Catenary-like pattern of stretching DNA molecules: experiments and models

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Abstract It was verified that our "s-suspension bridge" model may be not only responsible for catenary-like patterns of DNA molecules which were formed in our experiments, but also for catenary-like patterns of DNA molecules in literature .

Keywords DNA molecules, Atomic force microscope, Nanometer scale, Catenary-like pattern

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1 INTRODUCTION

A detail experimental and theoretical analysis of a two-dimensional pattern of grafted DNA molecules on the surface of a solid substrate by a moving meniscus was reported in 1995.[1] Bensimon *et al.* acquired a loop-like shape of grafted DNA molecules on the surface of a solid substrate in terms of his "molecular combing" technique in the range of micron scale.[1] However, only one of their loops in Fig.2(d) has a clear and complete outline. Make use of different experimental procedures, more clear nano-catenary-like patterns of DNA molecules has been formed in our studies, which were revealed by atomic force microscope (AFM) and could be understood quantitatively quite well by means of our "s-suspension bridge" model.[2] The success of "s-suspension bridge" model suggests that concerning Ref.[1] three points needing to discuss:

(1) Bensimon *et al.* obtained the solutions (i.e. Eq.(5) in Ref.[1])

$$\ell = \frac{(a+1)\ell_0}{1+a\ell_0^{1+\frac{1}{a}}}, \sin\Theta = \frac{1-\ell_0^{1+\frac{1}{a}}}{1+a\ell_0^{1+\frac{1}{a}}}, \tag{1}$$

of the followin set of differential equations:

$$\frac{F_0}{EA}\frac{d\ell}{ds} = 1 - \frac{\ell(s)}{\ell_0(s)}, \frac{d\ell_0}{ds} = -\frac{\ell_0(s)}{\ell(s)}, \tag{2}$$

where a≡ F_0/EA. Apart from the inconsistent dimension of same symbol ℓ_0(s) in the numerator and denominator of Eq.(1), they claimed that the calculated shape, for Fig.2(a)

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with a=1.36, for Fig.2(b) with a=0.47, are in excellent agreement with the observations. But they only compared the evaluating value of parameter "a" in Eq.(1) with the measured (observed) value "a" in Fig.2(a).

(2) They never compared the evaluating value $\ell_0(s)$ and $\ell(s)$ (might as well called ℓ_e) with the measured value $\ell_0(s)$ and $\ell(s)$ (might as well called ℓ_m) point by point in the loops.

(3) Whether the postulate of "the end result is a constant stretching force F_0 parallel to the tangential direction of a combed molecule" is reasonable?

In this paper we are going to report that not only our catenary patterns of DNA could be understood by means of "s-suspension bridge" model but also the loop in Fig.2(d) in Ref.[1].

2 EXPERIMENTIAL SECTION

The main experimental procedures may be found in Ref.[2]:

(1) DNA molecules were stretched on the APTES-mica[3] surface.[4]

(2) To use a second water flow to construct the catenary-like patterns of DNA.

(3) The treated DNA strands was dried and immediately imaged with AFM.

3 RESULTS AND DISCUSSION

Fig.1 and Fig.2 are two typical results adopted from our hundreds of AFM images. Patterns in Figs.1–2 were formed making use of two DNA strands at the same time. Curves 1–4 in Fig.1 and curves 1–5 in Fig.2 have the following three features: 1) the curves 1–4 in Fig.1 and curves 1–5 in Fig.2 bend to the moving direction of liquid flow (external force); 2) all size of curves display symmetric patterns approximately; 3) their symmetrical axes are all parallel to the moving direction of the liquid flow approximately. Besides, fortunately, there exists a half-tone-pattern labeled "ht" in Fig.2.

One may find that all shapes of the curves 1–4 in Fig.1 and curves 1–5 in Fig.2 as well as loop Fig.2(d) in Ref.[1] look like a "suspension bridge" or a "catenary-like" curve approximately so that we have presented a physical mechanism called "s-suspension bridge" model responsible for these phenomena,[2] in which a resultant was assumed to be perpendicular to DNA strands and distributed continuously and uniformly along the strands of DNA molecules, see the sketch Figs.3(a) and 3(b) in Ref.[2]. Starting from a cable being in static equilibrum at any moment, the equations of static equilibrium of the segment CD in Fig.3(b)in Ref.[2] are

$$T\sin\theta = fs, \quad T\cos\theta = T_0, \tag{3}$$

finally one may obtain a catenary equation

$$y = c\cosh\frac{x}{c}, \quad s = c\sinh\frac{x}{c}, \tag{4}$$

where f is the constant load per unit length of the cable , T the tangent tension Tat any point D in the cable, s the arclength of the cable CD, T_0 the horizontal tension at C. By using Eq.(4) catenary-like patterns of DNA molecules were understood quite well:

(1) According to Eqs.(3-4), one may infer that under the action of liquid flow perpendicular to the aligned DNA and distributed continuously and uniformly along the DNA strands, those segments not adhering firmly to the mica surface might be firstly stretched and bent meanwhile as a catenary-like curve with symmetrical axes parallel to the direction of the liquid flow and then stuck on the mica surface randomly.

(2) Let us use L and h to denote the span (width) and the sag (depth) of a catenary respectively. The curve labeled "ht" in Fig.2 would be "frozen" as a half-tone-pattern when the used liquid flow was tured off due to the span L of "ht" being bigger than others and having no enough time to take shape.

(3) Parameter c characterizes a catenary. The catenaries with the same parameter c are termed to be equal.[5] Parameter c is not an adjustable one, which is determined by the span, the sag and Eq.(4). For curves in Figs.1-2 we measure their spans as well as sags and evaluate the parameter c according to Eq.(4), then list data in Table 1(a) and Table 1(b) respectively. The ralative extension (2S/L) of a catenary is listed in Table 1 also.

(4) Obviously, in the nanometer scale, we have been unable to control the direction of the water flow strictly yet, so that the nano-scale patterns of DNA strands displays a symmetry approximately merely.

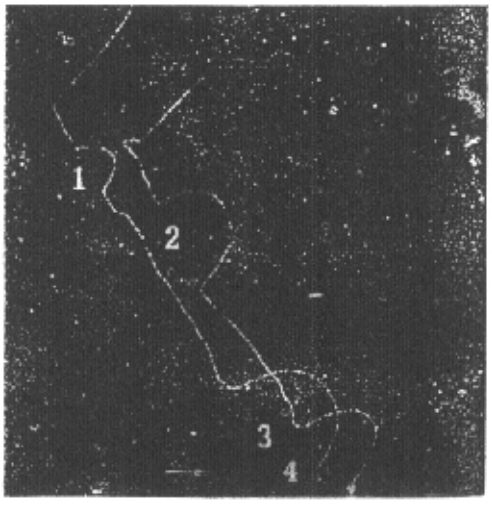

Fig.1 One typical AFM image adopted from our hundreds of AFM images. Data were collected by Tapping-Mode AFM[2] Scan size: 3.0μm× 3μm

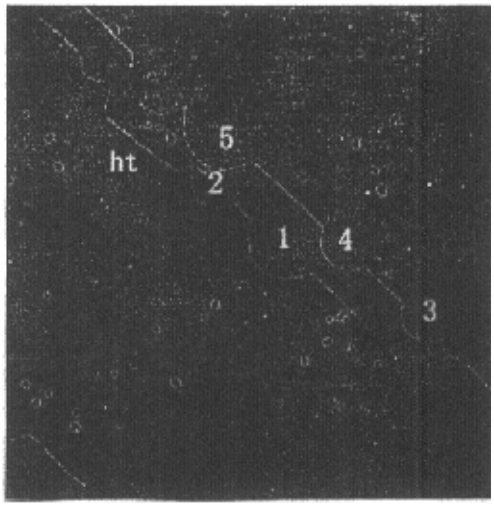

Fig.2 Another typical AFM image adopted from our hundreds of AFM imaged. Data were collected by the same way as in Fig.1. Scan size: 3.0μm × 3μm

Table 1 The evaluated value of parameter c and total length S

(a)

Fig.1	Span L ($\times 10^2$nm)	Sag h_{max} ($\times 10^2$nm)	C ($\times 10^2$nm)	$2S$ ($\times 10^2$nm)	$2S/L$
Curve 1	14.50±0.08	7.50±0.08	4.38	22.09	1.52
Curve 2	26.00±0.08	15.00±0.08	7.30	42.09	1.62
Curve 3	34.00±0.08	20.50±0.08	9.27	44.52	1.31
Curve 4	22.00±0.08	17.50±0.08	5.05	44.02	2.00

(b)

Fig.2	Span L ($\times 10^2$nm)	Sag h_{max} ($\times 10^2$nm)	C ($\times 10^2$nm)	$2S$ ($\times 10^2$nm)	$2S/L$
Curve 1	8.48± 0.08	3.01± 0.08	3.39	10.86	1.28
Curve 2	6.15± 0.08	2.19± 0.08	2.46	7.90	1.28
Curve 3	5.47± 0.08	1.91± 0.08	2.21	6.96	1.27
Curve 4	6.02± 0.08	2.19± 0.08	2.36	7.78	1.29
Curve 5	9.08± 0.08	3.56± 0.08	3.37	12.10	1.33

(5) The shape of all the curves in Figs.1-2 could be fitted quantitatively by Eq.(4) quite well. For simplicity, we only give two examples here. Table 2(a)-2(b), show the comparison between measuring values h_m and the evaluating values h_e for curve 3 in Fig.1 and curve 1 in Fig.2 by the use of following equations

$$y_c = c\cosh\frac{x}{c}, \qquad h_e = h_{max} + c - y_e, \tag{5}$$

where x is the measuring value of coordinates of points on the curve 3 in Fig.1 and on the curve 1 in Fig.2, h_{max} the sag of the curve 3 in Fig.1 and of the curve 1 in Fig.2, h_e the evaluating values corresponding to each x, the values of c are taken from Table 1. The comparison for other curves in Figs.1-2 are not listed and will be published elsewhere.

Table 2 The comparison between measuring values h_m and the evaluating values h_e

Table 2(a) [c=246nm, h_{max}=219± 8nm]

x ($\times 10^2$nm)	0.55	1.09	1.37	1.64	1.91	2.19
h_m ($\times 10^2$nm)	2.05± 0.08	1.91± 0.08	1.78± 0.08	1.59± 0.08	1.37± 0.08	1.09± 0.08
h_e ($\times 10^2$nm)	2.13	1.94	1.81	1.61	1.40	1.15

Table 2(b) [c=927nm, h_{max}=301± 8nm]

x ($\times 10^2$nm)	0.82	1.64	2.19	2.74	3.28	3.83
h_m ($\times 10^2$nm)	20.00± 0.08	18.50± 0.08	16.90± 0.08	14.60± 0.08	11.60± 0.08	7.80± 0.08
h_e ($\times 10^2$nm)	20.01	18.49	16.83	14.56	11.59	7.76

(6) Moveover, the shape of Fig.2(d) in Ref.[1] could be fitted by the use of Eq.(4) quite well also, see Table 3, where c=4.78 (μm) is evaluated in terms of Eq.(4), and the

measured values of the span (L=6.12×2 μm) as well as the sag (h_{max}=4.49 μm) of the curve Fig.2(d) in Ref.[1].

Table 3 The comparison between measuring values h_m and the evalues h_c for curve in Fig.2(d) in Ref.[1]

x (μm)	1.22	2.45	3.06	3.67	4.90	5.51
h_c (μm)	4.33	3.84	3.47	3.03	1.76	0.95
h_m (μm)	4.33± 0.3	3.92± 0.3	3.39± 0.3	3.27± 0.3	2.04± 0.3	1.06± 0.3

(7) As we know, the tension T at any point of the cable CD in Fig.3(a) in Ref.[2] is given by

$$T = T_0 \frac{ds}{dx} = fy \tag{6}$$

The tangent tension T at any point of any deforming DNA segment is a component of the total resultant force and is proportional to its vertical coordinate y. This point is different from the postulate of "a constant tangential force exerted on the molecule" used in Ref.[1]. Judging from this point that the total resultant force in Ref.[1] should be along the receding direction of a meniscus and was distributed continuously and uniformly along the loops, but not along the tangential direction of the combed DNA molecule.

4 CONCLUSION

The present work reveals further that, as a whole, the stretched DNA strands still behave like a flexible cable in nano-scale; the classical elastic mechanical works very well; the shape of two-dimensional patterns of stretching DNA molecules may be controlled, which can be used in the design of DNA based devices. But the size and c of patterns are still beyond control so far.

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