Magnetic torque tweezers: measuring torsional stiffness in DNA and RecA-DNA filaments

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We introduce magnetic torque tweezers, which enable direct single-molecule measurements of torque. Our measurements of the effective torsional stiffness $C$ of dsDNA indicated a substantial force dependence, with $C = \sim 40$ nm at low forces up to $C = \sim 100$ nm at high forces. The initial torsional stiffness of RecA filaments was nearly twofold larger than that for dsDNA, yet at moderate torques further build-up of torsional strain was prevented.

Magnetic tweezers are a powerful single-molecule technique that can be used to apply stretching forces and torques to biological molecules tethered between a surface and superparamagnetic particles. Although forces applied in conventional magnetic tweezers can readily be calibrated, direct measurement of torque has proven difficult. Here we report the design of magnetic torque tweezers (MTT), which can be used to apply and directly measure both forces and torques to single biomolecules and yet have the strengths of conventional magnetic tweezers: facile application of torque, natural operation in constant force mode, straightforward extension to parallel measurements, absence of sample heating and photodamage, and simplicity and robustness.

We introduce a protocol to monitor the bead’s rotation with simultaneous detection of the bead’s $x$, $y$ and $z$ position, and redesigned the magnet geometry to provide an angular clamp suitable for torque measurements. In contrast to a nanorod-based approach, our MTT do not require complicated nanofabrication of particles, they allow for application of torque by simple rotation of the magnets and maintain the position resolution of conventional magnetic tweezers. Unlike the torque measurement schemes using a rotor bead assay or an optical torque wrench, the MTT require neither lasers for fluorescence excitation, particle trapping or polarization control, nor special constructs for the tether. Our MTT cover the entire range of stretching forces relevant for studying supercoiled DNA from $\sim 10$ femtonewtons (fN) to 10 pN.

The principle of the MTT is based on the measurement of small angular deviations in a low-stiffness torsional trap (Fig. 1a,b). A superparamagnetic bead held in magnetic tweezers experiences a constant upward force, $F = \nabla \cdot (m(B) \cdot \vec{B}) / 2$, in which $\vec{B}$ is the magnetic field and the force, $\vec{F}$, is due to the magnetization, $\vec{m}$, and the gradient of the magnetic field. The upward force exerted by the magnetic tweezers on the bead is balanced by the restoring force of the DNA tether. In addition, the bead’s rotation about the $z$ axis (along the direction of the stretched DNA) is constrained by the magnetic field. The torque exerted on the bead by the magnetic field is given by $\vec{r}_T = \vec{m} \times \vec{B}$ in which $\vec{m}$ is exclusively the permanent component of the bead’s magnetization. Unlike the force exerted by the magnets, the torque depends on $\vec{m}$ (but $\vec{F}$ depends on the total magnetization, $\vec{m}$) and on the magnitude and direction of the magnetic field (but $\vec{F}$ depends on the gradient).

The stiffness of the torsional trap, $k_{\text{rot}}$, can be calibrated by observing the rotational thermal fluctuations $<\delta \theta^2>$ of the bead and applying the equipartition theorem

$$k_{\text{rot}} = \frac{k_B T}{\langle \delta \theta^2 \rangle}$$

in which $k_B$ is the Boltzmann constant, and $T$ is the temperature. If the DNA tether is over- or underwound by rotating the magnets, the DNA will exert a restoring torque $r_{\text{DNA}}$ on the bead (Fig. 1b). After calibrating the trap stiffness and the equilibrium angle $\theta_0$ of the trap for torsionally relaxed DNA, $r_{\text{DNA}}$ can be determined from the shift in the average angle $<\theta - \theta_0>$ away from this equilibrium

$$r_{\text{DNA}} = -k_{\text{rot}} (\theta - \theta_0)$$

To implement the necessary angular tracking, we attached non-magnetic, biotinylated 1.0-μm-diameter beads to streptavidin-coated 2.8-μm-diameter superparamagnetic beads that we tethered to a microscope coverslip by single DNA molecules (Fig. 1a,c). We analyzed slightly defocused charge-coupled device (CCD) images obtained by video microscopy (Fig. 1d) to track the magnetic bead’s $x$, $y$ and $z$ position with a resolution of $\sim 2-3$ nm as determined from the s.d. of the traces of immobile beads (Supplementary Fig. 1). The smaller bead was a clear fiducial marker that allowed us to track the rotation angle simultaneously with the position of the magnetic bead (Fig. 1d) by considering a ring-like radial section of the bead image that was centered on the magnetic bead and included the fiducial bead (Fig. 1e). We used a correlation algorithm to track the fiducial bead, after unfolding the image in polar coordinates (Fig. 1f and Supplementary Fig. 2). The angular resolution of our tracking protocol was $\sim 0.1^\circ$, as judged from angular traces of beads stuck to the surface (Fig. 1g and Supplementary Figs. 3 and 4).
To provide MTT with sufficient sensitivity for detecting small torques, we redesigned the magnet configuration in our tweezers. In conventional magnetic tweezers, $\vec{m}_0$ is closely aligned with a horizontal magnetic field and the torsional trap stiffness $k_{\text{rot}}$ is in the range of $10^3$–$10^4$ pN nm rad$^{-1}$, which is unsuitably large for torque measurements on DNA (Supplementary Figs. 5 and 6). We based our MTT magnet geometry on a large cylindrical magnet aligned vertically, with the field pointing in the $z$ direction (Fig. 1a), which provides a strong field gradient that pulls the magnetic bead upwards, but reduces $k_{\text{rot}}$ by multiple orders of magnitude. For perfect alignment of the field with the $z$ direction, we expected $\vec{m}_0$ to align in the $z$ direction and the bead to rotate freely about the $z$ axis, unconstrained by the magnets. Therefore, to maintain the ability to apply torques and rotate the bead, we added a small side magnet that provides a small horizontal component to the field and generates a weak angular trap with $k_{\text{rot}}$ of $\sim 100$–500 pN nm rad$^{-1}$ (Supplementary Figs. 5 and 7), allowing us to directly observe the shift in equilibrium angle induced by the torque exerted by DNA (Fig. 1g).

Using MTT we determined the DNA tether extension and torque response while over- and underwinding single DNA molecules (Fig. 2 and Supplementary Figs. 8 and 9). Starting with a torsionally relaxed molecule at 0 turns, DNA initially behaves like an isotropic flexible rod: as positive turns are added to the molecule, its extension remains approximately constant (Fig. 2d) and the shift in the mean angular signal decreases linearly with increasing number of turns (Fig. 2b,c). The shift in the mean angle can be directly converted to torque (Fig. 2b,c) because the stiffness of the torsional trap is independent of the applied number of turns (Fig. 2a). The effective twist persistence length, $C$, of DNA can be determined from a fit to the torque data in the region in which the torque builds up linearly with added turns (Fig. 2b,c) as the torque after $N$ turns equals $2\pi Nk_{\text{rot}}TC/L_C$, in which $L_C$ is the contour length of DNA (we determined $L_C$ independently; Supplementary Fig. 10). As we continued to apply positive turns, the build-up in torsional strain continued until a critical twist density was reached at which the molecule buckled to form plectonemic supercoils. Beyond this transition, the torque in the molecule remained constant at $\tau_c$ (Fig. 2b,c); additional turns led to an accumulation of plectonemic supercoils associated with a rapid decrease in extension (Fig. 2d). When we applied negative turns to torsionally relaxed DNA, the DNA initially behaved like an isotropic rod and exerted a restoring torque with opposite sign compared to the situation with positive turns. Under tensions of 1 pN or greater, DNA does not buckle upon further underwinding (the extension of the molecule remained approximately constant; Fig. 2d and Supplementary Fig. 11); instead the molecule denatured locally$^{10}$. Experimentally, we measured the corresponding denaturation torque $\tau_{\text{dennat}} = -10 \pm 1$ pN nm (Fig. 2b).

We systematically measured torque response of single DNAs to determine the buckling torque $\tau_c$ and effective twist persistence length $C$ as a function of the stretching force $F$ (Fig. 2e,f). $\tau_c$ increased systematically with increasing $F$ (Fig. 2e). A simple model of DNA elasticity$^{11}$ captured the observed behavior only qualitatively, whereas a more complicated model$^{12}$ described the data quantitatively (Fig. 2e). At forces above 6 pN, DNA no longer formed plectonemic supercoils upon overwinding and instead underwent a transition from B- to P-DNA$^{6,10}$. This transition occurred at $36 \pm 2$ pN nm (Fig. 2e), in agreement with published measurements (using two different methods: rotor bead assay$^6$ and optical torque wrench$^{13}$).

The effective torsional stiffness of DNA depended on $F$: $C$ decreased from $103 \pm 5$ nm at $F = 6.5$ pN to $43 \pm 4$ nm at $F = 0.25$ pN.
The value we obtained at 6.5 pN agrees with experimental error with the values determined at forces between 15 and 45 pN (ref. 6) (Fig. 2f), suggesting that the force-dependence of C effectively saturates for \( F \geq 6.5 \) pN. Our measurement for C at 0.25 pN agreed with values determined from fluorescence polarization anisotropy measurements of short linear DNA constructs\(^{14-16}\) that are effectively made at zero stretching force (Fig. 2f). Previous measurements with less well-defined stretching forces and theoretical treatments that integrate data at different forces have yielded C values that were intermediate between these limits (Supplementary Fig. 12). Our direct measurements over the entire force range can be compared to the Moroz-Nelson\(^{17}\) model for C(F) and to the data obtained using an indirect approach\(^{18}\) (Fig. 2f and Supplementary Fig. 12).

We also used the MTT to probe RecA filaments assembled on torsionally constrained duplex DNA in the presence of the non-hydrolyzable ATP analog ATP-γS\(^{19,20}\). In the filament one RecA monomer binds every three base pairs (bp), resulting in both stretching (0.51 nm increase in \( L_C \) per bound monomer) and unwinding (−45° per bound monomer) compared to bare DNA\(^{21}\) (Fig. 3a). RecA-dsDNA filaments had a dramatically increased bending stiffness \( L_P \), with \( L_P \) increased at least 15-fold compared to dsDNA (Supplementary Fig. 13).

Upon overwinding of the torsionally relaxed filament, we initially observed an increase in the torsional strain in the molecule (Fig. 3b and Supplementary Fig. 14) and subsequently, at \( \sim 50 \) turns, a saturation of the torque at 39 ± 3 pN nm. The initial buildup of torque was fitted to yield \( C_{\text{RecA}} = 173 \pm 5 \) nm at \( F = 3.5 \) pN, which was 1.8-fold larger than that of bare DNA at the same force. In contrast, we observed saturation of torsional stress at a lower value of \( \sim 10 \pm 5 \) pN nm upon underwinding. Given values are means ± s.e.m. from ten independent measurements.

These measurements suggest that upon initial application of torque, torsional strain builds up in the RecA-dsDNA filament, which exhibits a higher effective torsional stiffness than dsDNA, as might have been qualitatively expected from the increased \( L_P \) and diameter of the filament. However, at torques similar to 40 pN nm upon overwinding and \( \sim 10 \) pN nm upon underwinding, we...
observed no additional build-up of torsional strain. The modest decrease in length per turn (about 1 nm per turn upon overwinding and about 1.4 nm per turn upon unwinding) suggests that the filament did not buckle. The evidence from the torque and extension measurements combined with additional experiments probing the disassembly of the filament (Supplementary Fig. 15) suggest that a combination of RecA unbinding and supercoiled P-DNA formation upon overwinding and DNA denaturation upon unwinding might be responsible for the observed saturation of the torsional strain.

We anticipate that MTT can be generally applied to obtain information about the material properties of biological polymers and can be a platform with which to probe protein-protein or protein-nucleic acid interactions.

METHODS
Methods and any associated references are available in the online version of the paper at http://www.nature.com/naturemethods/.

Note: Supplementary information is available on the Nature Methods website.

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AUTHOR CONTRIBUTIONS
J.L., J.W.J.K. and N.H.D. designed the study, J.L. and T.J. performed the experiments, J.W.J.K. wrote the angular tracking routine and J.L. and N.H.D. wrote the manuscript.

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ONLINE METHODS

DNA construct. As tethers in our MTT setup, we used a 7.9-kbp DNA construct ligated at the ends to ~600-bp DNA PCR fragments that were functionalized with multiple biotin and digoxigenin groups, respectively. The 7.9-kbp DNA is the ligation product of residues 755–1153 of the plbluescrIISK plasmid (Stratagene), residues 4214–6163 and 9023–11220 of lambda-phage DNA (Promega) and residues 1945–5304 of the pSV1 plasmid (Stratagene). The DNA tethers were attached to streptavidin-coated 2.8-μm-diameter M270 superparamagnetic beads (Invitrogen) by incubation in PBS (Sigma).

Magnetic tweezers experimental configuration. Our MTT implementation extends the capabilities of conventional magnetic tweezers1, which have been described previously2,4,22–24. Briefly, a 100x oil-immersion objective (Olympus ACH 100X; numerical aperture (NA) = 1.25) connected to a CCD camera (Pullux TM-6710CL) was used to image superparamagnetic beads tethered by DNA molecules to the surface of a flow cell.

Flow cells were made from glass microscope cover slips with a double layer of parafilm as a spacer. The bottom surface was coated with nitrocellulose (0.01% wt/vol) in amyl acetate and flow cells were stored dry. Before measurements, 3.6-μm-diameter nonmagnetic latex beads (Invitrogen) were unspecifically attached to the bottom surface by incubation in PBS for 30 min to act as reference beads. Before addition of the DNA-linked magnetic beads, the bottom surface was functionalized by incubation with 100 μg ml⁻¹ anti-digoxigenin (Roche) in PBS for 30 min to provide for DNA attachment and was passivated by incubating for 30 min with 2 mg ml⁻¹ bovine serum albumin (Sigma). The positions of a DNA-tethered bead and a reference bead attached to the surface were tracked simultaneously at a rate of up to 120 Hz. From analysis of the CCD images, the bead positions in x, y and z dimensions were determined (see below).

After subtraction of the reference bead position to correct for mechanical drift, the tethered bead was tracked with an accuracy of < 5 nm in x, y and z dimensions (Supplementary Fig. 1). From analysis of the CCD images, the bead positions in x, y and z dimensions were determined (see below).

Magnets for MTT. To apply forces and torques, we placed magnets with a center opening for LED illumination above the flow cell. The main magnet was a cylindrical magnet formed by a stack of three magnets (R-06-02-02-G, Supermagnet). An additional magnet (S-04-07-N, Supermagnet) was added on one side of the cylindrical magnet to allow for the application of torque. The side magnet had the shape of a solid cylinder, with 4-mm diameter and a height of 7 mm. A detailed schematic of the magnet assembly is presented in Supplementary Figure 16.

Rotational tracking by video microscopy. After tethering the magnetic beads to the surface, we specifically attached smaller, nonmagnetic beads to act as fiducial markers for tracking the magnetic beads’ rotation. As fiducials, we used biotin-labeled 1.0-μm-diameter Fluosphere microspheres (Invitrogen). Incubation of the flow cell with 1,000-fold diluted Fluosphere beads for 30–60 min lead to attachment of typically one or more marker beads per tethered magnetic bead. The 1.0-μm-diameter marker beads provided sufficient asymmetry of the bead image to track the rotation angle via cross-correlation analysis of the CCD images with an accuracy of ~0.1° (Fig. 1g and Supplementary Fig. 4a) using the following algorithm.

The defocused microscope image of a magnetic bead with a smaller, nonmagnetic fiducial bead attached was still nearly circularly symmetric but contained a small protrusion on one side (Fig. 1d and Supplementary Fig. 2a). As most of the ring pattern is unaffected, the x-y-tracking procedure by cross-correlation analysis still closely approximated the symmetry center of the main bead and we achieved an accuracy of 2–3 nm as judged by the s.d. of traces recorded with surface attached beads (Supplementary Fig. 1). For tracking the relative angle of the protrusion, a polar coordinate grid [r,φ] grid was defined using the center position determined from the x-y tracking as the coordinate center. The range of the angular coordinate φ is 360 degrees and comprises 360 p steps, with p being the number of points per degree. The radial coordinate, r, runs from minimum to maximum values r_min to r_max with increments of p per pixel unit. The truncated image that results using a typical choice of r_min and r_max is shown in Supplementary Fig. 2b. Using these coordinates, we generated an image in polar coordinates P(r,φ) (Supplementary Fig. 2c) using interpolated pixel intensities S(i′,j′) from the original image, in which i′ and j′ are noninteger pixel coordinates:

\[ i' = i + \delta_i = r \sin(\phi) \quad \text{and} \quad j' = j + \delta_j = r \cos(\phi) \]

(3)

where i and j are the truncated integer values, and \( \delta_i \) and \( \delta_j \) is the difference between the fractional pixel coordinate and its truncated integer value. To track the rotation of the bead, which corresponds to pattern changes along the φ direction, we summed the polar map over r:

\[ P(\phi) = \sum_{r_{\min}}^{r_{\max}} P(r,\phi) \]

(4)

The resulting curve produced an angular signature of the bead and shifted proportionally and periodically with φ when the bead and its corresponding image pattern rotated. To quantify the relative change in φ, we performed a cross-correlation of \( P(\phi) \) with its own mirror function \( P(-\phi) \) (Supplementary Fig. 2d). To speed up the numerical calculation of this cross-correlation, it was performed via the respective fast Fourier transforms (FFT):

\[ C(\phi) = \text{FFT}^{-1}\left(\text{FFT}(P(\phi)) \times \text{FFT}(P(-\phi))\right) \]

(5)

The correlation function of the angular signatures (Supplementary Fig. 2e) exhibited a maximum that shifted twice as fast as a corresponding rotation (which caused the tracked angles to have a periodicity π). To achieve a resolution of less than one angular bin (of 1/\( p_d \) of a degree), a subpixel fitting step was performed by selecting a five-point subsection around the maximum (Supplementary Fig. 2f). This subsection was subjected to a parabolic fit, and the subpixel location of the maximum of the fit was scaled with \( p_d/2 \) to yield a relative angle. Unwrapping of the angle was performed posteriori in the angular trace by detecting sudden changes in the signal close to π. Such phase jumps were compensated for by adding a phase shift of π to all the signal values after the jump. Our implementation
of this tracking algorithm in Labview 2009 (National Instruments) is available as Supplementary Software.

**Buffer conditions and RecA stocks.** Experiments on bare DNA were carried out in PBS (137 mM NaCl, 2.7 mM KCl and 10 mM phosphate (pH 7.4); Sigma) supplemented with 100 μg ml⁻¹ BSA (Sigma), 0.1% Tween (Sigma) and 5 mM sodium azide (Sigma). RecA experiments were performed in a buffer of similar ionic strength, namely 20 mM MES (2-(N-morpholino)ethanesulfonic acid) buffer (Sigma), pH 6.2, with 1 mM MgCl₂ (Sigma), 50 mM NaCl (Sigma), 1 mM DTT (dithiothreitol; Sigma) and 0.1 mM ATP·γS (Roche Diagnostics). We used commercially available RecA stock (New England Biolabs) at a final concentration of 5 μM.

**Estimate of the torque measurement error.** We estimated the error of our torque measurement from basic considerations of error propagation and Brownian fluctuations. The torque measurement in the MTT was achieved from a measurement of the shift of the mean angle from its equilibrium value (equation (2)) after calibrating the trap stiffness \( k_{\text{rot}} \). The error in the torque measurement \( \sigma_\tau \) was approximately given by

\[
\sigma_\tau = k_{\text{rot}} \sigma_\theta
\]  

(6)

in which \( \sigma_\theta \) is the error in the determination of the angular deflection and \( k_{\text{rot}} \) the stiffness of the torsional trap. The measurement of the mean angle had two sources of measurement uncertainty: one kind of error, \( \sigma_{\text{BM}} \), stems from the fact that the particle was undergoing (rotational) Brownian motion and experienced thermal fluctuations; the second type of error, \( \sigma_{\text{meas}} \), stemmed from errors in the measurement, such as inaccuracies of the tracker, drifts of the flow cell, small changes in the illumination, inaccuracies of the magnet positioning and other sources of experimental error. As these two sources of error are approximately independent, they add in quadrature

\[
\sigma_\theta = \sqrt{\sigma_{\text{BM}}^2 + \sigma_{\text{meas}}^2}
\]  

(7)

The magnitude of the error owing to Brownian motion of the particle can be estimated as follows. The particle undergoes fluctuations with a width \( \delta \theta \) given by the stiffness of the trap, by rearranging equation (1)

\[
\langle \delta \theta^2 \rangle = \frac{k_B T}{k_{\text{rot}}}
\]  

(8)

The effect of the Brownian fluctuations can be averaged out by measuring the rotation angle over a time period \( t_{\text{meas}} \). The resulting estimate, which is essentially the s.e.m., will have an uncertainty given by \( \delta \theta / (N(\tau_C))^{1/2} \), where \( N(\tau_C) \) is the number of independent measurements, spaced by approximately one characteristic time of the system, that is, \( N(\tau_C) = t_{\text{meas}} / \tau_C \).

The characteristic time \( \tau_C \) was determined by the rotational friction coefficient \( \gamma \) and the trap stiffness \( \tau_C = \gamma k_{\text{rot}} \) (Supplementary Fig. 7). Combining the expression for \( N(\tau_C) \) with equation (8), we find

\[
\sigma_{\text{BM}}^2 = \frac{k_B T}{k_{\text{rot}} t_{\text{meas}}} \frac{\tau_C}{\tau_{\text{rot}}} = \frac{k_B T \gamma}{k_{\text{rot}} t_{\text{meas}}}
\]  

(9)

This expression is analogous to the thermal limit of position detection\(^{25}\).

**Limit \( \sigma_{\text{BM}} \gg \sigma_{\text{meas}} \).** If we consider a ‘perfect’ measurement in which the intrinsic measurement error is zero, that is, \( \sigma_{\text{meas}} = 0 \), the accuracy of the torque measurement will be limited by Brownian motion alone. More realistically, we consider the case in which the Brownian motion error dominates the overall error, which will be the case for weak traps and short measurements, that is, when \( k_{\text{rot}} \) and \( t_{\text{meas}} \) are small. In this limit, the error on the torque measurement simplifies to

\[
\sigma_\tau = k_{\text{rot}} \sigma_{\text{BM}} = \frac{k_B T \gamma}{\sqrt{t_{\text{meas}}}}
\]  

(10)

We note that in the limit in which \( \sigma_{\text{meas}} \) is negligible, the accuracy of the torque measurement is independent of the trap stiffness: a softer trap leads to a smaller torque error for a given level of accuracy in the angle determination, but to achieve a given accuracy in angle, we have to integrate much longer with the softer trap. Overall, the two effects cancel and the factor \( k_{\text{rot}} \) drops out of the expression for \( \sigma_\tau \).

**Limit \( \sigma_{\text{BM}} \ll \sigma_{\text{meas}} \).** For any real measurement, there will be a contribution to the error on the torque measurement from measurement uncertainties because of tracker error, drift of the instrument and illumination, among others, which are summarized in \( \sigma_{\text{meas}} \). It is instructive to consider the limit in which \( \sigma_{\text{meas}} \) dominates, that is, the limit of negligible Brownian motion. In this limit, the error in the torque for a given measurement error \( \sigma_{\text{meas}} \) is directly proportional to \( k_{\text{rot}} \). This is the reason why we redesigned the magnet geometry for the MTT to substantially lower the trap stiffness. An instrument error of \( \sigma_{\text{meas}} = 0.1° \) corresponds to an error in the torque measurement of \( < 1 \) pN nm for trap stiffnesses in the range of 100–500 pN nm rad⁻¹ (Supplementary Fig. 5b), which is acceptable if measuring DNA in which the characteristic torques are on the order of \( ~10 \) pN nm. In contrast, in conventional magnetic tweezers, the torque trap has a stiffness of \( 10^{3}–10^{4} \) pN nm rad⁻¹ (Supplementary Fig. 5b), corresponding to a torque error of \( 18–180 \) pN nm, which makes systematic measurement of DNA unfeasible (Supplementary Fig. 6b).

In practice, in our instrument \( \sigma_{\text{meas}} = 0.1–0.2° \) (Fig. 1g, Supplementary Figs. 4a and 6), and we measured each torque value, that is, each plateau in the twist curve, for typically \( t_{\text{meas}} = 300 \) s. In this regime, both \( \sigma_{\text{BM}} \) and \( \sigma_{\text{meas}} \) contributed to the total torque error, which was \( ~1–3 \) pN nm from measurement to measurement.