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Rigid DNA Beams for High-Resolution Single-Molecule Mechanics**

Emanuel Pfizter, Christian Wachauf, Fabian Kilchherr, Benjamin Pelz, William M. Shih, Matthias Rief, and Hendrik Dietz*

Single molecule mechanical techniques like AFM or optical tweezers provide insight into the conformational dynamics of macromolecules and allow reconstructing details of the free energy landscapes that direct such processes.\(^{[1]}\) Single-molecule mechanical assays have been successfully applied to analyze large conformational changes like the ones that occur in protein unfolding or in the motion of molecular motors. However, conformational transitions in many native proteins involve much smaller length changes, on the order of a nanometer or less.\(^{[2]}\) Conventional force spectroscopy at such fine resolution is affected by significant signal-to-noise limitations in the regime of low forces (less than 10 pN). Yet it is precisely the regime of low forces that deserves attention, because the functionally relevant conformational dynamics of proteins and other biological macromolecules are located here.

In a typical single-molecule mechanical assay, the molecule of interest is attached to a sensitive probe such as two micron-sized beads held in optical tweezers (Figure 1A). To avoid non-specific interactions with the surface of the probe, the attachment of the molecule of interest to the probe typically occurs through molecular linkers such as double-stranded DNA (dsDNA).\(^{[3]}\) The mechanical stiffness of those linkers is critical for the signal-to-noise ratio of the measurement.\(^{[4]}\) This can be modeled through Monte Carlo simulations using the consideration that every degree of freedom in a thermodynamic ensemble has the energy \(k_B T / 2\). For soft flexibly linkers, thermal forces will drive the probe through large displacements, but stiff linkers clamp the probe and suppress unwanted noise (Figure 1B,C).

Previously, noise suppression was achieved by taking advantage of the tensile stiffening of polymeric linkers upon stretching to high forces above 10 pN (Figure 1C).\(^{[5]}\) Short (less than 50 nm) B-form DNA linkers were also tested for
their ability to stiffen the connection between the beads,[9] but the noise suppression was minor, presumably because of the unusual flexibility of short duplex DNA molecules[7] and the flexibility of the DNA-bead attachment.[9] Molecular self-assembly with DNA offers unique possibilities to create functional structures with user-defined shape and mechanical properties.[9] Herein, we took advantage of this technique to establish rigid beam-like molecular linkers that enable the study of conformational transitions of single molecules with unprecedented resolution.

We tested four linker designs for rigid-beam-like mechanical behavior. We constructed helix bundles consisting of six, eight, ten, and twelve DNA double helices that were aligned and cross-linked in parallel at contour-length extension (Supporting Information, Figure S1).[9c] Because the bundles form from a DNA molecule 7560 bases in length, the bundle length decreases with increasing number of DNA double helices in the bundle. The bundles were self-assembled in one-pot thermal renaturation reactions, as previously described.[9c] Assembly was confirmed by agarose gel electrophoresis (Figure S2) and by direct imaging using negative-stain transmission electron microscopy (TEM; Figure S3). Single particle TEM micrographs were aligned against a randomly chosen reference particle micrograph using cross-correlation maximization within a 25 pixel radial interval centered in the middle of each bundle micrograph. Average bundle images were computed (Figure S4 A) that reflected decreasing shape fluctuations with increasing cross-sectional area of the bundles. The ten- and twelve-helix bundles in particular appeared as rigid beams with little shape variation. Particle backbone tracing in single-bundle micrographs was used to determine the contour lengths and end-to-end distances (Figure S4B,C). This data agreed with predictions from a semi-flexible beam theory[9b] when assuming persistence lengths of 2 μm for the six-helix bundle and 3.5 μm for the eight-helix bundle. The value found for the six-helix bundle is consistent with previous results.[11] For the ten- and twelve-helix bundles, the measured end-to-end distances were identical to the measured contour lengths within the resolution of the backbone tracing method. For all bundles, the measured average contour lengths matched the expected lengths to 2% accuracy. The standard deviation from the average contour length was 3% or less for all bundle types. We attributed fluctuations in the measured contour lengths mostly to limitations of backbone tracing, rather than actual absolute contour length fluctuations.

To analyze the mechanics of individual helix bundles in a dual-beam optical tweezer setup (Figure 2 A), the two opposing helical interfaces of the bundles were functionalized with multiple biotin- and digoxigenin-modified DNA oligonucleotides (see Figure S1), respectively, and then attached to streptavidin- and anti-digoxigenin-modified one micrometer silica beads. The force-extension responses of individual helix bundles (Figure 2 B) were as expected (Figure 1 C), except for a false impression of extensibility when stretched to the contour length (Figure 2 B). This data gave stretching stiffness values $k_{\text{app}}$ that were an order of magnitude smaller than expected ($k_\text{expected} = NK/L$, where $L$ is the contour length, $K$ the stretch modulus of a single dsDNA,[12] and $N$ the number of helices in the bundle). However, the observed apparent bundle extensibility also correlated directly with the stiffness of the laser traps used in the experiments (Figure 2 C), thus pointing to errors in determining the absolute bead displacements rather than an actual significant stretching of the bundles beyond their unloaded contour length. These errors directly propagate into the quantity extension for the special case of linkers that are significantly stiffer than the laser traps themselves. Importantly, the force-extension data obtained, for example, with the ten-helix bundles had the desired noise suppression in the force regime from 1 to 10 pN (Figure 2 D). The noise suppression remained comparable when using two copies of the ten-helix bundles that flanked a short dsDNA element as a mimic for a molecule under study that lacks conformational dynamics (Figure 2 D). Because the ten-helix bundle combined attractive geometrical properties with an absolute length of approximately 250 nm and rigid-beam-like mechanical properties, we used it for the experiments that are described next. However, the other bundle types also offer noise suppression, with a slight trend toward greater noise suppression for thicker bundles (Figure S5).

For proof-of-concept purposes we compared the unfolding and refolding dynamics of a previously studied stable 20 base-pair (bp) long DNA hairpin[13] using conventional dsDNA linkers (Figure 3 A,B) versus using stiff ten-helix bundle linkers (Figure 3 C,D; see Figure S6 for design
details). The data were consistent with each other (see also Figure S7), except for a larger separation between the two dominant deflection states corresponding to the unfolded and folded states of the hairpin in the stiff linker data (Figure 3B versus Figure 3D), which is an expected consequence of the inextensibility of the ten-helix bundle linkers. We also determined the force-dependent unfolding- and refolding-transition rate constants of the 20 bp hairpin (Figure 3E) by analyzing the distribution of dwell times in the constant-distance data (see also Figure S7). The rate constants obtained from the experiments with the stiff linker system agreed well—within experimental error—with those from our reference experiments and also with previous experiments\[13a\] that were both performed with the conventional dsDNA linkers. Notably, the noise suppression that was supplied by the stiff linker system even at the relatively high force load of around 14 pN gave access to more detailed information about the energy landscape that directs the hairpin transition. Histograms of the deflection states visited at a load of approximately 14 pN as measured with the conventional dsDNA (orange) versus the ten-helix bundles (cyan). G) Free-energy landscape reconstructed from (F) using deconvolution\[22\] of the deflection statistics.

Finally, we used the stiff linker system to study equilibrium unfolding and refolding transitions of a weak six bp DNA hairpin. The force-extension response when pulling on constructs in which the six bp hairpin was either flanked by stiff linkers or the conventional dsDNA linkers featured, in both cases, increased extension fluctuations in the force range 4–8 pN (Figure 4A–C), consistent with previous data for this hairpin.\[13a\] When monitoring the extension at a constant trap distance in this force range, the data collected with the stiff linkers exhibited two-state hopping signatures on the timescale of milliseconds that reflected reversible folding and unfolding transitions of the short hairpin (Figure 4D). Such transitions could not be discerned in the data that we collected with the conventional dsDNA linkers (Figure 4E). Hidden Markov modeling\[14\] assuming a two-state system was successful when applied to the data acquired with the stiff linkers (Figure 4D) and allowed for extraction of the force-dependent transition rate constants for the short hairpin (Figure 4F). The corresponding analysis failed when applied to the data obtained with the conventional dsDNA linkers (Figure 4E) because of the greater noise amplitude. Histograms of the extension signals obtained with the stiff linker system show two distinct populations that are separated by approximately 3 nm along the extension axis (Figure 4G). These two populations are masked in noise for the case of the conventional linkers (Figure 4H). The higher-resolution data acquired with the stiff linker system thus allowed construction of a meaningful free-energy landscape for the short hairpin that contains two minima (Figure 4I).
The average force load on the folded and unfolded states was 6.5 pN and 6.0 pN in the bead attachment may further enhance the performance of Angew. Chem. Int. Ed.

**Figure 4.** Conformational dynamics of a 6 bp DNA hairpin. A,B) Force-extension data at full measurement bandwidth collected with A) ten-helix bundles or B) conventional dsDNA linkers. C) Fluctuation amplitude in the data from (A,B) or when the linkers were connected directly (gray). D) Solid line: extension data for constant trap distance at full measurement bandwidth for the ten-helix bundles. Dashed line: fitted two-state hidden Markov transition trajectory. E) As in (D) but with conventional dsDNA. F) Force-dependent folding (falling branch) and unfolding (rising branch) rate constants as determined from dwell-time analysis of constant distance data as in (D) acquired at different loads. Vertical and horizontal bars indicate branch) rate constants as determined from dwell-time analysis of constant distance for C) the ten-helix bundles or H) conventional dsDNA. Solid lines: fits using a single Gaussian (red) or a linear combination of two Gaussians (gray). The average force load on the folded and unfolded states was 6.5 pN and 6.0 pN in (G), respectively. I) Free-energy landscape reconstructed from the data in (G).

Our results thus establish DNA helix bundles as an attractive linker system for single-molecule mechanical assays. In addition to enabling single-molecule force spectroscopy with higher resolution in the low force regime, the system provides a multivalent and thus presumably longer-lasting attachment to the beads. It may also be conjugated to a wide range of target molecules using previously established methods. We speculate that also reducing the flexibility of the bead attachment may further enhance the performance of the stiff linker system. For the future studies of the energy landscape of enzymes and other functional protein systems, where conformational changes take place in the sub-nanometer range, these rigid DNA beams offer significant advantages over conventional approaches. Hence, we anticipate that our stiff linker system, based on self-assembled DNA nanostructures, may become a standard technique for the study of the functionally relevant dynamics of biological macromolecules.

**Experimental Section**

DNA-templated design and synthesis: The multi-helix bundles were designed using caDNAno v0.2.[3] DNA scaffold strands were prepared as previously described.[5] DNA staple oligonucleotide strands (Table S1) were prepared by solid-phase chemical synthesis (Eurofins MWG) with Eurofins MWG high purity salt free purification grade. The objects were synthesized in a one-pot mixture containing 20 mm of a 7560 base long M13mp18-phase-derived genomic DNA, 200 nm oligonucleotide staples in a pH 8 buffer that included 5 mm Tris-base, 1 mm EDTA, 20 mm MgCl2, and 5 mm NaCl. The mixture was incubated at 65°C for 15 min, then annealed from 60°C to 43°C over the course of 16 h, and then stored at 4°C. Analysis of the reaction products by agarose gel electrophoresis (Figure S2) showed that the helix bundles assembled with acceptable yield.

Monte-Carlo simulations for Figure 1: The combined free-energy function for two tethered beads held in an optical trap was constructed by considering 3D harmonic potentials for the laser traps with a curvature of 0.4 pN nm⁻¹ in the directions perpendicular to the laser beam, and 0.04 pN nm⁻¹ along the beam direction, plus the expected energetic contributions of the tether as a function of its extension. To model the elasticity of the tether, the extensible worm-like chain (eWLC) model was used in the case of the conventional dsDNA linkers ( persistence length \( p = 50 \) nm, contour length \( L = 530 \) nm, and stretch modulus \( K = 1 \) nN), while an extensible freely-jointed chain with two elements [Eq. (1)] was used to model the elasticity of the rigid ten-helix bundles with \( K = 10 \) nN and \( L = 4885 \) nm.

The expression for the free energy of the eWLC model is given by Eq. (1):

\[
F(e) = k_B T \frac{2 \left( \frac{e}{L} \right)}{L \left( 1 - \frac{e^2}{L^2} \right)}
\]

To account for the additional elasticity of the DNA single strands that were used to connect the stiff helix bundles to the beads, the worm-like chain model was employed using a contour length \( L = 15 \) nm and a persistence length \( p = 1 \) nm. The stochastic dynamics of the system were simulated using a Monte Carlo method.[17] Every degree of freedom was varied randomly and simultaneously in discrete steps \( n \). The difference in free energy with respect to the previous iteration was computed. The variations were accepted with Boltzmann-weighted probability. If the step was accepted, one trap position was moved away by \( dx = (500 \text{ nm s}^{-1})/(100 \text{ kHz}) \). If the step was not accepted, another random variation was performed. The resulting force-extension traces were downsampled to 20 kHz to maintain comparability to experimental data. The standard deviation of the extension signal versus force was determined in the same way as for the experimental data. For the standard-deviation plots shown.
in Figure 1C, 200 individual force-extension traces were simulated and the average force-dependent standard deviation was determined.

Preparation of conventional dsDNA linkers conjugated to DNA hairpins: Autosticky-PCR[9] was performed on a segment of M13mp18 genomic DNA to produce two products: 1) 5' biotin + 1024 bp + abasic site + hairpin + 30 nt 5' overhang, and 2) 30 nt 5' overhang (complementary to 5' overhang in product (1)) + 563 bp + 5' digoxigenin. The two products (1) and (2) were each purified by agarose gel electrophoresis followed by physical extraction using freeze'n'squeeze columns (Biorad), and then incubated together in a 1:1 volumetric ratio for dimerization. The dimerized product was again gel purified as above and thus gave an approximately 530 nm long dsDNA construct that included the hairpin at about 2/3 of its length.

Preparation of ten-helix bundles with hairpins: The bundles were self-assembled as described above. One version was prepared that included four biotinylated-DNA overhangs on one helical-bundle interface plus the desired hairpin sequence (extended by a single-stranded DNA overhang) on the opposing helical-bundle interface (see Figure S6). Another version was prepared that included four digoxigenin-modified DNA overhangs on one helical-bundle interface and a single-stranded DNA overhang on the opposing interface that was complementary to the 5' single-stranded overhang of the hairpin on the other ten-helix bundle. These bundles were gel-purified (2% agarose, 0.5xTBE) plus the desired hairpin sequence plus the desired hairpin sequence. These bundles were self-assembled as described above. One version was prepared that included four biotinylated-DNA overhangs on one helical-bundle interface and a single-stranded DNA overhang on the opposing interface that was complementary to the 5' single-stranded overhang of the hairpin on the other ten-helix bundle. These bundles were gel-purified (2% agarose, 0.5xTBE) plus the desired hairpin sequence plus the desired hairpin sequence.
[10] J. Wilhelm, E. Frey, *Phys. Rev. Lett.* **1996**, *77*, 2581 – 2584.

[11] D. J. Kauert, T. Kurth, T. Liedl, R. Seidel, *Nano Lett.* **2011**, *11*, 5558 – 5563.

[12] Z. Bryant, M. D. Stone, J. Gore, S. B. Smith, N. R. Cozzarelli, C. Bustamante, *Nature* **2003**, *424*, 338 – 341.

[13] a) M. T. Woodside, W. M. Behnke-Parks, K. Larizadeh, K. Travers, D. Herschlag, S. M. Block, *Proc. Natl. Acad. Sci. USA* **2006**, *103*, 6190 – 6195; b) M. T. Woodside, P. C. Anthony, W. M. Behnke-Parks, K. Larizadeh, D. Herschlag, S. M. Block, *Science* **2006**, *314*, 1001 – 1004.

[14] J. Stigler, M. Rief, *ChemPhysChem* **2012**, *13*, 1079 – 1086.

[15] S. M. Douglas, A. H. Marblestone, S. Teerapittayanon, A. Vazquez, G. M. Church, W. M. Shih, *Nucleic Acids Res.* **2009**, *37*, 5001 – 5006.

[16] S. M. Douglas, J. J. Chou, W. M. Shih, *Proc. Natl. Acad. Sci. USA* **2007**, *104*, 6644 – 6648.

[17] N. Metropolis, A. W. Rosenbluth, M. N. Rosenbluth, A. H. Teller, E. Teller, *J. Chem. Phys.* **1953**, *21*, 1087 – 1092.

[18] J. Gal, R. Schnell, S. Szekeres, M. Kalman, *Mol. Gen. Genet.* **1999**, *260*, 569 – 573.

[19] L. Rognoni, J. Stigler, B. Pelz, J. Ylanne, M. Rief, *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 19679 – 19684.

[20] Y. von Hansen, A. Mehlich, B. Pelz, M. Rief, R. R. Netz, *Rev. Sci. Instrum.* **2012**, *83*, 095116.

[21] S. F. Tolić-Nørrelykke, E. Schaffer, J. Howard, F. S. Pavone, F. Julicher, H. Flyvbjerg, *Rev. Sci. Instrum.* **2006**, *77*, 103101.

[22] M. Hinczewski, J. C. Gebhardt, M. Rief, D. Thirumalai, *Proc. Natl. Acad. Sci. USA* **2013**, *110*, 4500 – 4505.