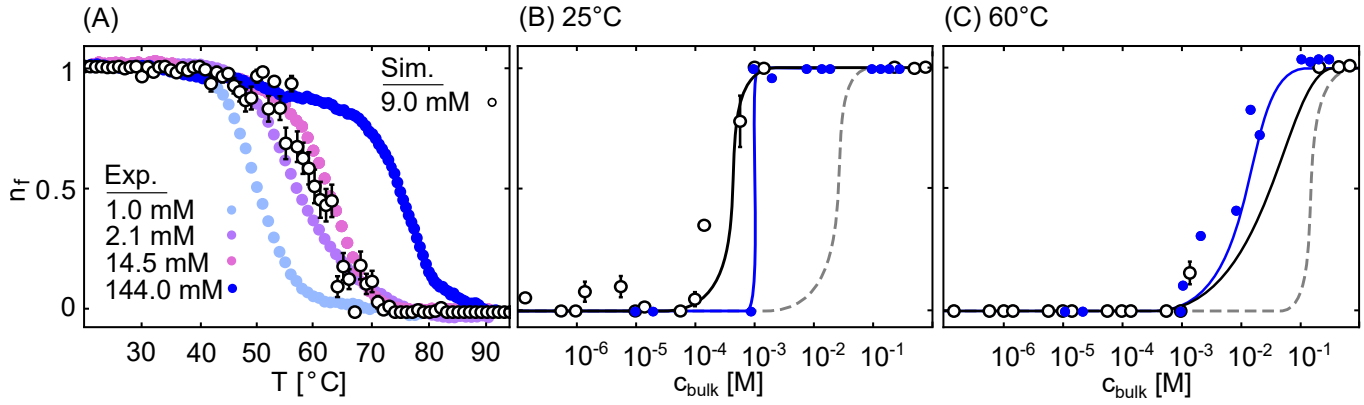

Figure 3. Comparison of the population of the folded state n_f from simulations and experiments. (A) n_f as function of the temperature from experimental melting curves and CG simulations. (B, C) n_f as function of the K^+ concentrations at 25°C and 60°C. With increasing salt concentration, the equilibrium is shifted to the folded state with $n_f = 1$. The lines are a guide to the eye and indicate the folded/unfolded transition region. The dashed lines are the uncorrected results neglecting the effect of the ionic double layer.

bulk concentration (as measured in the experiments) and the local concentration in the double layer by performing all-atom MD simulations. The simulations were done at two different KCl concentrations ($c_{\text{bulk}} = 190$ mM and $c_{\text{bulk}} = 1.19$ M). Figure 2A shows the radial concentration profile at $c_{\text{bulk}} = 1.19$ M. The formation of an electric double layer is clearly visible. The highest peak ($r = 0.2$ nm) corresponds to K^+ in the central pore and the second peak ($r = 1.23$ nm) corresponds to adsorption of K^+ at the phosphate oxygens of the backbone. From the simulated profiles, we calculated the local concentration by averaging from the center of the channel up to $R_{\text{RNA}} + R_{\text{C}}$. $R_{\text{RNA}} = 1.23$ nm is the radius of the rG4 from central axis to phosphodiester groups (Figure 2A) and R_C corresponds to the bilayer thickness and is treated as a free parameter. Since the results are not sensitive to the exact choice of R_C, we chose $R_C = 1.1$ nm at 1.19 M and scaled the value at the lower concentrations of 190 mM due to decreased screening according to $R_C = 1.1 \cdot (1.19\ \text{M}/190\ \text{mM})^{1/2}$ nm.

The matching was done in two regimes: For large concentrations ($c_{\text{bulk}} > 2$ mM), the simulation box is neutral with 24 cations to neutralize the negative charge of the rG4. In this regime, the relation is derived from a straight line fit of the simulation results obtained at $c_{\text{bulk}} = 190$ mM and $c_{\text{bulk}} = 1.19$ M (Figure 2C). Note that 2 mM corresponds to the situation where there is one additional cation in the simulations box (in addition to the cations neutralizing charge of the rG4). Since it is not possible to simulate a lower concentration while keeping the simulation box neutral, we extrapolate from $c_{\text{bulk}} > 2$ mM to the limit of vanishing concentration i.e. point (0, 0) in Figure 2C.

The following relation between the bulk salt concentration (c_{bulk}) and the local concentration (c_{CG}) is obtained

$$c_{\text{CG}} = \begin{cases} \alpha c_{\text{bulk}} + \beta & \text{for} \quad c_{\text{bulk}} > 2\ \text{mM} \\ \gamma c_{\text{bulk}} & \quad\ \ \text{otherwise} \end{cases} \tag{4}$$

with fit parameters $\alpha = 1.17$, $\beta = 0.14$ M and $\gamma = 70$. The results from the matching procedure are validated by CD experiments as will be discussed further below.

Experiments

Sample preparation:

TERRA25 (5'-UAGGGUUAGGGUUAGGGUUAGGGUU-3') was purchased from Dharmacon (Cambridge, UK). The oligomer was HPLC purified using a tetrabutylammonium acetate buffer and precipitated with five volumes of $LiClO_4$ (2% in acetone (w/v)) at -20 °C over night. Subsequently, desalting with an ultracentrifuge filtration device (Vivacon 2 kD cut-off, VWR) was performed to remove residual Li^+ cations and acetone.

Circular dichroism (CD) experiments:

CD measurements were performed using a JASCO J-810 spectropolarimeter with a Peltier temperature control system. 10 μM RNA were used per measurement and dissolved in ddH_2O containing 1, 2.1, 14.5 or 144 mM KCl. A quartz cuvette with 2 mm pathlength was used. The CD spectra were recorded with a scanning speed of 50 nm/min and three accumulations between 200 and 320 nm. CD melting curves were recorded at the maximum of the CD signal (264 nm) with a heating rate of 0.5°C/min.

Native polyacrylamide gel electrophoreses (PAGE):

Correct folding of TERRA25 was checked via native PAGE (15% acrylamide gel). 400 pmol samples were loaded in 50% glycerol and 5 mM KCl. Gels were prepared in 50 mM Tris-borate buffer (pH = 8.4) supplemented with 5 mM KCl. Bands were separated in the same buffer at 0.8 W for 90 min with water cooling (13°C water temperature). The bands were visualized by UV shadowing (254 nm).

Fraction of folded structures from CD melting curves:

Conversion of CD absorbance into population of the folded state was calculated according to the method highlighted by Mergny and Lacroix (72). Firstly, upper and lower baselines were corrected for temperature correction to determine the CD signal for the unfolded and folded states, respectively. The baselines were then used to normalize the absorbance values and yield fraction of folded states.

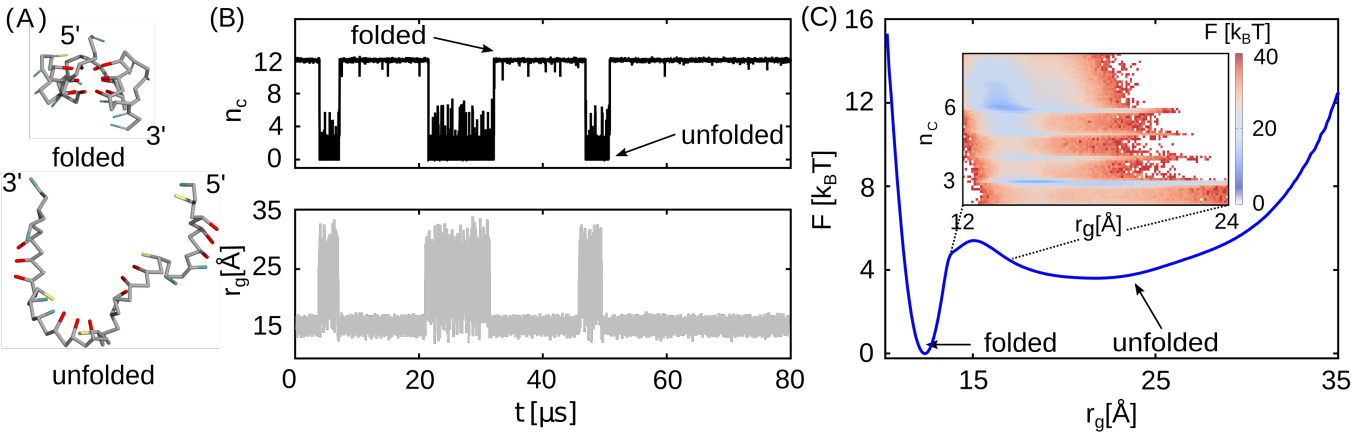

Figure 4. Folding pathway and folding free energy landscape of TERRA25 from CG simulations. (A) Snapshots in the folded and unfolded state from the CG simulations. Guanosine is represented in red, uridine in teal and adenosine in yellow. (B) Number of native contacts n_C and radius of gyration r_g as function of time. (C) One-dimensional free energy profile F as a function of r_g. The inset shows the two-dimensional free energy landscape as function of r_g and n_C in the region of the barrier.

The melting temperatures were calculated by fitting the normalized melting curves to a sigmoidal function

$$n_f = 1/\left(1+e^{(T_m-T)/s}\right) \quad (5)$$

where T_m is the melting temperature and s the slope of the curve. The fitting was done according to the nonlinear least-squares Marquardt-Levenberg algorithm.

Table 1. Melting temperatures of TERRA25 at different KCl concentrations from CD experiments and CG simulations using concentration matching from all-atom MD simulations.

	c_{bulk} [mM]	c_{CG} [mM]	T_m [°C]
Exp.	1.0		50.67 ± 0.04
	2.1		59.21 ± 0.09
	14.5		62.6 ± 0.2
	144.0		76.9 ± 0.1
Sim.	9	150	60.1 ± 0.1

RESULTS AND DISCUSSION

Quantitative comparison of the fraction of folded structures from simulations and experiments

Initially, we validated the CG model by CD experiments and provided a direct comparison of the fraction of folded structures in dependence of the temperature or the K^+ concentration (Figure 3). To obtain quantitative agreement between experiments and CG simulations, the ion atmosphere surrounding the highly charged G4 has to be taken into account. Since the cations are attracted to the negatively charged phosphodiester backbone while the anions are repelled, a pronounced double layer is formed. Given the high negative charge, the local ion concentration in the double layer is significantly larger compared to bulk (Figure 2C). It is therefore crucial to take the local concentration in the CG simulations into account to correctly capture the population of the folded state at a given bulk salt concentration. To achieve this, we derived a matching relation from all-atom MD simulations which relates the bulk salt concentration to the local concentration in the double layer (Figure 2C). Based on the relation, the CG concentration was chosen such that it reproduces the average concentration in the double layer.

To validate the procedure, we first investigated the temperature-induced unfolding of the TERRA25 and obtained melting curves from experiments and simulations (Figure 3A). At low temperatures, rG4 is folded in presence of K^+ ($n_f = 1$). With increasing temperature, the equilibrium shifts toward the unfolded state and n_f decreases. At high temperatures, rG4 is unfolded ($n_f = 0$). The melting point T_m depends on the salt concentration (Table 1) and the rG4 becomes more stable with increasing K^+ concentration. The direct comparison of experiments and simulations reveals a similar dependence of n_f on the temperature (Figure 3A). Moreover, the melting temperature of 60°C from the CG simulations at 9 mM (derived from the matching relation in Figure 2C) is in between the experimental results of 59°C and 62°C for 2.1 and 14.5 mM (see Table 1). Note that without the matching relation, a melting temperature of 60°C corresponds to 150 mM salt concentration. Hence, without the details of the ionic double layer, the CG model clearly overrates the population of the unfolded state.

The importance of including the local salt concentration via the matching relation becomes even more evident from the dependence of n_f on the concentration at 25°C or 60°C (Figure 3B,C). Without matching, the CG model overrates the unfolded state stability, and the folded/unfolded transition is predicted at too high salt concentrations. On the other hand, quantitative agreement of CD experiments and CG simulations is obtained by taking the local concentration in the double layer into account via the matching relation from additional MD simulations.

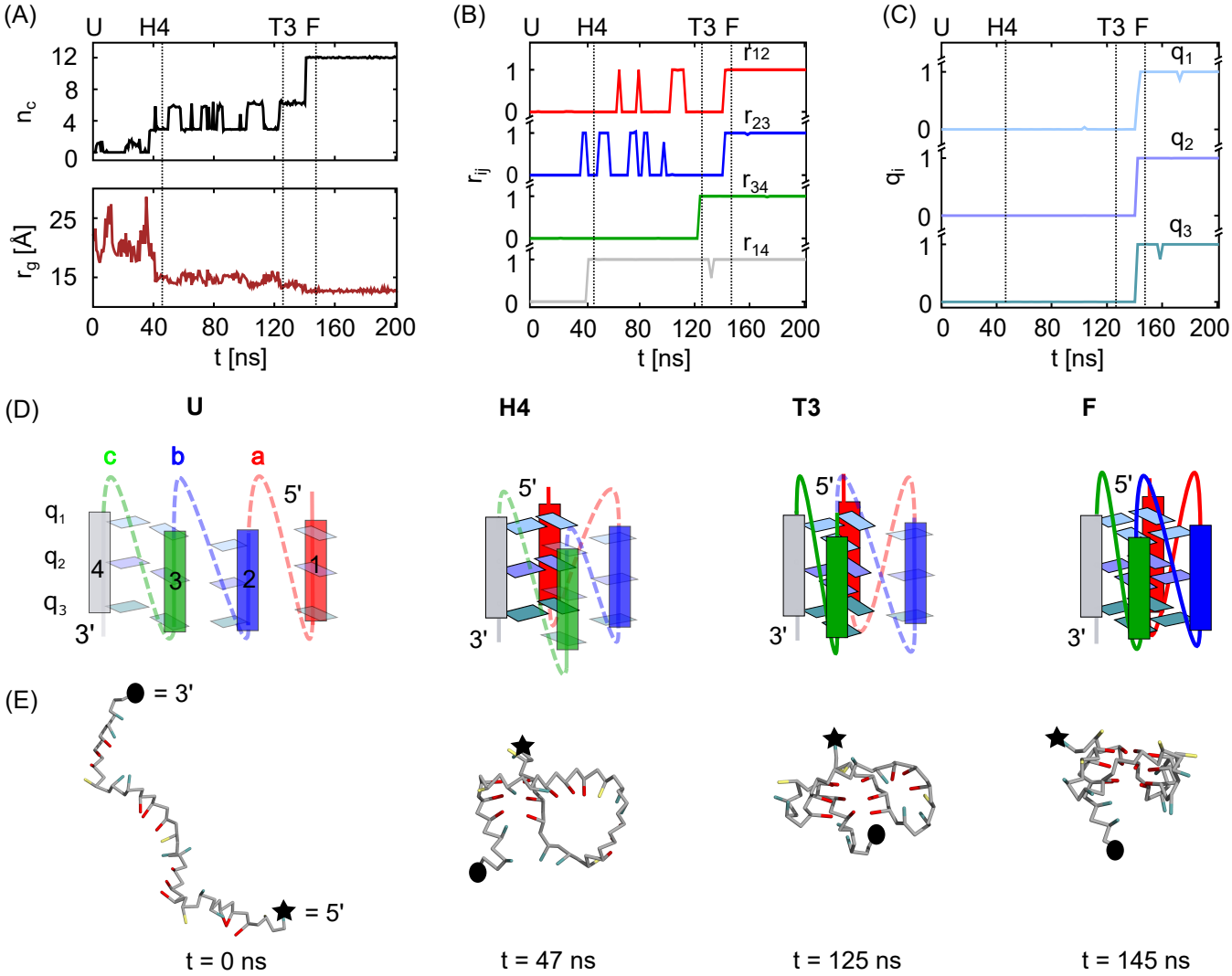

Figure 5. Representative folding pathway and intermediates of TERRA25 from CG simulations. (A) Number of native contacts n_C and radius of gyration r_g during the folding transition. (B) Repeat order parameter r_{ij} describing the assembly of repeat i and j (with $i \neq j$ and $i,j = 1-4$). r_{ij} is one if three native contacts have formed neighboring repeats. (C) Quartet order parameter q_i describing the formation of the guanosine quartets ($i = 1-3$). q_i is one if all four native contacts have formed in a quartet. (D) Schematic representation of the folding pathway. Assembled parts of the structure (repeats, quartets, propeller loops) are shown in solid colors; non-assembled parts are transparent or dashed. (E) Simulation snapshots along the folding pathway at times indicated in A-C.

Folding and unfolding of TERRA25 is a sequential but multi-pathway process

After successful validation, we analyzed the CG simulations to extract information regarding the folding and unfolding of TERRA25.

Figure 4B shows the number of native contacts n_c and the radius of gyration r_g for a 80 µs simulation at 25 °C and $c_{\text{bulk}} = 0.7$ mM. Multiple transitions between the folded ($n_c = 12$ and $r_g \approx 15$ Å) and unfolded ($n_c = 0$ and $r_g \approx 24$) states are observed. Energy and entropy contributions to the folding are obtained by calculating the free energy profile $F(r_g)$ (Figure 4C). The folded state is characterized by the sharp and deep minimum in the free energy profile while the unfolded state is broader with r_g ranging from 15 to 25 Å. This reflects an energy-entropy compensation mechanism in which the folded state is energetically favored while the unfolded state competes with a larger entropy due to a variety of unfolded conformations. The folded and unfolded structures are separated by a barrier of 5 k_BT. The two-dimensional free energy landscape $F(n_c, r_g)$ in the region of this barrier reveals several distinct intermediate states (Figure 4C, inset). The intermediate states are broad indicating that multiple different conformations contribute to them (as will be discussed in detail further below).

Figure 5 shows the computation of one representative folding pathway of TERRA25. The number of native contacts n_C increases stepwise while the radius of gyration r_g decreases (Figure 5A). The repeat order parameter r_{ij} and the quartet order parameter q_i reveal that rG4 is formed repeat after repeat and not quartet after quartet (Figure 5B,C), suggesting that stacking interactions drive the initial formation of rG4 rather than Hoogsten interactions. In this example, repeat 1 and 4 assemble first and form the parallel hairpin H4 without propeller loop (Figure 5D,E at t=47 ns). Subsequently,

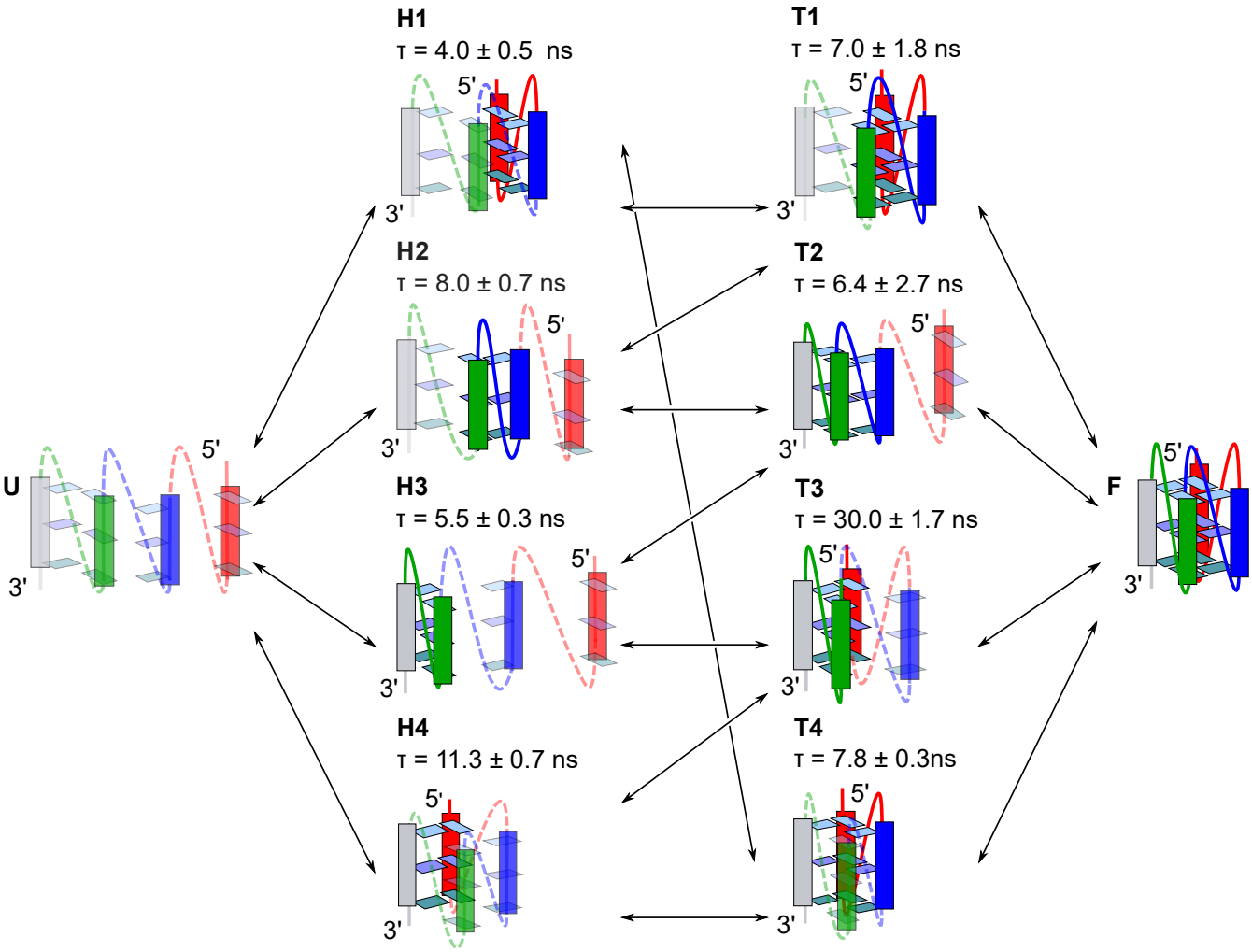

Figure 6. Folding and unfolding pathways of TERRA25. The arrows correspond to the transitions between the conformations. The pathways pass through two intermediate states: hairpin and triplex state. In total four different hairpin (H1, H2, H3, H4) and four different triplex (T1, T2, T3, T4) conformations are observed. The lifetimes τ of the intermediates are shown above the structures.

repeat 3 assembles and forms the triplex structure T3 with three planar units formed by three h-bonded guanosines, called triads. At this point, the propeller loop c is formed at the 3' end (Figure 5D,E at t=125 ns). Folding is completed once the last repeat assembles, creating the loops a and b (Figure 5D,E at t=145 ns) and all three quartets are formed simultaneously as visible from the quartet order parameter in Figure 5C.

In summary, during rG4 folding the repeats assemble and the corresponding propeller loops are formed. During the folding, two intermediate structures are observed, a hairpin and a triplex, supporting previous observations and predictions of hairpin and triplex structures as intermediates in the folding of rG4s and dG4s in experimental (27, 29, 35, 73) and computational (39, 74) work.

From simple combinatorics, there are four possibilities to form a hairpin from a nucleic acid structure with four repeats. Similarly, there are four possibilities to form a triplex. For the folding of G4s the question arises whether all these intermediates can be observed or whether their formation is inhibited kinetically or energetically.

To gain further insights, we determined the folding pathways from CG simulations and classified the intermediates from about 200 folding and unfolding events (Figure 6 and 7). The results reveal that all four possible hairpin conformations are accessible in the simulations. However, their stability is different as indicated by the different lifetimes τ. The hairpin structure formed by the two terminal guanosine repeats (labeled H4 in Figure 6) is most stable with a lifetime of $\tau = 11.3$ ns. Hairpin structures with propeller loops have shorter lifetimes. The shortest lifetime is observed for the hairpin structure formed by the first two repeats at the 5' end (labeled H1, $\tau = 4$ ns). These results agree with previous all-atom simulations for propeller loop hairpins from human telomeric rG4s, revealing that these hairpins unfold rapidly (37, 75). Moreover, a hairpin intermediate at the 5' end, similar to H1 in Figure 6 and Figure 7, was recently observed in smFRET experiments on the folding pathway of a plant rG4 (36).

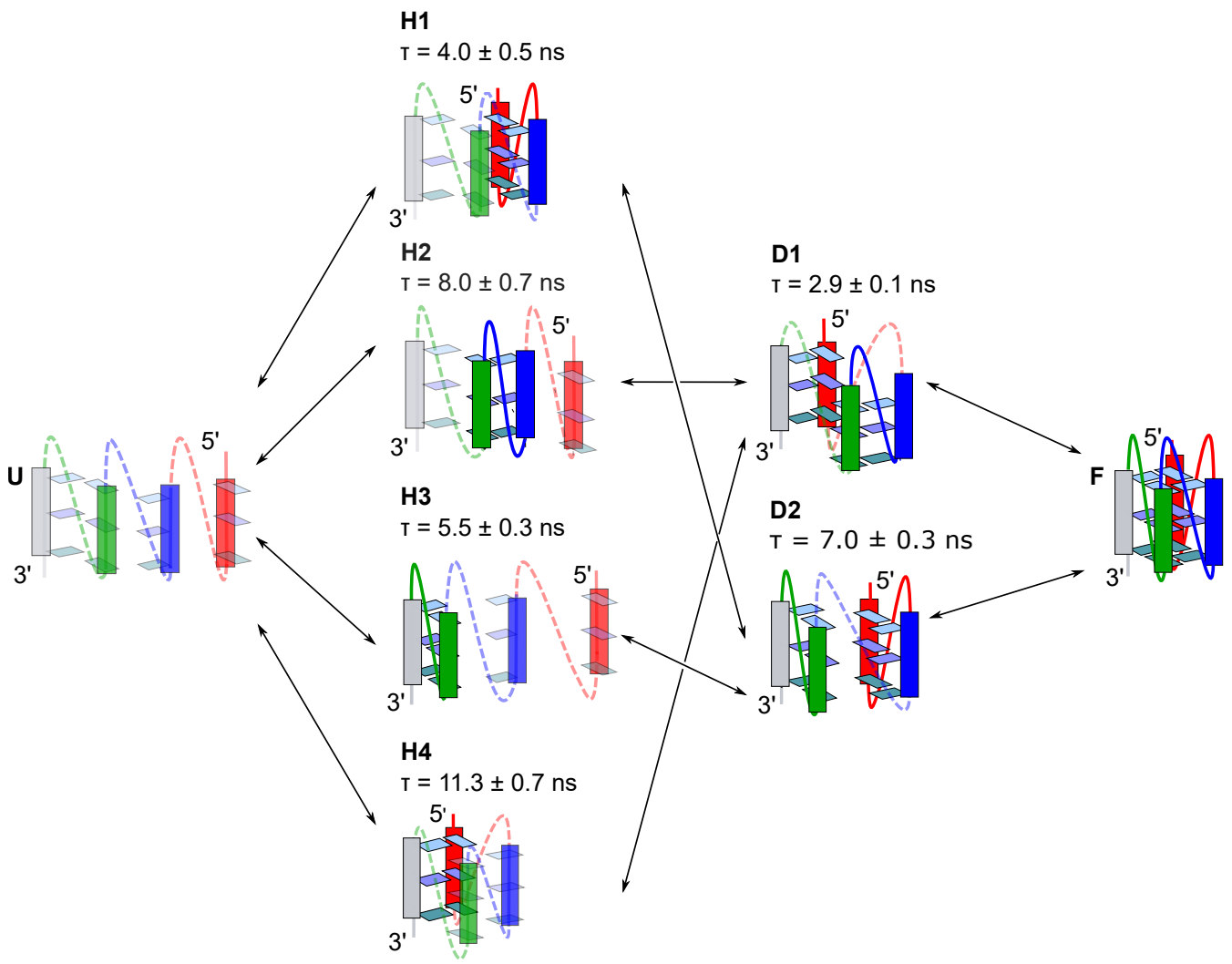

Figure 7. Folding and unfolding pathways of TERRA25. The arrows correspond to the transitions between the conformations. The pathways pass through two intermediate states: hairpin and double-hairpin state. As in Figure 5, four different hairpin (H1, H2, H3, H4) and two different double-hairpin (D1, D2) conformations are observed. The lifetimes τ of the intermediates are shown above the structures.

The situation is similar for the triplex intermediates. Again, all four possible triplex conformations are observed in the simulations. A triplex intermediate with $\tau = 30$ ns is formed by the two terminal repeats and one central repeat (T3 in Figure 6). The other triplexes (T1, T2, T4) have significantly shorter lifetimes, likely due to the high entropy of the free guanosine repeats at the 3' or 5' end. Interestingly, a triplex similar to T1 has been observed in smFRET experiments for a plant rG4 (36). Moreover, RNA triplexes with propeller loops have been proposed for rG4s and dG4s with two quartets (35).

In addition to hairpin and triplex, an additional class of intermediates is observed: Two hairpins are created sequentially and form a double-hairpin intermediate state (Figure 7). In pathways containing a double-hairpin intermediate, no triplex state is observed. The double-hairpin structure D2, in which each hairpin comprises one free end, is the most stable with $\tau = 7$ ns. This is further supported by a similar double-hairpin conformation from NMR spectroscopy on a hybrid G4 of human telomeric DNA (29).

In summary, the pathways between the unfolded and folded state of TERRA25 pass through two transient intermediate states. The first intermediate is a hairpin and the second one is either a triplex or a double-hairpin state. Each state comprises several different conformations leading to the high conformational entropy of the intermediate states. In total, four different hairpin, four different triplex and two different double-hairpin structures are observed along the folding pathways of TERRA25.

CONCLUSION

The folding kinetics of rG4s is essential for their function in cellular processes. In the current work, we resolve the folding pathways of a G4 derived from human telomeric repeat-containing RNA (TERRA25) by combining all-atom MD, CG simulations and CD experiments.

Initially, we develop a matching procedure based on atomistic simulations in explicit water to correctly capture

the ionic double layer in the implicit solvent CG simulations. The matching correctly reproduces the local salt concentration in the vicinity of the negatively charged phosphate groups and therefore yields close agreement of the fraction of folded structures obtained from CG simulations and experiments at a given salt concentration.

Folding of rG4s is on the timescale of minutes (21) and therefore out of reach for atomistic simulations. CG simulations using the TIS model, on the other hand, reach beyond this limit and allow us to resolve the folding pathways and intermediate states with sufficient statistics. The simulations reveal on-pathways intermediates corresponding to hairpin, triplex or double-hairpin states. The intermediates are transient and possess a high conformational entropy with two to four structures contributing to each state. However, properties that are easy to measure such as the end-to-end distance are insufficient to discriminate between the different structures. Here, the insights from the simulations can guide the experiments to detect all intermediate structures, for instance by strategically placed fluorophores in smFRET experiments (35, 36).

In the future, more complex models could be employed to explore or rule out off-pathway intermediates by including strand-shifts or syn-anti G-patterns. In any case, combining atomistic MD, CG simulations and experiments is a valuable starting point to capture the influence of the ionic environment and to resolve the multi-pathway folding landscape.

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Conflict of interest statement None declared.

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