PHYSICAL REVIEW E **70**, 010902(R) (2004)

Bubble relaxation dynamics in double-stranded DNA

D. J. Bicout[1,2] and E. Kats[1,3]
[1]*Institut Laue-Langevin, 6 rue Jules Horowitz, B.P. 156, 38042 Grenoble, France*
[2]*Biomathematics and Epidemiology, ENVL, B.P. 83, 69280 Marcy l'Etoile, France*
[3]*L. D. Landau Institute for Theoretical Physics, RAS, 117940 GSP-1, Moscow, Russia*
(Received 17 November 2003; revised manuscript received 27 February 2004; published 28 July 2004)

This paper deals with the two-state (opening–closing of base pairs) model used to describe the fluctuation dynamics of a single bubble formation. We present an exact solution for the discrete and finite size version of the model that includes end effects and derive analytic expressions of the correlation function, survival probability, and lifetimes for the bubble relaxation dynamics. It is shown that the continuous and semi-infinite limit of the model becomes a good approximation to an exact result when $a^N \ll 1$, where N is bubble size and a, the ratio of opening to closing rates of base pairs, is the control parameter of DNA melting.

DOI: 10.1103/PhysRevE.70.010902 PACS number(s): 87.14.Gg, 02.50.Ga, 82.39.Jn, 87.15.−v

Upon heating, a double stranded DNA (ds DNA) undergoes a denaturation process with the formation of bubbles of increasing size and number and, eventually, leading to the separation of the two strands [1]. On the other hand, many DNA biological activities require the unzipping of the two strands by breaking hydrogen bonds between base pairs (see e.g., Ref. [2] for an idea of the background to the problem). Such open regions of complex DNA, enclosing up to 10–30 broken base pairs, represent a first step of the transcription processes and are called the transcription bubbles. Several theoretical models have been proposed to describe the phenomenon of bubble formation (for a review see, e.g., [3]). However, the issue remains unsettled with various, and even contradictory, results reported in the literature. This is indicative of the complexity of the problem which involves number of factors (e.g., base pair sequences, molecular environment, counterions, etc.) that can influence the denaturation process in various ways (see, e.g., [4–6]). In addition, as a one- or quasi-one-dimensional system, the ds DNA is expected to be very sensitive to thermal fluctuations. Therefore, it seems appropriate in a first step to study the fluctuations of local breathing or unzipping of a ds DNA that opens up bubbles of a few tens of base pairs.

The characteristic dynamics of these local denaturation zones (bubbles) in the structure of a ds DNA have been recently probed through fluorescence correlation spectroscopy [7,8]. This is an essential issue not only for physiological processes involving ds DNA but also for providing insights on the general nature of fluctuations in such systems. From a theoretical modeling perspective, however, we have just begun to understand these experimental results. In their recent paper [8], Altan-Bonnet, Libchaber, and Krichevsky (ALK) have presented a measurement of the dynamics of a single bubble formation in ds DNA construct. The authors proposed a simple discrete and finite size model for the description of the dynamics of bubbles while they used a continuous and semi-infinite version of the model to fit their experimental data. In this continuous and semi-infinite limit, the survival probability of the bubble reads [8]:

$$B_{\infty,c}(t) = \left(1 + \frac{x}{2}\right)\mathrm{erfc}\left[\frac{\sqrt{x}}{2}\right] - \left(\frac{x}{\pi}\right)^{1/2} e^{-x/4}, \qquad (1)$$

where $x = t/\tau_{\infty,c}$ and the bubble lifetime is

$$\tau_{\infty,c} = \frac{(1+a)}{2k_-(1-a)^2}; \quad a = \frac{k_+}{k_-} = e^{-\varepsilon/k_BT}, \qquad (2)$$

where k_+ and k_- are the opening and closing rates of base pair, respectively, ε the bubble extension energy and k_BT the thermal energy. In the same spirit, the dynamics of bubble formation have been studied in terms of Fokker-Planck equation [9]. In this paper, we go one step forward in providing the exact solution of the generalized ALK model, taking into account both the discreteness of the system and the finite size and including end effects. Figure 1 displays an illustration of the reaction we are dealing with. Our motivation in this investigation is to provide analytic expressions for bubble relaxation function, relaxation time, and lifetime. Such exact solutions may significantly improve data analyzes and be very relevant for any systems with arbitrary ε and size N.

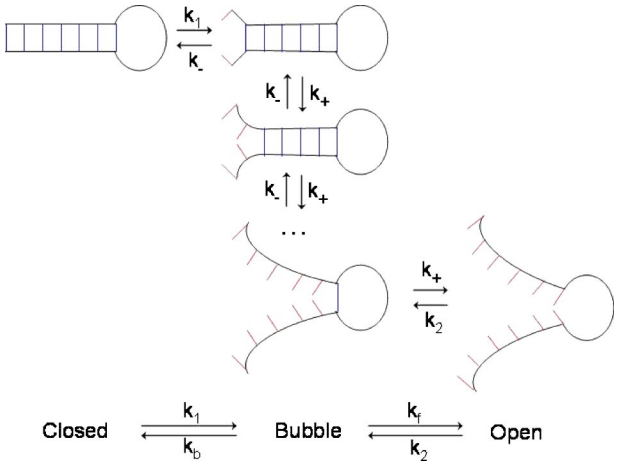

FIG. 1. Sketch illustrating the opening–closing bubble reaction kinetics.

Following ALK, we denote by $b_n(t)$ the probability density of bubbles of size n at time t in the system. Assuming that all conformations of the ds DNA can be described as two states (closed or open), the fluctuations dynamics in the number n of open base pairs in the bubble is described by the master equation:

$$\begin{cases} \frac{db_0}{dt} &= k_- b_1 - k_1 b_0 \\ \frac{db_1}{dt} &= k_1 b_0 + k_- b_2 - (k_+ + k_-) b_1 \\ \cdots & \cdots \\ \frac{db_n}{dt} &= k_+ b_{n-1} + k_- b_{n+1} - (k_+ + k_-) b_n \\ \cdots & \cdots \\ \frac{db_N}{dt} &= k_+ b_{N-1} + k_2 b_{N+1} - (k_+ + k_-) b_N \\ \frac{db_{N+1}}{dt} &= k_+ b_N - k_2 b_{N+1}, \end{cases} \tag{3}$$

where, in addition to the rates $k_\pm$ in ALK model [8], we have explicitly introduced the opening and the closing rates k_1 and k_2, respectively, for opening the first and closing the last pairs since two ends of the DNA helix are sealed (see Fig. 1).

Stationary distribution: When $k_1 \neq 0$ and $k_2 \neq 0$, Eq. (3) admits a stationary solution given by

$$\frac{b_{\rm st}(n)}{b_{\rm st}(0)} = \begin{cases} k_1 a^{n-1}/k_- & ; \quad 1 \leqslant n \leqslant N \\ k_1 a^N / k_2 & ; \quad n = N+1 \end{cases}, \tag{4}$$

where $b_{\rm st}(0) = 1/[1 + (k_1 Q/k_-) + (k_1 a^N/k_2)]$ with $Q = (1 - a^N)/(1-a)$. The equilibrium fraction of DNA molecules that are closed, open, and with bubbles in the system are given by $b_{\rm st}(0)$, $b_{\rm st}(N)$, and f_b, respectively, where

$$f_b = \sum_{n=1}^{N} b_{\rm st}(n) = \left(\frac{k_1 Q}{k_-} \right) b_{\rm st}(0). \tag{5}$$

The equilibrium constants K_1 and K_2 for the concentrations of species in the reactions in Fig. 1 are:

$$K_1 = \frac{(\text{bubble})}{(\text{closed})} = \frac{k_1}{k_{\rm b}} \quad \text{and} \quad K_2 = \frac{(\text{open})}{(\text{bubble})} = \frac{k_{\rm f}}{k_2}. \tag{6}$$

where the backward k_b and forward k_f rates are,

$$k_{\rm b} = \frac{k_{\rm f}}{a^N} = k_- \left(\frac{1-a}{1-a^N} \right). \tag{7}$$

When $k_1 = k_2 = 0$, the concentration of bubbles tends zero and we have $[\text{open}]/[\text{closed}] = a^N$.

Relaxation function: To study the fluctuations of bubbles, we consider $\Pi(z,t|n_0) = \Sigma_{n=0}^{N+1} z^n b_n(t|n_0)$ (where $b_n(t|n_0)$ is conditional the probability density of finding a DNA molecule with a bubble of size n at time t given that the size was n_0 at time $t=0$) the characteristic function for the system prepared with the initial condition, $b_n(t=0|n_0) = \delta_{n,n_0}$. The Laplace transform $[\hat{\Pi}(z,s|n_0) = \int_0^\infty dt \Pi(z,t|n_0) e^{-st}]$ of $\Pi(z,t|n_0)$ is obtained as,

$$\hat{\Pi}(z,s|n_0) = \frac{1}{D(z,s)} \{ -z^{n_0+1} + [D(z,0) + k_1(1-z)z] \hat{b}_0(s|n_0) + [D(z,0) - k_2(1-z)] z^{N+1} \hat{b}_{N+1}(s|n_0) \} \tag{8}$$

where $D(z,s) = k_+ [z - z_1(s)][z - z_2(s)]$ and $z_{1,2}(s) = [s/k_- + 1 + a \mp \sqrt{(s/k_- + 1 + a)^2 - 4a}]/2a$. The functions $\hat{b}_0(s|n_0)$ and $\hat{b}_{N+1}(s|n_0)$, obtained by requiring that the numerator of $\hat{\Pi}(z,s|n_0)$ cancels at the roots of $D(z,s)$, are given by

$$\hat{b}_0(s|n_0 = \frac{1}{\Delta} \begin{vmatrix} z_1^{n_0} & [sz_1 - k_2(1-z_1)] z_1^N \\ z_2^{n_0} & [sz_2 - k_2(1-z_2)] z_2^N \end{vmatrix}, \tag{9}$$

and

$$\hat{b}_{N+1}(s|n_0 = \frac{1}{\Delta} \begin{vmatrix} s + k_1(1-z_1) & z_1^{n_0} \\ s + k_1(1-z_2) & z_2^{n_0} \end{vmatrix}, \tag{10}$$

with

$$\Delta(s) = \begin{vmatrix} s + k_1(1-z_1) & [sz_1 - k_2(1-z_1)] z_1^N \\ s + k_1(1-z_2) & [sz_2 - k_2(1-z_2)] z_2^N \end{vmatrix}. \tag{11}$$

To fit with the experimental conditions by ALK, we assume that the system is prepared in the initial conditions $b_{\rm st}(n_0)/f_b$ for $1 \leqslant n_0 \leqslant N$ and zero otherwise. The quantity of interest is the correlation function $C_N(t)$ that describes fluctuations in the bubble population at equilibrium and is measured by fluorescence correlation spectroscopy method [8]:

$$C_N(t) = \sum_{n_0=1}^{N} \sum_{n=1}^{N} \frac{[b_n(t|n_0) - b_n(\infty|n_0 b_{\rm st}(n_0)}{f_b(1-f_b)} = 1 - \sum_{n_0=1}^{N} \frac{[b_0(t|n_0) + b_{N+1}(t|n_0 b_{\rm st}(n_0)}{f_b(1-f_b)}, \tag{12}$$

in which $b_n(0|n_0) = \delta_{n,n_0}$, and we have used the conservation of the probability density, $\Sigma_{n=0}^{N+1} b_n(t|n_0) = 1$. Note that $C_N(0) = 1$ since $b_n(\infty|n_0) = b_{\rm st}(n)$ and $C_N(\infty) = 0$. Performing the summation in Eq. (12), we find the Laplace transform of $C_N(t)$ as

$$\hat{C}_N(s) = \frac{1}{s} - \left[\frac{k_-}{(1-f_b)Q} \right] \times \frac{[(1-z_1)F(z_2) - (1-z_2)F(z_1)]}{s}, \tag{13}$$

where $F(z) = (1-z^N)[s(1-z^{N+1}) + (1-z)(k_1 + k_2 z^N)]/[z^N \Delta]$. From this, the bubble relaxation time is obtained as $\tau_N = \hat{C}(s=0)$. Two limiting cases are considered depending on k_1 and k_2.

(1) $(k_1 + k_2) > 0$ *limit:* In this case, the bubble relaxation time is given by

$$\tau_N = \left\{ \frac{(1+a^{N+1})}{(1-a)^2}\left[\frac{k_1+k_2}{a^N k_1 k_- + k_2 k_- + Q k_1 k_2}\right] - \frac{2Na^N}{(1-a)(1-a^N)}\left[\frac{k_1+k_2}{a^N k_1 k_- + k_2 k_- + Q k_1 k_2}\right] + \left(\frac{1-a^{N+1}}{1-a}\right) \times \left[\frac{k_-}{a^N k_1 k_- + k_2 k_- + Q k_1 k_2}\right] - \left(\frac{1-a^{N+1}}{1-a}\right) \times \left[\frac{1}{a^N k_1 + k_2}\right]\right\} H(k_1+k_2), \quad (14)$$

where H is Heaviside step function defined as $H(z)=0$ for $z<0$ and $H(z)=1$ for $z>0$. When either k_1 or k_2 tends to zero, τ_N linearly decreases, respectively, with either k_1 or k_2 towards $\tau_N(0)$ defined as

$$k_-\tau_N(0) = \left[\frac{(1+a^{N+1})(1-a^N) - 2Na^N(1-a)}{(1-a)^2(1-a^N)}\right] \times \begin{cases} 1 & ; \quad k_1=0, k_2>0 \\ a^{-N} & ; \quad k_1>0, k_2=0. \end{cases} \quad (15)$$

Note, that $\tau_N(0)$ is independent of k_1 and k_2 because the kinetics in these limits is dominated by the bubbles decay. As $N\to\infty$, the fluctuations of bubbles become independent of N with the relaxation function;

$$\hat{C}(s) = \frac{1}{s} - \frac{k_-(1-a)(1-z_1)}{(1-f_b)s[s+k_1(1-z_1)]}, \quad (16)$$

and lifetime,

$$\tau_\infty = \frac{1}{(1-a)[(1-a)k_- + k_1]}. \quad (17)$$

(2) $k_1=k_2=0$ limit: In this case, $\hat{C}_N(s)=\hat{B}_N(s)$, where $B_N(t)$ is the survival probability of bubbles. Likewise, the bubble lifetime $\tau_N=\hat{B}_N(s=0)$ is given by

$$\tau_N = \frac{(1-a^N)(1-a^{N+2}) - N(N+2)(1-a)^2 a^N}{k_-(1-a)^2(1-a^N)(1-a^{N+1})}. \quad (18)$$

When $N\to\infty$, Eq. (13) reduces to $\hat{B}_\infty(s)=(1/s)-k_-(1-a)[1-z_1]/s^2$, and,

$$B_\infty(t) = 1 - \frac{x}{1-a} + \frac{(1-a)}{2a}\int_0^y dz\left(\frac{y}{z}-1\right)\exp\left[-\frac{(1+a)}{2\sqrt{a}}z\right] I_1(z), \quad (19)$$

where $I_1(\cdots)$ is the modified Bessel function of order one, $y=2x\sqrt{a}/(1-a)^2$ and $x=t/\tau_\infty$. It is worth noting that even in the $N\to\infty$ limit the exact solution Eq. (19) for the bubble survival probability is different from Eq. (1) given in [8]. The fact is that, depending on the size N and the parameter "a," the discreteness of the system is an ingredient which might be taken into account to capture the correct bubble dynamics. This is illustrated in Fig. 2 where the exact survival probability is compared with its $N\to\infty$ limit and the ALK continuous model. Figure 3 shows the departure in the bubble lifetime to the continuous limit as a function of bubble size. It clearly appears from Figs. 2 and 3 that the continuous limit as done by ALK [8] becomes a fairly good approximation to exact result for $a^N \ll 1$ (where $a \leqslant 1$ is the control parameter for the ds DNA melting [8,10]).

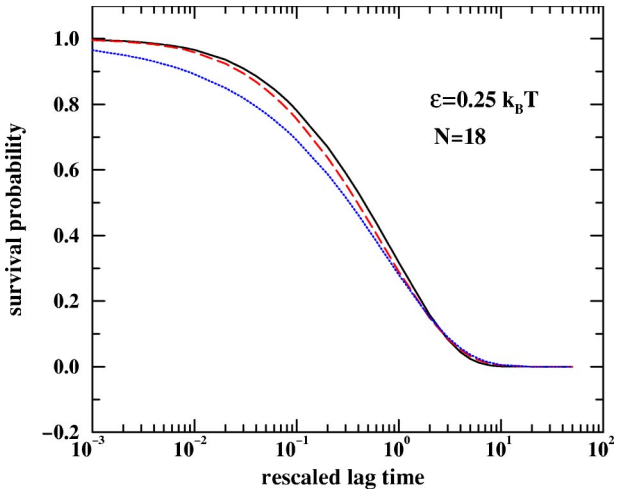

FIG. 2. Bubble survival probabilities, from the top to the bottom, $B_N(t)$ (solid line), $B_\infty(t)$ (long-dashed line), and $B_{\infty,c}(t)$ (dotted line) vs the rescaled lag times t/τ_N, t/τ_∞, and $t/\tau_{\infty,c}$, respectively.

Simple inspection of expressions in Eqs. (13), (14), and (18), and of the figures, indicate that the behavior of bubble dynamics is controlled by the bubble size N and the parameter a (ratio of opening to closing rates of base pairs). As $a \leqslant 1$ according to the experimental situation in [8], the closing of bubbles is the fastest process in the bubbles kinetics. The parameter a also controls the denaturation transition. As $a\to 1$, there is a kind of "critical slowing down" where the fluctuations of bubbles are described by an unbiased diffusion process. For instance, the bubble lifetime in Eq. (18) reduces to

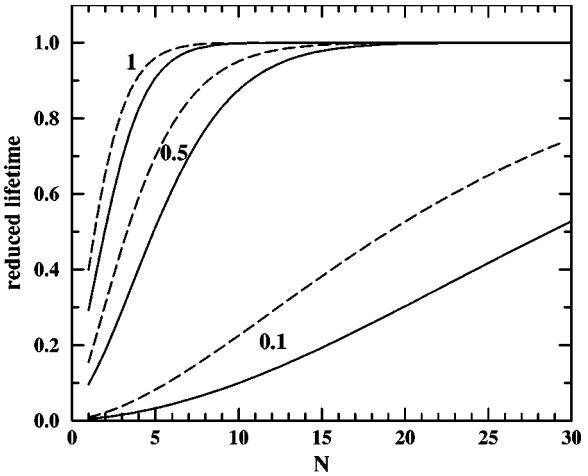

FIG. 3. Reduced lifetime, τ_N/τ_∞ in Eq. (14) for $k_1=0$ (dashed line) and Eq. (18) (solid line), as a function of bubble size, N. Quoted numbers represent the bubble extension energy ε/k_BT.

TABLE I. Estimate of k_- using the expressions of the bubble lifetime in the case of $k_1=k_2=0$. In Ref. [8], the experimental bubble lifetime is equal to 95 μs at $T=303$ K for $N=18$ and DNA samples M_{18} and A_{18}.

ε/k_BT		0.1	0.5	1
Lifetime (μs)			$k_-(10^6\ s^{-1})$	
τ_N	95	0.300	0.0675	0.0263
τ_∞	95	1.162	0.0680	0.0263
$\tau_{\infty,c}$	95	1.110	0.0550	0.0180

$$\tau_N = \frac{(N+1)(N+2)}{12k_-}, \tag{20}$$

in the $a \to 1$ limit, and τ_N diverges with the bubble size.

It may be useful for practical purposes to have an idea of numerical values of physical parameters entering in the problem. In the absence of direct measurement of k_-, for instance, one can use the experimental data in [8] in conjunction with theoretical results to estimate the closing rate k_-. The results of such an estimation are presented in Table I.

To summarize, we have presented an exact solution of the discrete and finite size model in Eq. (3) for the description of the fluctuations dynamics of bubble formation. The twofold merit of this two-state (open and closed) model is to already include sufficient complexity of the bubble dynamics over biomolecular relevant scales and to allow exact analytical solution. The main results of this paper are the expressions in Eqs. (13), (14), and (18) for the bubble correlation function, relaxation time, and bubble lifetime, respectively. These results, consistent with available data, may prove to be useful for analysis and interpretation of experimental data on bubble fluctuations and they are amenable for further experimental tests. It is worthwhile to mention in addition that different expressions for the relaxation function and time can be generated within the theoretical framework developed above by simply using different initial conditions in Eq. (12) for the preparation of the system.

Given the closing and opening rates of base pair, the model discussed above allows study phenomena related to the denaturation mechanisms of DNA such as heating, changing buffer surrounding, or applying external torques or forces [11–14]. Likewise, the model can easily be modified to include more than two states in order to describe, for instance, the intermediates states between bond and broken states. Finally, although the calculations may become more involved and intricate, the theory outlined above can be extended in several directions including in Eq. (3), for example, the effects of base pair sequence in the opening and closing rates (two and three hydrogen bonds being involved in A–T and G–C base pairs, respectively), initiation of several bubbles, bubbles fission and fusion processes, etc.

E.K. acknowledges partial support of this work by INTAS Grant No. 01-0105.

[1] D. Poland and H. A. Sheraga, *Theory of Helix–Coil Transitions in Biopolymers* (Academic, New York, 1970).
[2] H. M. Sobell, Proc. Natl. Acad. Sci. U.S.A. **82**, 5328 (1985).
[3] R. M. Wartell and A. S. Benight, Phys. Rep. **126**, 67 (1985).
[4] M. Peyrard and A. R. Bishop, Phys. Rev. Lett. **62**, 2755 (1989).
[5] Y. Kafri, D. Mukamel, and L. Peliti, Phys. Rev. Lett. **85**, 4988 (2000).
[6] N. Singh and Y. Singh, Phys. Rev. E **64**, 042901 (2001).
[7] G. Bonnet, O. Krichevskii, and A. Libchaber, Proc. Natl. Acad. Sci. U.S.A. **95**, 8602 (1998).
[8] G. Altan-Bonnet, A. Libchaber, and O. Krichevsky, Phys. Rev. Lett. **90**, 138101 (2003).
[9] A. Hanke and R. Metzler, J. Phys. A **36**, L473 (2003).
[10] T. Hwa, E. Marinani, K. Sneppen, and L.-H. Tang, Proc. Natl. Acad. Sci. U.S.A. **100**, 4411 (2003).
[11] J. F. Marko and E. D. Siggia, Phys. Rev. E **52**, 2912 (1995); R. M. Fye and C. J. Benham, *ibid.* **59**, 3408 (1999).
[12] S. Cocco and R. Monasson, Phys. Rev. Lett. **83**, 5178 (1999).
[13] D. K. Lubensky and D. R. Nelson, Phys. Rev. Lett. **85**, 1572 (2000).
[14] J. Chuang, Y. Kantor, and M. Kardar, Phys. Rev. E **65**, 011802 (2002).