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The elastic theory of a single DNA molecule

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Abstract. We study the elastic responses of double- (ds) and single-stranded (ss) DNA at external force fields. A double-strand-polymer elastic model is constructed and solved by path integral methods and Monte Carlo simulations to understand the entropic elasticity, cooperative extensibility, and supercoiling property of dsDNA. The good agreement with experiments indicates that short-ranged base-pair stacking interaction is crucial for the stability and the high deformability of dsDNA. Hairpin-coil transition in ssDNA is studied with generating function method. A threshold force is needed to pull the ssDNA hairpin patterns, stabilized by base pairing and base-pair stacking, into random coils. This phase transition is predicted to be of first order for stacking potential higher than some critical level, in accordance with experimental observations.

Keywords. DNA; elastic theory; stacking interaction; supercoiling; hairpin-coil transition.

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1. Introduction

During the last decade, single-molecule mechanical manipulation experiments have revealed many novel mechanical properties of nucleic acids, going from elastic behaviors to complex structure transitions. Detailed elastic results about double-stranded DNA (dsDNA) have been given. At low external forces, dsDNA is a semiflexible polymer with a large stretching modulus ($\sim$1000 pN [1]) and bend persistence length ($\sim$50 nm [2,3]); but, if pulled with a force of about 70 pN, the molecule as a whole can suddenly be driven to an almost fully stretched state with a contour length 1.7 times its native value [1,4]. On the other hand, if there is a negative torsional stress, a pulling force as small as 0.3 pN can distort the native structure of DNA considerably [5,6]. Related to the latter, there has been recent progress in understanding the force–extension curves of single-stranded DNA (ssDNA) and RNA [7–12]. Many distinct transitions have been shown in experiments: the transition can be gradual [7–10] or abrupt [11,12], depending on the ssDNA or RNA sequence concerned.

In an attempt to understand the above-mentioned dsDNA entropic elasticity, cooperative extensibility and supercoiling property, we introduce and solve a simple elastic model for dsDNA in §§2 and 3 and compare the results with experiments. It appears that the short-ranged base-pair stacking interaction can account for both the stability of dsDNA double-

helix and its high deformability at large external forces. In §4 we study structure transition process of ssDNA theoretically, and show that the transition cooperativity is controlled by the base-pair stacking interaction in the DNA hairpin structure. Finally our conclusions will be presented in §5.

2. Double-stranded DNA with axial stress

We model a dsDNA polymer as composed of two inextensible strings which are linked together by many rigid rods of fixed length. The two inextensible backbones of DNA are characterized by the same bending rigidity $\kappa = k_{\mathrm{B}}Tl_{\mathrm{p}}$ ($l_{\mathrm{p}} \approx 1.5$ nm [1]). Their position vectors are $\mathbf{r}_i = \int^S \mathbf{t}_i(s')\mathrm{d}s'$, where $\mathbf{t}_i$ ($i = 1, 2$) is the unit tangent of the ith backbone and s its arc length. We regard each nucleotide base-pair as a rigid rod of length $2R$ pointing along direction $\mathbf{b}$ from $\mathbf{r}_1$ to $\mathbf{r}_2$, with $\mathbf{r}_2(s) - \mathbf{r}_1(s) = 2R\mathbf{b}(s)$; we further suppose $\mathbf{b}\cdot\mathbf{t}_1 = \mathbf{b}\cdot\mathbf{t}_2 \equiv 0$. DNA central axis is $\mathbf{r}(s) = \mathbf{r}_1(s) + R\mathbf{b}(s)$, and its tangent is denoted by $\mathbf{t}$, with $\mathbf{t}\cdot\mathbf{b} = 0$. We see that $\mathbf{t}_1 = \mathbf{t}\cos\varphi + \mathbf{n}\sin\varphi$ and $\mathbf{t}_2 = \mathbf{t}\cos\varphi - \mathbf{n}\sin\varphi$, where $\mathbf{n} = \mathbf{b}\times\mathbf{t}$ and φ, the folding angle, is half the rotational angle from $\mathbf{t}_2$ to $\mathbf{t}_1$ ($\mathbf{b}$ being the rotational axis): $-\pi/2 < \varphi < +\pi/2$ ($\varphi > 0$ for right-handed rotations and < 0 for left-handed ones). Geometrically, we have $\mathrm{d}\mathbf{b}/\mathrm{d}s = (\mathbf{t}_2 - \mathbf{t}_1)/2R = -\mathbf{n}\sin\varphi/R$ and $\mathrm{d}\mathbf{t}/\mathrm{d}s = (\mathbf{t}_1 + \mathbf{t}_2)/2 = -\mathbf{t}\cos\varphi$.

The bending energy of the backbones, $E_{\mathrm{b}} = \int(\kappa/2)[(\mathrm{d}\mathbf{t}_1/\mathrm{d}s)^2 + (\mathrm{d}\mathbf{t}_2/\mathrm{d}s)^2]\mathrm{d}s$, is shown to be

$$E_{\mathrm{b}} = \int_0^L \left[\kappa\left(\frac{\mathrm{d}\mathbf{t}}{\mathrm{d}s}\right)^2 + \kappa\left(\frac{\mathrm{d}\varphi}{\mathrm{d}s}\right)^2 + \frac{\kappa}{R^2}\sin^4\varphi\right]\mathrm{d}s, \tag{1}$$

where L is the total contour length of each backbone. The second and the third terms in eq. (1) is deformation energy caused by folding of the backbones with respect to the central axis, and the first term, $\kappa(\mathrm{d}\mathbf{t}/\mathrm{d}s)^2$, is the bending energy of DNA central axis contributed by the two backbones. So far, base-pairs are viewed as thin rods and their contribution to the bending rigidity of DNA chain is not considered. The simplest way to consider base-pair steric effect is to replace κ in the first term of eq. (1) with a phenomenological parameter $\kappa^* = k_{\mathrm{B}}Tl_{\mathrm{p}}^*$, with $l_{\mathrm{p}}^* > l_{\mathrm{p}}$. Hereafter this is assumed.

Besides steric effects, nucleotide base-pairs also contribute to stacking energy. This energy mainly originates from non-covalent van der Waals interactions between adjacent base-pairs. Stacking interaction is short ranged and is characterized by an attractive potential proportional to $1/r^6$ and a strong repulsive potential proportional to $1/r^{12}$ (r is the axial distance between adjacent base-pairs). In the continuous model, the line density of such Lennard–Jones-type potential is written as

$$\rho(\varphi) = \begin{cases} \frac{\varepsilon}{r_0}\left[\left(\frac{\cos\varphi_0}{\cos\varphi}\right)^{12} - 2\left(\frac{\cos\varphi_0}{\cos\varphi}\right)^{6}\right] & (\varphi \geq 0) \\ \text{constant} \sim 0 & (\varphi < 0) \end{cases}, \tag{2}$$

and the total stacking energy is $E_{\mathrm{LJ}} = \int_0^L \rho\mathrm{d}s$. In eq. (2), r_0 is the backbone arc length between adjacent bases, φ_0 is a parameter related to the equilibrium distance between a DNA dimer, ε is the stacking intensity which is generally sequence dependent. Here, we

focus on macroscopic properties of DNA and consider ε in the average sense and take it as a constant, $\varepsilon \approx 14.0 k_{\mathrm{B}}T$ [13]. The asymmetric stacking potential (eq. (2)) ensures a relaxed DNA to take on a right-handed double-helix folding angle $\varphi \sim \varphi_0$. However, if adjacent base-pairs are pulled apart slightly from the equilibrium distance, the stacking interaction intensity quickly decreases because of its short-range nature. In other words, the stacking potential can endure only a limited pulling force. We suggest this to be closely related to the observed DNA highly cooperative extensibility at 70 pN.

Under external force $\mathbf{F} = f\mathbf{z}_0$ along the direction $\mathbf{z}_0$, the total energy functional is then $E = E_{\mathrm{b}} + E_{\mathrm{LJ}} - \int_0^L f\cos\varphi\mathbf{t}\cdot\mathbf{z}_0\mathrm{d}s$, and the Green function $G(\mathbf{t},\varphi;\mathbf{t}',\varphi';s)$ which determines the probability distribution of $\mathbf{t}$ and φ along the DNA chain [14,15], is governed by

$$\frac{\partial G}{\partial s} = \left[\frac{\partial^2}{4l_{\mathrm{p}}^*\partial\mathbf{t}^2} + \frac{\partial^2}{4l_{\mathrm{p}}\partial\varphi^2} + \frac{f\cos\varphi}{k_{\mathrm{B}}T}\mathbf{t}\cdot\mathbf{z}_0 - \frac{\rho(\varphi)}{k_{\mathrm{B}}T} - \frac{l_{\mathrm{p}}}{R^2}\sin^4\varphi\right]G. \tag{3}$$

The spectrum of eq. (3) is discrete; for long chains, the average extension is obtained by a direct integration with its normalized ground-state eigenfunction $\Phi_0(\mathbf{t},\varphi)$

$$\langle Z\rangle = L\int\int|\Phi_0|^2\mathbf{t}\cdot\mathbf{z}_0\cos\varphi\,\mathrm{d}\mathbf{t}\,\mathrm{d}\varphi. \tag{4}$$

The resulting force vs. extension curve is shown in figure 1a, which is obtained with one adjustable parameter [14,15]. The agreement with experiments is satisfactory. According to the model, the onset of cooperative extension at forces of about 70 pN is mainly caused by the yielding of the base-pair stacking interaction (where the base-pair stacked pattern is severely distorted [14]). Below the onset of cooperative elongation, the DNA is very stiff and calculations show that at $f = 50$ pN the total extension of the DNA is only 4.1% longer than its B-form length, in close accordance with the value of 4.6% reported in ref. [1]. This is related to the fact that the base-pair stacking intensity ε is very strong. At low forces ($f < 10$ pN), the DNA elasticity is dominated by thermal fluctuations of the axial direction $\mathbf{t}$ (entropic elasticity). The now well-known worm-like chain model with contour length $L\langle\cos\varphi\rangle_{f=0}$ and persistence length $2l_{\mathrm{p}}^*\langle\cos\varphi\rangle_{f=0}$ (see figure 1b) is just an excellent approximation theory (see figure 1b).

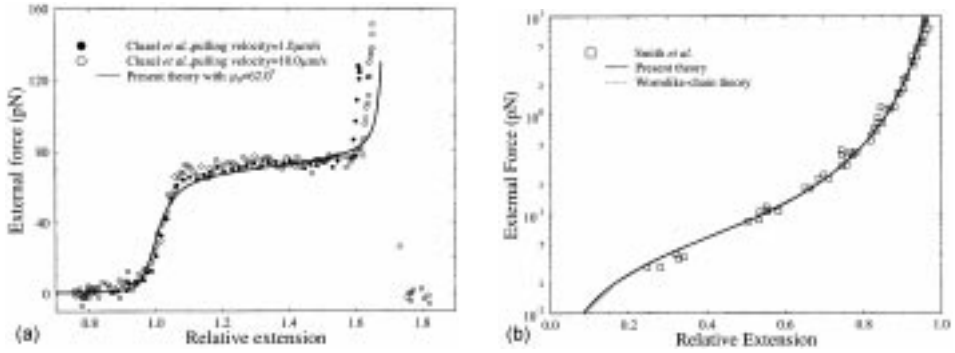

Figure 1. Force–extension relationship for dsDNA. (**a**) The whole force range, with experimental data from figure 2A of ref. [4]. (**b**) Low force range, experimental data from figure 5B of ref. [2].

3. Double-stranded DNA with torsional stress

As dsDNA is composed of two sugar–phosphate strands, torsional stress can be introduced by twisting the molecule [5]. Torsionally stressed dsDNA is termed 'supercoiled'. Mathematically, a supercoiled dsDNA is characterized by its fixed value of linking number Lk. It measures the total topological turns by which one DNA backbone winds around the other or around the central axis, and can be expressed as the sum of the twisting number, $Tw(\mathbf{r}_1, \mathbf{r})$, of backbone $\mathbf{r}_1$ around the central axis $\mathbf{r}$ and the writhing number $Wr(\mathbf{r})$ of the central axis, $Lk = Tw + Wr$. For dsDNA, $Tw(\mathbf{r}_1, \mathbf{r}) = (1/2\pi) \int \mathbf{t} \times (-\mathbf{b}) \cdot \mathrm{d}(-\mathbf{b}) = (1/2\pi) \int \sin\varphi \mathrm{d}s/R$ [14]; and Wr is expressed as a double integral [16]:

$$Wr = \frac{1}{4\pi} \int \int \mathrm{d}s\,\mathrm{d}s' \frac{\partial_s \mathbf{r}(s) \times \partial_s \mathbf{r}(s') \cdot [\mathbf{r}(s) - \mathbf{r}(s')]}{|\mathbf{r}(s) - \mathbf{r}(s')|^3}. \tag{5}$$

Torsionally relaxed dsDNA is a right-handed double-helix, and the equilibrium linking number Lk_0 is non-zero; we introduce the supercoiling degree as $\sigma = (Lk - Lk_0)/Lk_0$. The complicated expression of writhing number (eq. (5)) makes analytical calculation difficult, and so we use Monte Carlo simulation instead. The dsDNA model introduced in §2 is simulated under the constraint of fixed supercoiling degree, and the average extension of the molecule is obtained at each applied force [17]. The simulation result is demonstrated in figure 2a and compared with experimental data. Both experiment and theory showed that at low stretching, negatively and positively supercoiled dsDNAs behave symmetrically while at intermediate force ranges (about 1.0 pN) the extension of negatively supercoiled dsDNA is almost independent of supercoiling degree, indicating the existence of a structural transition. The nature of this transition is investigated in the following.

Suppose a torque Γ is acting on dsDNA, then the energy functional is $E = E_\mathrm{b} + E_\mathrm{LJ} - f \int \cos\varphi \mathbf{t} \cdot \mathbf{z}_0 \mathrm{d}s - 2\pi\Gamma Lk$. For considerably straight dsDNA, $Wr(r) = (1/4\pi) \int (t_x \mathrm{d}t_y/\mathrm{d}s - t_y \mathrm{d}t_x/\mathrm{d}s)\mathrm{d}s$ [15], where t_x and t_y are the x and y components of $\mathbf{t}$. The Green equation for the supercoiled dsDNA is [15]

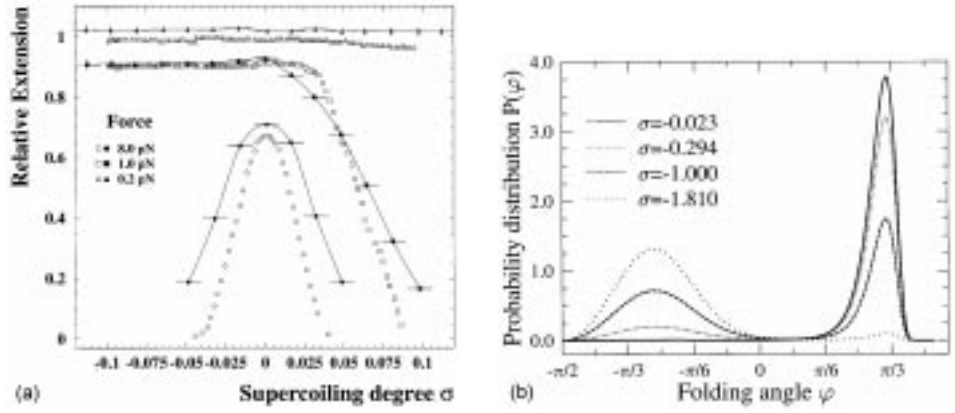

Figure 2. Supercoiling property of dsDNA. (**a**) Relative extension vs. supercoiling degree at fixed forces. Open points denote experimental data [6] and solid points, MC results [17]. (**b**) Folding angle distribution for negatively supercoiled dsDNA pulled with a force of 1.3 pN.

$$\frac{\partial G}{\partial s} = \left[\frac{\partial^2}{4l_{\mathrm{p}}^* \partial \mathbf{t}^2} + \frac{\partial^2}{4l_{\mathrm{p}} \partial \varphi^2} + \frac{f \cos\varphi}{k_{\mathrm{B}}T} \mathbf{t} \cdot \mathbf{z}_0 - \frac{\rho(\varphi)}{k_{\mathrm{B}}T} - \frac{l_{\mathrm{p}}}{R^2} \sin^4\varphi \right.$$
$$\left. + \frac{\Gamma}{Rk_{\mathrm{B}}T} \sin\varphi - \frac{\Gamma}{4k_{\mathrm{B}}T l_{\mathrm{p}}^*} \frac{\partial}{\partial \phi} + \frac{\Gamma^2}{16 l_{\mathrm{p}}^* (k_{\mathrm{B}}T)^2} \sin^2\theta \right] G. \tag{6}$$

The folding angle distribution $P(\varphi)$ is calculated by $P(\varphi) = \int \Phi_0^*(\mathbf{t}, \varphi)\Phi_0(\mathbf{t}, \varphi)\mathrm{d}\mathbf{t}$, with Φ_0 the ground-state eigenfunction of eq. (6). The numerically determined folding angle distribution for negatively supercoiled dsDNA is shown in figure 2b.

We find that as the torsional stress becomes large (with $|\sigma| \geq 0.025$), two peaks appear in the distribution, one at $\varphi = +57.0^\circ$ (B-form DNA), the other at $\varphi = -48.6^\circ$ (left-handed configuration). Between these two peaks, there exists an extended region of folding angle from 0° to 30° with an extremely small probability of occurrence. Thus, a negatively supercoiled DNA can have two possible stable configurations. A transition between these two structures will pass through the intermediate state where the two adjacent base-pairs are not stacked. At this point the base-pairs may break, because a single unstacked base-pair is not stable; and it is possible that the left-handed dsDNA is composed of two sugar–phosphate strands which are not mutually base-paired [5,18]. Another possibility is that dsDNA is in the Z-DNA configuration [19].

4. Hairpin-coil transition in stretched ssDNA

In a ssDNA, one nucleotide base can interact with another (complementary) base on the same chain to form a base-pair. In high salt conditions the possibility of forming such a base-pair is considerable and hence ssDNA will be in the compact hairpin state. Some threshold force is needed to drive the polymer into a random coil [7–12]. In the following we discuss the influence of stacking interaction on the cooperativity of this hairpin-coil transition process.

Consider a fictitious polymer chain made of N tiny beads (bases) with index i from 1 to N. Between any two adjacent bases (i and $i+1$) there is an elastic bond of equilibrium length b and length variance l ($l \ll b$). For any two bases i and j, if their mutual distance $|\mathbf{r}_{ij}|$ is less than a there could be a pairing potential $V_{\mathrm{pair}}^{i,j}(\mathbf{r}_{ij})$; we extend the work of ref. [20] to suppose that if any two base-pairs are nearest neighbours there is an additional stacking interaction $J_{i,i+1}^{j,j-1}(\mathbf{r}_{ij}, \mathbf{r}_{i+1,j-1})$ between them. Only the secondary pairing patterns are considered: (1) each base can be unpaired or be paired to at most one other base; (2) if base i is paired to base j (suppose $i < j$) and k to l ($k < l$), then either $i < j < k < l$ or $i < k < l < j$.

The partition function can be calculated iteratively. The total statistical weight $Z_i^j(\mathbf{r})$ for a polynucleotide segment (from base i to j) whose ends are separated by a distance $\mathbf{r}$ is expressed as [20,21]

$$Z_i^j(\mathbf{r}) = \int \mathrm{d}\mathbf{u}\, \mu(\mathbf{u}) Z_i^{j-1}(\mathbf{r} - \mathbf{u}) + f_{ij}(\mathbf{r}) \left[\prod_{i=1}^{2} \int \mathrm{d}\mathbf{u}_i\, \mu(\mathbf{u}_i) \right] Z_{i+1}^{j-1}(\mathbf{r} - \mathbf{u}_1 - \mathbf{u}_2)$$
$$+ \sum_{k=i+1}^{j-2} \left[\prod_{i=1}^{3} \int \mathrm{d}\mathbf{u}_i\, \mu(\mathbf{u}_i) \right] \mathrm{d}\mathbf{v} f_{jk}(\mathbf{v}) Z_i^{k-1}(\mathbf{r} - \mathbf{u}_1 - \mathbf{v}) Z_{k+1}^{j-1}(\mathbf{v} - \mathbf{u}_2 - \mathbf{u}_3)$$

$$+s(a-|\mathbf{r}|)(1+f_{ij}(\mathbf{r}))\left[\prod_{i=1}^{2}\int \mathrm{d}\mathbf{u}_i\,\mu(\mathbf{u}_i)\right] g_{i,i+1}^{j,j-1} Z_{i+1}^{(p)^{j-1}}(\mathbf{r}-\mathbf{u}_1-\mathbf{u}_2)$$
$$+\sum_{k=i+1}^{j-2}\prod_{i=1}^{3}\int \mathrm{d}\mathbf{u}_i\,\mathrm{d}\mathbf{v}s(a-|\mathbf{v}|)(1+f_{ij}(\mathbf{r}))g_{k,k+1}^{j,j-1}$$
$$\times Z_i^{k-1}(\mathbf{r}-\mathbf{u}_1-\mathbf{v})Z_{k+1}^{(p)^{j-1}}(\mathbf{v}-\mathbf{u}_2-\mathbf{u}_3). \tag{7}$$

Here, $\mu(\mathbf{r}) \propto \exp(-(|\mathbf{r}|-b)^2/2l^2)$, $f_{ij}(\mathbf{r}) = \exp[-\beta V_{\mathrm{pair}}^{j,i}(\mathbf{r}_{ij})]-1$, and $s(x)=1$ if $x \geq 0$ and 0 otherwise, $g_{i,i+1}^{j,j-1} = \exp[-\beta J_{i,i+1}^{j,j-1}(\mathbf{r}_{ij},\mathbf{r}_{i+1,j-1})]-1$. $Z_i^{(p)^j}$ is the statistical weight for a ssDNA segment whose two end bases (i and j) form a base pair:

$$Z_i^{(p)^j}(\mathbf{r}) = s(a-|\mathbf{r}|)(1+f_{ji}(\mathbf{r}))\left[\prod_{i=1}^{2}\int \mathrm{d}\mathbf{u}_i\,\mu(\mathbf{u}_i)\right] Z_{i+1}^{j-1}(\mathbf{r}-\mathbf{u}_1-\mathbf{u}_2)$$
$$+s(a-|\mathbf{r}|)(1+f_{ji}(\mathbf{r}))\left[\prod_{i=1}^{2}\int \mathrm{d}\mathbf{u}_i\,\mu(\mathbf{u}_i)\right] g_{i,i+1}^{j,j-1} Z_{i+1}^{(p)^{j-1}}(\mathbf{r}-\mathbf{u}_1-\mathbf{u}_2). \tag{8}$$

To simplify the calculation, we assume the polymer chain to be homogeneous. Then in eqs (7) and (8) we can write $f_{ji}(\mathbf{r})$ as $f(\mathbf{r})$; $Z_{j,i}(r)$ as $Z_{j-i}(r)$, etc. and we just denote the stacking potential to be a constant J and denote $g = g_{i,i+1}^{j,j-1}(\mathbf{r}_{i,j},\mathbf{r}_{i+1,j-1}) = \text{const.}$ Define $\Xi(\zeta,\mathbf{p}) = \int \mathrm{d}\mathbf{r}(\sum_{n=0}^{\infty} Z_n(\mathbf{r})\zeta^n)\exp(i\mathbf{p}\cdot\mathbf{r})$ [20]. After considering eqs (7) and (8), we can show [21] that $\Xi(\zeta,\mathbf{p}) = D(\zeta)/[1-\sigma(\mathbf{p})D(\zeta)]$. Here

$$D(\zeta) = \zeta + \Xi(\zeta,p) = -\eta_1\zeta^3 + \eta_2\zeta^2 + \zeta \tag{9}$$

with coefficient η_1 being a constant and η_2 related to D:

$$\eta_1 = g\gamma(4\pi)^{-3/2}(b/l),$$

and

$$\eta_2(D) = D\eta_1\left[1+(b^2 l/g\pi^{3/2})\int \mathrm{d}\mathbf{q}\,\sigma^2(\mathbf{q})/(1-\sigma(\mathbf{q})D)\right].$$

When an external force $\mathbf{F} = F\mathbf{z}_0$ is applied at the end of the ssDNA chain, the total partition function is $Z_N^F = \int \mathrm{d}\mathbf{r}\,Z_N(\mathbf{r})\exp(-\beta\mathbf{F}\cdot\mathbf{r})$. The Laplace transform of this partition function is calculated to be $\sum_{N=0}^{\infty} Z_N^F\zeta^N = \Xi(\zeta,-i\beta\mathbf{F})$. The smallest positive singularity point of the function $\Xi(\zeta,-i\beta\mathbf{F})$ in the variable ζ corresponds to the free energy density of the ssDNA chain [22]. We see that $\Xi(\zeta,-i\beta\mathbf{F})$ has a pole ζ_{pole} determined by

$$D(\zeta_{\mathrm{pole}}) = 1/\sigma(-i\beta\mathbf{F}) = [\beta Fb/\sinh(\beta Fb)]\exp(-\beta^2F^2l^2/2). \tag{10}$$

The function $D(\zeta)$ is related to the Laplace transform of the statistical weight of hairpin state and has a finite radius of convergence. The singularity of $D(\zeta)$ is related to the roots of eq. (9). To see this, we consider two extreme cases:

Case A: *Stacking potential* $J=0$. In this case, $g=0$ and $\eta_1=0$ and eq. (9) reduces to second order. This situation has been studied in ref. [20] and it was found that $D(\zeta)$ has

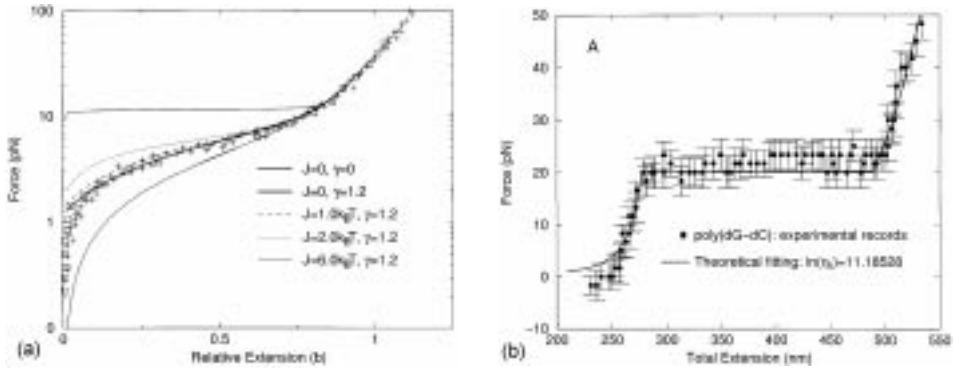

Figure 3. Force–extension relationship for ssDNA. (**a**) The ssDNA bases are randomly ordered (experimental data come from ref. [7] (+) and [9] (□)). (**b**) Poly(dG-dC) sequence (experimental data from ref. [10]). J is the stacking potential, γ accounts for the pairing potential intensity, and η_1 accounts for the combined intensity of pairing and stacking.

a second-order branching point at $\zeta_{\rm bp}$ equalling the maximum of the expression $(-1+\sqrt{1+4D\eta_2})/2\eta_2$, which is reached at $D = D_{\rm bp} < 1$. When the force is less than the threshold value $F_{\rm cr}$ determined by eq. (10) at $D = D_{\rm bp}$, the polymer resides in the hairpin phase with zero extension. At $F = F_{\rm cr}$, there is a second-order continuous hairpin-coil phase-transition (because $\mathrm{d}\zeta/D = 0$ at $D_{\rm bp}$).

Case B: *The stacking potential J is so strong that* $J \gg 1$. In this case, $\eta_2 = D\eta_1$ and eq. (9) is equivalent to $(\zeta + 1/\sqrt{\eta_1})(\zeta - D)(\zeta - 1/\sqrt{\eta_1}) = 0$. When $D \leq 1/\sqrt{\eta_1}$, its smallest positive root is $\zeta = D$; and when $D > 1/\sqrt{\eta_1}$, its smallest positive solution is a constant $\zeta = 1/\sqrt{\eta_1} \propto (g\gamma)^{-1/2}$. As a consequence, for $F < F_{\rm cr}$ which is determined by eq. (10) with $D = 1/\sqrt{\eta_1}$, the polymer is in the hairpin state, for $F > F_{\rm cr}$ the system is in the random coil state and at $F = F_{\rm cr}$ there is a first-order hairpin-coil phase-transition, resulting from the fact that $\mathrm{d}\zeta/\mathrm{d}D|_{D=1/\sqrt{\eta_1}} = 1$.

Comparing Cases A and B, we have the impression that the inclusion of base-pair stacking interaction may dramatically change the statistical property of the ssDNA system, even the order of the hairpin-coil phase transition. There is a critical strength of stacking interaction $J_{\rm cr}$, above which the ssDNA system shows first-order phase transition behavior, and below which it shows continuous behavior (cf. ref. [21] for more detailed analysis). This insight is used to understand some recent experimental facts. In figure 3 the theoretical and experimental force–extension profiles for two ssDNA sequences are shown.

5. Conclusion

We have studied the elasticity of double- and single-stranded DNA polymers by theoretical means, with the stacking interaction between nucleotide base-pairs being explicitly incorporated. This work demonstrated the possibility of understanding DNA elasticity by simple models and suggested the significance of stacking interaction to the mechanical stability

and deformability of DNA double-helix. The improved understanding of DNA mechanics should be helpful for one to investigate the mechanical property of DNA–protein complex, an outstanding example being chromatin.

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