Physical origin of DNA unzipping

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Received: 30 December 2014 / Accepted: 14 July 2015 / Published online: 26 August 2015
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Abstract In DNA transcription, the base pairs are unzipped in response to the enzymatic forces, separating apart two intertwined nucleotide strands. Consequently, the double-stranded DNA (dsDNA), in which two nucleotide strands wind about each other, transits structurally to the single-stranded DNA (ssDNA) in which two nucleotide strands are completely unwound and separated. The large interstrand separation is intimately related to the softening nucleotide strands. This conceptual framework is reinforced with the flow of the bending modulus toward zero under recursion relations derived from the momentum shell renormalization group. Interestingly, the stretch modulus remains the same under recursion relations. The renormalization of the bending modulus to zero has a profound implication that ssDNA has the shorter bending persistence length than does dsDNA in accordance with experiments.

Keywords DNA unzipping · Momentum shell renormalization group · Linking number

1 Introduction

In both prokaryotic and eukaryotic cells, DNA stores the genetic information in the sequence of base pairs. To transcribe the genetic code, two nucleotide strands forming a double helix must be unwound and the complementary base pairs must be unzipped, opening a space for RNA to get access to the base pairs. The enzymatic force competing against the hydrogen bonds tries to pull apart two nucleotide strands. Exploiting the advances in single-molecule

Electronic supplementary material The online version of this article (doi:10.1007/s10867-015-9393-0) contains supplementary material, which is available to authorized users.

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techniques, the DNA unzipping *in vivo* can be mimicked extracellularly by the experiments in which one end of the nucleotide strand is held in an optical tweezer and the other end is anchored to a glass slide. Displacing the glass slide generates a force sufficiently large to initiate DNA unzipping, which occurs at about 15 pN and the unzipping rate is sequence dependent [1]. At room temperature $T = 300$ K, the adenine-thymine (A-T) base pair is bound by two hydrogen bonds whose energy is $4k_B T = 1.66 \times 10^{-20}$ J, and the guanine-cytosine (G-C) base pair is bound by three hydrogen bonds whose energy is $6k_B T = 2.49 \times 10^{-20}$ J [2]. Hence, the force required to displace over the distance 2 nm, which is the helix diameter, is about 8 pN for A-T base pair and 12 pN for G-C base pair in good agreement with the 15 pN critical force observed in experiments.

The breaking of the hydrogen bonds due to the force relieves the torsional stress stored in a double helix. As a result, the nucleotide strands rotate more freely about the axis of a helix and start unwinding. The DNA unwinding occurs simultaneously with the DNA unzipping. Without the hydrogen-bond binding the nucleotide strands are separated by the large distance relative to the 2-nm helix diameter, so they are completely independent of each other. This separated, independent structure with all base pairs unzipped is called ssDNA. The DNA unzipping and the DNA unwinding result in a structural transformation from dsDNA to ssDNA. Given the number of base pairs per turn of 10.5, the number of hydrogen bonds ranges from 21 bonds, for these 10.5 base pairs all being A-T, to 31.5 bonds for these 10.5 base pairs all being G-C. Roughly speaking, two tightly intertwined nucleotide strands would unwind one turn for every 21–31.5 hydrogen bonds being broken. In Fig. 1, as more base pairs are unzipped, the DNA unwinding gradually proceeds from one end of the nucleotide strands to the other end, decreasing the linking number Lk . Until the force exceeding the critical value F_c , the nucleotide strands no longer wind about each other, i.e., $Lk = 0$. The dsDNA-to-ssDNA transition can be alternately viewed as the $Lk \neq 0$ state to $Lk = 0$ state transition.

2 DNA elasticity

The intrinsic DNA rigidity arises from the base stacking and the phosphate–phosphate charge repulsion [3]. The dominant deformations of dsDNA are stretching, bending, and twisting. The dsDNA has the bending persistence length, $\xi = 50$ nm, and the twist persistence length, $\xi_t = 75$ nm [4]. The fact that the bending persistence length is shorter than the twist persistence length suggests that the nucleotide strands resist more strongly to twist than to bending. Twisting is therefore less energetically favorable, so neglecting it would not alter qualitatively the main features of the dsDNA-to-ssDNA transition. However, the consideration of twisting is essential to the plectoneme formation resulted from the release of the excess of the twist energy [5].

The 50 nm bending persistence length is much longer than the 0.34 nm separation of the adjacent base pairs, justifying the continuum description of DNA. In such a continuum model, the DNA elasticity is quantitatively characterized by the stretch modulus A and by the bending modulus B , which are 1100 pN and 230 pN.nm², respectively [6]. The bending modulus is related to the bending persistence length via $B = \xi k_B T$ [7]. As shown in Fig. 2a, two nucleotide strands of the DNA with arbitrary conformations are represented by two curves $\mathbf{r}_1(s)$ and $\mathbf{r}_2(s)$, whose length L , is parameterized by arc length s . The hydrogen bonding responsible for the base pairing is phenomenologically described by an interstrand potential $U(\mathbf{r}_2 - \mathbf{r}_1)$ whose strength depends on the specific sequence of base pairs. The constant force $\mathbf{F}$ is applied to one end of each nucleotide strand equally in magnitude but

Fig. 1 The force-induced DNA unzipping causes the dsDNA-to-ssDNA transition. In dsDNA, two nucleotide strands wind about each other a number of turns, $Lk \neq 0$, while in ssDNA they are completely unwound, $Lk = 0$, and are separated by the large distance relative to the helix diameter. Linking number Lk could play a role of the order parameter in analogy to the magnetization being an order parameter of the ferromagnetic-to-paramagnetic transition

opposite in direction, mimicking the displacement of the glass slide that tears two nucleotide strands apart [1]. The Hamiltonian of the system thus consists of the stretching energy, bending energy, interstrand potential, and the work done by the force

$$\begin{aligned}
 H = & \frac{A}{2} \int_0^L ds \left[\left(\frac{d\mathbf{r}_1}{ds} \right)^2 + \left(\frac{d\mathbf{r}_2}{ds} \right)^2 \right] + \frac{B}{2} \int_0^L ds \left[\left(\frac{d^2\mathbf{r}_1}{ds^2} \right)^2 + \left(\frac{d^2\mathbf{r}_2}{ds^2} \right)^2 \right] \\
 & + \int_0^L ds U(\mathbf{r}_2(s) - \mathbf{r}_1(s)) + \mathbf{F} \cdot \mathbf{r}_1(0) - \mathbf{F} \cdot \mathbf{r}_2(0).
 \end{aligned} \quad (1)$$

This Hamiltonian without the first and third terms is used to study the DNA stretching and gives the end-to-end distance approaching the length L in the $F^{-1/2}$ fashion [8]. The discrete version of (1) with the diagonal interaction of the base pairs on different nucleotide strands is the Hamiltonian for studying the helix-ladder transition [9]. The stacking interaction originating from the cooperativity of three consecutive base pairs can be

Fig. 2 Schematic of the coarse-grained model of DNA. **a** Two nucleotide strands winding arbitrarily are represented by two fluctuating curves $\mathbf{r}_1(s)$ and $\mathbf{r}_2(s)$ interacting via the interstrand potential $U(\mathbf{r}_2 - \mathbf{r}_1)$. DNA unzipping is initiated by the constant force $\mathbf{F}$ pulling them apart at one end of each nucleotide strand. **b** In the absence of the force, the ground state configuration of DNA is a double helix with a diameter of $2R = 2$ nm and pitch of $P = 3.4$ nm

introduced to the Hamiltonian, if desired, by assigning the interstrand separation dependence to the bending modulus, namely $B(|\mathbf{r}_2 - \mathbf{r}_1|)$ [10]. However, in our simple model we treat both stretch modulus A and bending modulus B as constants.

In the remainder of this section, the explicit form of the interstrand potential U will be determined on a basis that the ground state configuration in the absence of the force, i.e., $\mathbf{F} = 0$, is the well-known double helix with radius $R = 1$ nm and pitch $P = 3.4$ nm [11]. One nucleotide strand displaces by the axial distance $3P/8$ relative to the other, creating a minor groove, as depicted in Fig. 2b. To decouple two curves $\mathbf{r}_1$ and $\mathbf{r}_2$, change the coordinates to the “center-of-mass” coordinates $\mathbf{r}_{cm} \equiv (\mathbf{r}_2 + \mathbf{r}_1)/2$ and to the relative coordinates $\mathbf{r} \equiv \mathbf{r}_2 - \mathbf{r}_1$ results in

$$\begin{aligned}
 H = & A \int_0^L ds \left(\frac{d\mathbf{r}_{cm}}{ds} \right)^2 + B \int_0^L ds \left(\frac{d^2\mathbf{r}_{cm}}{ds^2} \right)^2 + \frac{A}{4} \int_0^L ds \left(\frac{d\mathbf{r}}{ds} \right)^2 \\
 & + \frac{B}{4} \int_0^L ds \left(\frac{d^2\mathbf{r}}{ds^2} \right)^2 + \int_0^L ds U(\mathbf{r}(s)) - \mathbf{F} \cdot \mathbf{r}(0).
 \end{aligned} \quad (2)$$

The force $\mathbf{F}$ applied at one end of each nucleotide strand, where the relative coordinates are $\mathbf{r}(0)$, gives rise to the term $\mathbf{F} \cdot \mathbf{r}(0)$ [12]. The interstrand potential $U(\mathbf{r})$ affects only the relative coordinates $\mathbf{r}$ as expected intuitively. The stretch modulus and bending modulus associating with the relative coordinates $\mathbf{r}$ are fourfold smaller than those associating with the “center-of-mass” coordinates $\mathbf{r}_{cm}$. This means that the relative coordinates $\mathbf{r}$ are more sensitive to stretching and to bending than the “center-of-mass” coordinates $\mathbf{r}_{cm}$. Set the force $\mathbf{F} = 0$ the ground state configuration is obtained by $\delta H / \delta r_{cm\ i}(s) = 0$ and $\delta H / \delta r_i(s) = 0$ yielding, respectively

$$\begin{aligned} B \frac{d^4 r_{cm\ i}}{ds^4} - A \frac{d^2 r_{cm\ i}}{ds^2} &= 0 \\ \frac{B}{2} \frac{d^4 r_i}{ds^4} - \frac{A}{2} \frac{d^2 r_i}{ds^2} &= -\frac{\partial U}{\partial r_i}. \end{aligned} \quad (3)$$

Substituting the relative coordinates $\mathbf{r}(s)$ of the double helix, which is the ground state configuration, in the second line of (3) gives the interstrand potential

$$U(\mathbf{r}) = \frac{1}{4} k_0^2 (A + B k_0^2) r^2 + U_0 \quad (4)$$

where defining the helix wavevector $k_0 \equiv 2\pi / \sqrt{(2\pi R)^2 + P^2} \approx 0.88 \text{ nm}^{-1}$. The positive constant U_0 is added to account for the repulsive potential due to the excluded volume effect that prevents two nucleotide strands from being at the same position. The more realistic interstrand potential of the hydrogen bonding is the Morse potential $U(\mathbf{r}) = D \exp(-a(r - 2R)) [\exp(-a(r - 2R)) - 2]$ whose minimum $-D$ at separation $r = 2R$ has the width a^{-1} [10]. The harmonic interstrand potential, (4), describes approximately the Morse potential in the vicinity of $r = 2R$. Expanding the Morse potential as a Taylor series around $r = 2R$ up to second order, its curvature Da^2 is equivalent to $k_0^2(A + B k_0^2)$ in our harmonic interstrand potential.

Let the axis of a helix be the z-axis. The relative coordinates $\mathbf{r}(s)$, whose length measures the interstrand separation transverse to the axis of a helix, thus have only the x and y components. The “center-of-mass” coordinates $\mathbf{r}_{cm}$ describes the rigid translation of the double helix as a whole. DNA unzipping results in the separation of two nucleotide strands, thus concerning only the relative-coordinate part of Hamiltonian. With the interstrand potential (4) and ignoring the “center-of-mass” part, the Hamiltonian takes the form

$$\begin{aligned} H &= \frac{1}{4} \int_0^L ds \left[A \left(\left(\frac{dx}{ds} \right)^2 + k_0^2 x^2(s) \right) + B \left(\left(\frac{d^2 x}{ds^2} \right)^2 + k_0^4 x^2(s) \right) \right] \\ &+ \frac{1}{4} \int_0^L ds \left[A \left(\left(\frac{dy}{ds} \right)^2 + k_0^2 y^2(s) \right) + B \left(\left(\frac{d^2 y}{ds^2} \right)^2 + k_0^4 y^2(s) \right) \right] \\ &- \mathbf{F} \cdot \mathbf{r}(0) \end{aligned} \quad (5)$$

or is written in momentum space as

$$\begin{aligned} H &= \frac{1}{4} \int \frac{dq}{2\pi} \left[A (q^2 + k_0^2) + B (q^4 + k_0^4) \right] x(q)x(-q) \\ &+ \frac{1}{4} \int \frac{dq}{2\pi} \left[A (q^2 + k_0^2) + B (q^4 + k_0^4) \right] y(q)y(-q) \\ &- \int \frac{dq}{2\pi} (F_x x(q) + F_y y(q)). \end{aligned} \quad (6)$$

The stretching part of the Hamiltonian depends quadratically on the wavevector, whereas the bending part of the Hamiltonian depends quartically on the wavevector. Bending the nucleotide strands thus causes a more rapidly spatial variation than does stretching them.

3 Enhancement of interstrand separation by softening the nucleotide strands

Basically, the DNA elasticity would dictate the interstrand separation. The stiff nucleotide strands are resistant to DNA unzipping. There are a large number of configurations that correspond to the same interstrand separation. Each configuration is sampled according to the Boltzmann distribution. The root-mean-square separation, $r_{rms}(s) \equiv \sqrt{\langle x^2(s) \rangle + \langle y^2(s) \rangle}$, is statistically a measure of the interstrand separation. The ensemble averages of the square of the x and y components are calculated by [13]

$$\langle x^2(s) \rangle = \frac{(k_B T)^2}{Z} \frac{\delta^2 Z}{\delta F_x(s) \delta F_x(s)}, \quad \langle y^2(s) \rangle = \frac{(k_B T)^2}{Z} \frac{\delta^2 Z}{\delta F_y(s) \delta F_y(s)} \quad (7)$$

where the partition function is an integral over all the possible configurations [14]

$$\begin{aligned} Z &= \int Dx(s) Dy(s) \exp \left(-\frac{H[x(s), y(s)]}{k_B T} \right) \\ &= C \exp \left(\frac{1}{k_B T} \int \frac{dq}{2\pi} \frac{F_x^2 + F_y^2}{A(q^2 + k_0^2) + B(q^4 + k_0^4)} \right) \end{aligned} \quad (8)$$

with defining the constant

$$C \equiv \exp \left(- \int \frac{dq}{2\pi} \ln \frac{A(q^2 + k_0^2) + B(q^4 + k_0^4)}{4\pi k_B T} \right). \quad (9)$$

The force pulling two nucleotide strands at one end $s = 0$ is described by the force field $F_x(s) = F_x \delta(s)$, $F_y(s) = F_y \delta(s)$. Using (7) and (8) the root-mean-square separation is [14]

$$r_{rms}(s) = \frac{1}{\sqrt{2}} \frac{F}{B k_0 k_1} \exp \left(-\frac{1}{\sqrt{2}} k_+ s \right) \left[\frac{1}{k_-} \sinh \left(\frac{1}{\sqrt{2}} k_- s \right) + \frac{1}{k_+} \cosh \left(\frac{1}{\sqrt{2}} k_- s \right) \right] \quad (10)$$

where defining the wavevectors

$$k_1 \equiv \sqrt{k_0^2 + \frac{A}{B}}, \quad k_+ \equiv \sqrt{\frac{A}{2B} + k_0 \sqrt{k_0^2 + \frac{A}{B}}}, \quad k_- \equiv \sqrt{\frac{A}{2B} - k_0 \sqrt{k_0^2 + \frac{A}{B}}}. \quad (11)$$

With stretch modulus $A = 1100$ pN, bending modulus $B = 230$ pN.nm², and helix wavevector $k_0 = 0.88$ nm⁻¹, the above wavevectors take the values $k_1 = 2.36$ nm⁻¹, $k_+ = 2.11$ nm⁻¹, $k_- = 0.56$ nm⁻¹. Note that the quantity $B k_0 k_1$ whose dimension is force gives the value 477 pN. As shown in Fig. 3, the root-mean-square separation $r_{rms}(s)$ is largest at arc length $s = 0$, where the constant force $\mathbf{F}$ is applied, and is smaller when moving toward arc length $s = L$. The decrease in bending modulus B enlarges the root-mean-square separation $r_{rms}(s)$, promoting DNA unzipping. The other consequence of the smaller bending modulus B is that the local orientation of the nucleotide strands changes rapidly from one segment to the other, namely the shorter bending persistence length ξ . Taking for simplicity the largest root-mean-square separation $r_{rms}(0)$ at arc length $s = 0$ as

Fig. 3 The “softer” nucleotide strands with the smaller value of the bending modulus B are further separated. Using the stretch modulus $A = 1100$ pN, helix wavevector $k_0 = 0.88 \text{ nm}^{-1}$, and force $F = 10$ pN, the graph shows a profile of the root-mean-square separation $r_{rms}(s)$ over the one-turn arc length $L = 7.14$ nm for three different values of the bending modulus B

a representative measure of the interstrand separation, Fig. 4 shows a decrease in the bending persistence length ξ with increasing $r_{rms}(0)$ in qualitative agreement with the step-like decrease of the bending persistence length from 50 nm of dsDNA to 0.75 nm of ssDNA shown in the inset. Regardless of the origins of the bending modulus reduction, either force induced DNA unzipping or thermally induced DNA denaturation, the structural instability of dsDNA leads to the shortening of the bending persistence length. Keeping in mind that our results are realized on the harmonic interstrand potential, (4), which is a good description for small deformation prior to DNA unzipping, the magnitude of the root-mean-square separation $r_{rms}(s)$ is likely the one that the nucleotide strands of dsDNA start to displace from the double-helix equilibrium configuration.

4 Renormalization of bending modulus

In the preceding section, the root-mean-square separation $r_{rms}(s)$, which represents the interstrand separation, grows with a decrease in the bending modulus B . Moreover, it is generally accepted that two nucleotide strands in ssDNA are largely separated because of all the base pairs unzipped. Combining these two relevant facts seems to suggest that DNA unzipping accompanies the bending modulus B renormalized to the smaller value. This plausible conjecture is supported by the experimental results that the ssDNA has the bending persistence length $\xi_{ssDNA} = 0.75$ nm [15] which yields, via $B = \xi k_B T$, an estimate of the ssDNA bending modulus $B_{ssDNA} = 3 \text{ pN.nm}^2$ at room temperature. Upon DNA unzipping, the 230 pN.nm^2 bending modulus of dsDNA must be renormalized to the 3 pN.nm^2 bending modulus of ssDNA. In what follows, this renormalization of the bending modulus B emerges naturally from its flow under the recursion relations. Having approached the critical force F_c of the dsDNA-to-ssDNA transition, the bending modulus B would scale,

Fig. 4 The direct consequence of the larger root-mean-square separation $r_{rms}(s)$ with smaller bending modulus B , shown in Fig. 3, is that the bending persistence length, $\xi = B/k_B T$, is shortened as the two nucleotide strands are pulled apart. Using the stretch modulus $A = 1100$ pN, helix wavevector $k_0 = 0.88 \text{ nm}^{-1}$, force $F = 10$ pN, and temperature $T = 300$ K, this graph resembles a shaded region of the inset [10] illustrating the local variation of the bending persistence length ξ depending on interstrand separation

to some extent, with the force F . The exponent of such scaling, as well as the critical force F_c , can be determined by the renormalization group. The critical force F_c appears as a fixed point of the recursion relations and the exponent is obtained by linearizing the recursion relations about the fixed point.

The nucleotide strands are regarded as the continuous curves not defined discretely on the lattice sites. The renormalization group in momentum space is preferable to that in real space. Hence, the momentum shell renormalization group is used to derive the recursion relations that govern the flow of the parameters of the Hamiltonian (6), such as stretch modulus A , bending modulus B , helix wavevector k_0 , and the force components F_x, F_y . The relative coordinates $\mathbf{r}(q)$, whose magnitude measures the interstrand separation, play a role of the field. Split the relative coordinates $\mathbf{r}(q)$ into two parts, the low momentum field $\mathbf{r}^<(q)$ and the high momentum field $\mathbf{r}^>(q)$ [13] gives

$$\mathbf{r}(q) = \mathbf{r}^<(q) + \mathbf{r}^>(q). \quad (12)$$

The wavevector is in the range $0 < q < \Lambda/b$ for the low momentum field $\mathbf{r}^<(q)$, and is in the range $\Lambda/b < q < \Lambda$ for the high momentum field $\mathbf{r}^>(q)$, where Λ denotes the momentum cutoff. The decomposition of the relative coordinates $\mathbf{r}(q)$ splits accordingly the Hamiltonian into two parts

$$H[\mathbf{r}(q)] = H^< + H^>. \quad (13)$$

The first part of Hamiltonian involving only the low momentum field $\mathbf{r}^<(q)$ is

$$\begin{aligned} H^< = & \frac{1}{4} \int_0^{\frac{\Lambda}{b}} \frac{dq}{2\pi} \left[A \left(q^2 + k_0^2 \right) + B \left(q^4 + k_0^4 \right) \right] x^<(q) x^<(-q) \\ & + \frac{1}{4} \int_0^{\frac{\Lambda}{b}} \frac{dq}{2\pi} \left[A \left(q^2 + k_0^2 \right) + B \left(q^4 + k_0^4 \right) \right] y^<(q) y^<(-q) \\ & - \int_0^{\frac{\Lambda}{b}} \frac{dq}{2\pi} \left(F_x x^<(q) + F_y y^<(q) \right). \end{aligned} \quad (14)$$

The second part of Hamiltonian involving both the low momentum field $\mathbf{r}^<(q)$ and the high momentum field $\mathbf{r}^>(q)$ is

$$\begin{aligned} H^> = & \frac{1}{4} \int_{\frac{\Lambda}{b}}^{\Lambda} \frac{dq}{2\pi} \left[A \left(q^2 + k_0^2 \right) + B \left(q^4 + k_0^4 \right) \right] \\ & \times \left[x^>(q) x^>(-q) + x^<(-q) x^>(q) + x^<(q) x^>(-q) \right] \\ & + \frac{1}{4} \int_{\frac{\Lambda}{b}}^{\Lambda} \frac{dq}{2\pi} \left[A \left(q^2 + k_0^2 \right) + B \left(q^4 + k_0^4 \right) \right] \\ & \times \left[y^>(q) y^>(-q) + y^<(-q) y^>(q) + y^<(q) y^>(-q) \right] \\ & - \int_{\frac{\Lambda}{b}}^{\Lambda} \frac{dq}{2\pi} \left(F_x x^>(q) + F_y y^>(q) \right). \end{aligned} \quad (15)$$

To thinning the degrees of freedom with the wavevector in the shell $\Lambda/b < q < \Lambda$, we integrate out the high-momentum field $\mathbf{r}^>(q)$, resulting in the new Hamiltonian $H_{\Lambda/b}[\mathbf{r}^<(q)]$, via

$$\exp \left(- \frac{H_{\Lambda/b}[\mathbf{r}^<(q)]}{k_B T} \right) = \exp \left(- \frac{H^<[\mathbf{r}^<(q)]}{k_B T} \right) \int D\mathbf{r}^>(q) \exp \left(- \frac{H^>[\mathbf{r}^<(q), \mathbf{r}^>(q)]}{k_B T} \right). \quad (16)$$

Note that the new Hamiltonian $H_{\Lambda/b}[\mathbf{r}^<(q)]$ contains only the low momentum field $\mathbf{r}^<(q)$, and thus has the reduced momentum cut off Λ/b . To restore the momentum cutoff to Λ as that of the original Hamiltonian $H[\mathbf{r}(q)]$, we rescale the wavevector by $q = q'/b$ and the field by $\mathbf{r}^<(q) = \zeta \mathbf{r}'(q')$. The wavevector and field rescaling generates the other new Hamiltonian $H'_{\Lambda}[\mathbf{r}'(q')]$ of which the parameters are stretch modulus A' , bending modulus B' , helix wavevector k'_0 , and the force components F'_x, F'_y . The momentum cut-off of this new Hamiltonian $H'_{\Lambda}[\mathbf{r}'(q')]$ now becomes the same Λ as that of the original Hamiltonian $H[\mathbf{r}(q)]$. Due to the invariance under the scale transformation, both original Hamiltonian $H[\mathbf{r}(q)]$ and new Hamiltonian $H'_{\Lambda}[\mathbf{r}'(q')]$ share the identical form except the parameters of the latter being renormalized. The comparison between original Hamiltonian $H[\mathbf{r}(q)]$ and new Hamiltonian $H'_{\Lambda}[\mathbf{r}'(q')]$ gives the recursion relations for the parameters of Hamiltonian, with the detailed calculation presented in an [Appendix](#),

$$A' = A, \quad B' = \frac{1}{b^2} B, \quad k'_0 = b k_0, \quad F'_x = \frac{1}{\sqrt{2}} b^{3/2} F_x, \quad F'_y = \frac{1}{\sqrt{2}} b^{3/2} F_y. \quad (17)$$

The successive iterations of the recursion relations drive the system toward the fixed point where the dsDNA-to-ssDNA transition occurs. Upon iterating the recursion relations, the stretch modulus A remains the same, the bending modulus B diminishes, the helix wavevector k_0 grows, and the force components F_x, F_y grow. Stretch modulus A controls the displacement of the nucleotide strands in the direction parallel to the axis of the helix. While

DNA unzipping mainly gives rise to the displacement of the nucleotide strands in the directions perpendicular to the axis of the helix. The result that the stretch modulus A does not change under the recursion relations is thus physically reasonable. The recursion relations of the defined wavevectors k_1 , k_+ , and k_- , (11), can be obtained from (17)

$$\begin{aligned} k'_1 &\equiv \sqrt{(k'_0)^2 + \frac{A'}{B'}}, \quad k'_+ \equiv \sqrt{\frac{A'}{2B'} + k'_0 \sqrt{(k'_0)^2 + \frac{A'}{B'}}}, \quad k'_- \equiv \sqrt{\frac{A'}{2B'} - k'_0 \sqrt{(k'_0)^2 + \frac{A'}{B'}}} \\ &= bk_1, \quad \quad \quad = bk_+, \quad \quad \quad = bk_-. \end{aligned} \quad (18)$$

To see how the DNA unzipping takes place in this context, let the root-mean-square separation $r_{rms}(0)$, where the pulling force $\mathbf{F}$ applied, as a representative interstrand separation. Given the fact that $r_{rms}(0) = F/\sqrt{2}Bk_0k_1k_+$ from (10), using the recursion relations (17) and (18) gives the recursion relation of the root-mean-square separation $r'_{rms}(0) = (1/\sqrt{2})b^{1/2}r_{rms}(0)$. Upon iterating the recursion relations, the root-mean-square separation $r_{rms}(0)$ grows infinitely, indicating that the interstrand separation becomes extremely large as dsDNA transits to ssDNA.

The inverses of these three wavevectors k_1 , k_+ , and k_- have the dimensions of length leading to define

$$\xi_1 \equiv \frac{1}{\sqrt{k_0^2 + \frac{A}{B}}}, \quad \xi_+ \equiv \frac{1}{\sqrt{\frac{A}{2B} + k_0 \sqrt{k_0^2 + \frac{A}{B}}}}, \quad \xi_- \equiv \frac{1}{\sqrt{\frac{A}{2B} - k_0 \sqrt{k_0^2 + \frac{A}{B}}}} \quad (19)$$

which are to some extent the typical length scales over which the root-mean-square separation $r_{rms}(s)$ changes appreciably. Their recursion relations are simply the reciprocal of those of three wavevectors

$$\xi'_1 = \frac{1}{b}\xi_1, \quad \xi'_+ = \frac{1}{b}\xi_+, \quad \xi'_- = \frac{1}{b}\xi_-. \quad (20)$$

Upon iterating the recursion relations, ξ_1 , ξ_+ , and ξ_- all diminish to zero with the same rate, reflecting an experimental finding that the only length scale strongly influenced by the dsDNA-to-ssDNA transition is the bending persistence length.

In Fig. 5, by increasing the force $F = \sqrt{F_x^2 + F_y^2}$, the bending modulus of dsDNA, $B_{dsDNA} = 230 \text{ pN.nm}^2$ decreases appreciably to zero over the force scale 5 pN. Experimentally, the bending persistence length is found to be $\xi_{ssDNA} = 0.75 \text{ nm}$ for ssDNA [15] from which the bending modulus of ssDNA, $B_{ssDNA} = 3 \text{ pN.nm}^2$, at room temperature is deduced by the relation $B = \xi k_B T$. This small value $B_{ssDNA} = 3 \text{ pN.nm}^2$ is reminiscent of the $B = 0$ value at the fixed point ($F = \infty$, $B = 0$) of the recursion relations. Although our recursion relations successfully capture what happens in DNA unzipping, they do not give the quantitatively satisfactory critical force $F_c = 15 \text{ pN}$ [1]. The overestimate of the critical force F_c would stem from the interstrand potential $U(\mathbf{r})$, (4), which is so long ranged that two nucleotide strands still feel attraction even at the large interstrand separation, thereby requiring the unusually large force to separate them. Expectedly, the finite critical force F_c could be obtained if using the more realistic interstrand potential, such as the short-ranged Morse potential describing faithfully the hydrogen bonding [16]. The renormalization of the bending modulus B will definitely remain valid for the actual interstrand potential except from being renormalized to the very small value instead of zero.

The different behaviors of the stretch modulus A and of the bending modulus B under the recursion relations render evidence that in some respects DNA does not respond to the force like the classical Kirchhoff elastic rod does. If DNA was a Kirchhoff elastic rod for which the bending modulus B is linearly proportional to the stretch modulus A , by $B = R^2 A/4$

Fig. 5 The flow of the force $F = \sqrt{F_x^2 + F_y^2}$ and the bending modulus B under the recursion relations, (17), is toward the fixed point ($F = \infty$, $B = 0$). As dsDNA transits structurally, via DNA unzipping, to ssDNA, the bending modulus $B = 230 \text{ pN.nm}^2$ of dsDNA is renormalized to zero, suggesting that ssDNA does not resist bending. This is analogous to the behavior of a fluid with zero shear modulus that does not resist shear

[17] with the helix radius $R = 1 \text{ nm}$, both A and B would have behaved exactly in the same way under the recursion relations.

5 Discussion and conclusions

The force-induced interstrand separation in DNA unzipping results in the dsDNA-to-ssDNA transition interpreted as a transition from the $Lk \neq 0$ state to the $Lk = 0$ state. Being inferred from the bending persistence length of dsDNA, $\xi_{dsDNA} = 50 \text{ nm}$ [18], and of ssDNA, $\xi_{ssDNA} = 0.75 \text{ nm}$ [15], their bending moduli are correspondingly $B_{dsDNA} = 230 \text{ pN.nm}^2$ and $B_{ssDNA} = 3 \text{ pN.nm}^2$. The smaller bending modulus of ssDNA suggests a notion that the dsDNA-to-ssDNA transition is a manifestation of the renormalization of the bending modulus B as being evident from the flow of the bending modulus toward zero under the recursion relation depicted in Fig. 5. Under physiological conditions, DNA is in a salt solution, such as NaCl, whose Na^+ ions mediate the counterintuitive attraction between two like negatively charged nucleotide strands and at the same time screen the interstrand potential to be short ranged [19]. For monovalent ions, the interstrand potential is well described by a Debye-Hückel potential. Remarkably, the bending persistence length ξ , proportional to the bending modulus B , is also renormalized smaller with increasing the ionic concentration [20].

The mechanistic response of DNA to the force has attracted much interest because this intracellular phenomenon can be studied *in vitro* by an optical tweezer, providing a framework for understanding how DNA deforms when bound specifically to the proteins. For medical purposes DNA could be potentially used as the sensitive viral detection. The underlying principle relies on the effect that viruses induce mechanical stress on a bundle of

ssDNA strands, when embedded in a hydrogel, leading to the measurable contraction of hydrogel [21]. The study of DNA will certainly continue for many years to come with a large variety of applications.

Acknowledgments The author is indebted to N. Chaichit for his insightful discussions and to Thammasat University for the TU new research scholar, contract number 2557. He also gratefully acknowledges the anonymous reviewers for their constructive comments and invaluable suggestions.

Appendix: Derivation of recursion relations by momentum shell renormalization group

We present the detail of calculation leading to the recursion relations, (17), governing how the stretch modulus A , bending modulus B , helix wavevector k_0 , and the force components F_x , F_y change as approaching to the dsDNA-to-ssDNA transition. The elastic properties, like stretch modulus A and bending modulus B , are insensitive to the short distance structure, i.e., large wavevector q . The dsDNA-to-ssDNA transition can be equally described by the Hamiltonian, which involves only the small wavevector q but with the parameters in the Hamiltonian being renormalized. The large wavevector corresponds to the high momentum. Integrating out the high momentum part of the field $\mathbf{r}^>(q)$ appearing in the Hamiltonian $H^>$, (15), leads to the new Hamiltonian $H_{\Lambda/b}[\mathbf{r}^<(q)]$, involving only the low momentum part of the field $\mathbf{r}^<(q)$ with small wavevector $0 < q < \Lambda/b$

$$\exp\left(-\frac{H_{\Lambda/b}[\mathbf{r}^<(q)]}{k_B T}\right) = \exp\left(-\frac{H^<[\mathbf{r}^<(q)]}{k_B T}\right) \int D\mathbf{r}^>(q) \exp\left(-\frac{H^>[\mathbf{r}^<(q), \mathbf{r}^>(q)]}{k_B T}\right). \quad (21)$$

The new Hamiltonian therefore takes the form

$$\begin{aligned} H_{\Lambda/b}[\mathbf{r}^<(q)] = & \frac{1}{8} \int_0^{\Lambda/b} \frac{dq}{2\pi} \left[A (q^2 + k_0^2) + B (q^4 + k_0^4) \right] x^<(q) x^<(-q) \\ & + \frac{1}{8} \int_0^{\Lambda/b} \frac{dq}{2\pi} \left[A (q^2 + k_0^2) + B (q^4 + k_0^4) \right] y^<(q) y^<(-q) \\ & - \frac{1}{2} \int_0^{\Lambda/b} \frac{dq}{2\pi} (F_x x^<(q) + F_y y^<(q)) + D \end{aligned} \quad (22)$$

where the constant is

$$D = - \int_0^{\Lambda/b} \frac{dq}{2\pi} \frac{F_x^2 + F_y^2}{A (q^2 + k_0^2) + B (q^4 + k_0^4)} + k_B T \int_0^{\Lambda/b} \frac{dq}{2\pi} \ln \frac{A (q^2 + k_0^2) + B (q^4 + k_0^4)}{4\pi k_B T}. \quad (23)$$

Note that the second term in D is $-k_B T \ln C$, recalling the constant C from (9). To restore the momentum cutoff Λ/b back to Λ , the momentum is rescaled by $q = q'/b$ and the field is rescaled by $\mathbf{r}^<(q) = \zeta \mathbf{r}'(q')$, corresponding to, in real space, the arc length rescaled by $s = bs'$ and the field rescaled by $\mathbf{r}^<(s) = (1/\zeta) \mathbf{r}'(s')$. This momentum and field rescaling

results in a new Hamiltonian $H'_\Lambda[\mathbf{r}'(q')]$, but now with the same momentum cutoff Λ as does the original Hamiltonian H ,

$$\begin{aligned} H'_\Lambda[\mathbf{r}'(q')] = & \frac{\zeta^2}{8b^3} \int_0^\Lambda \frac{dq'}{2\pi} \left[A \left(q'^2 + b^2 k_0^2 \right) + \frac{B}{b^2} \left(q'^4 + b^4 k_0^4 \right) \right] x'(q') x'(-q') \\ & + \frac{\zeta^2}{8b^3} \int_0^\Lambda \frac{dq'}{2\pi} \left[A \left(q'^2 + b^2 k_0^2 \right) + \frac{B}{b^2} \left(q'^4 + b^4 k_0^4 \right) \right] y'(q') y'(-q') \\ & - \frac{\zeta}{2b} \int_0^\Lambda \frac{dq'}{2\pi} \left[F'_x x'(q') + F'_y y'(q') \right]. \end{aligned} \quad (24)$$

This new Hamiltonian $H'_\Lambda[\mathbf{r}'(q')]$, (24), has the identical form of the original Hamiltonian $H[\mathbf{r}(q)]$, (6), suggesting that the stretch modulus A , bending modulus B , helix wavevector k_0 , and the force components F_x , F_y must be renormalized according to

$$A' = \frac{\zeta^2}{2b^3} A, \quad B' = \frac{\zeta^2}{2b^5} B, \quad k'_0 = b k_0, \quad F'_x = \frac{\zeta}{2} F_x, \quad F'_y = \frac{\zeta}{2} F_y. \quad (25)$$

The rescaling parameter ζ for the field is chosen to satisfy the scaling law of correlation. The inverse of the correlation $G_{ii}^{-1}(s, s')$ is the second functional derivative evaluated at the mean-field solution $\langle r_i(s) \rangle$ [13]

$$G_{ii}^{-1}(s, s') = \frac{1}{k_B T} \left. \frac{\delta^2 H}{\delta r_i(s) \delta r_i(s')} \right|_{r_i(s) = \langle r_i(s) \rangle}. \quad (26)$$

Using the relative-coordinate part of Hamiltonian (5) gives

$$\frac{\delta^2 H}{\delta r_i(s) \delta r_i(s')} = -\frac{A}{2} \frac{d^2}{ds^2} \delta(s - s') + \frac{B}{2} \frac{d^4}{ds^4} \delta(s - s') + \frac{k_0^2}{2} (A + B k_0^2) \delta(s - s'). \quad (27)$$

With the Fourier transform of the delta function, $\delta(s - s') = \int (dq/2\pi) \exp(iq(s - s'))$, substitute (27) in (26) gives the inverse of the correlation

$$G_{ii}^{-1}(s, s') = \int \frac{dq}{2\pi} \frac{1}{k_B T} \left(\frac{A}{2} (q^2 + k_0^2) + \frac{B}{2} (q^4 + k_0^4) \right) \exp(iq(s - s')) \quad (28)$$

which is the Fourier transform of $G_{ii}^{-1}(s, s')$. Apart from $\exp(iq(s - s'))$, the integrand is the inverse of the correlation in momentum space $G_{ii}^{-1}(q)$, resulting in the correlation

$$G_{ii}(q) = \frac{2k_B T}{A(q^2 + k_0^2) + B(q^4 + k_0^4)}. \quad (29)$$

Rescale the momentum $q = q'/b$ changes the correlation to

$$G_{ii}(q) = \frac{2k_B T b^2}{A(q'^2 + b^2 k_0^2) + \frac{B}{b^2} (q'^4 + b^4 k_0^4)} \quad (30)$$

whose the scaling law is $G_{ii}(q) = b^2 G'_{ii}(q')$, where the correlation $G'_{ii}(q')$ has the identical form with $G_{ii}(q)$ but with the renormalized stretch modulus A' , the renormalized bending modulus B' , and the renormalized helix wavevector k'_0

$$G'_{ii}(q') = \frac{2k_B T}{A'(q'^2 + k_0'^2) + B'(q'^4 + k_0'^4)}. \quad (31)$$

To fulfill the scaling law of correlation, we choose the rescaling parameter $\zeta^2 = 2b^3$, which simplifies (25) to

$$A' = A, \quad B' = \frac{1}{b^2}B, \quad k'_0 = bk_0, \quad F'_x = \frac{1}{\sqrt{2}}b^{3/2}F_x, \quad F'_y = \frac{1}{\sqrt{2}}b^{3/2}F_y. \quad (32)$$

which are indeed the recursion relations (17) in the main text.

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