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Biochemical and Biophysical Research Communications 349 (2006) 15–19
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Barrier height of free energy on confined polymer translocation through a short nano-channel

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Received 21 June 2006
Available online 21 July 2006

Abstract

The translocation of a confined polymer chain through a nano-channel has been simulated by using two-dimensional bond fluctuation model (BFM) with Monte Carlo dynamics. It is found that the trapping time for the polymer chain to overcome the free energy barrier during the translocation, τ_{trap}, depends exponentially on the chain length N and the channel length M, respectively. The results suggest that the barrier height of free energy depends linearly on N and M, which is different from that predicted for the *Gaussian* chain.

Keywords: Monte Carlo simulation; Polymer translocation; Confinement; Free energy barrier

The translocation of biopolymers through a nano-pore or nano-channel plays an important role in many biological phenomena. Examples include translocation of protein across a cellular membrane or endoplasmic reticulum [1,2], injection of RNA and RNA from a virus to bacteria after their synthesis [3], gene swapping between the guest and the host bacteria through pili, etc. Understanding this process will enable us to deepen our comprehension of many fundamental problems in cell biology, and may eventually provide various useful applications in biotechnologies and industrial processes, e.g., in DNA sequencing [4,5], in oil recovery and separation, and in gene therapy [6,7], etc. Accordingly, the polymer translocation dynamics has attracted considerable interests in recent years (experimental [5–8] and theoretical [9–13]).

The translocation of a polymer through a nano-channel faces a free energy barrier due to the loss of a great number of available configurations [9,10]. Experimental [14] and simulation [15–17] results have indicated that the polymer chain experienced a period of trapping time, τ_{trap}, to overcome this barrier under an external electric field. Theoretically, Muthukumar indicated that a *Gaussian* chain confined in a finite size container could thread through a nano-pore due to the free energy difference between the donor and recipient containers [10]. However, the trapping time during the translocation was omitted in his work and, the *Gaussian* chain could be only used to describe polymer translocation in a θ solution, which is difficult to make in experiments. For the excluded volume effect, the self-avoiding walk chain should exhibit different dynamical behaviors.

In this spirit, we follow the suggestion by Muthukumar that a polymer chain confined in a finite size container may be threaded through a nano-scale channel spontaneously due to the free energy difference between two connected containers. In this study, we use a lattice Monte Carlo simulation, focusing on the trapping stage during the translocation of a self-avoiding walk chain. Our simulation results show that the trapping time, τ_{trap}, exponentially decreases with N and increases with M. Then the barrier height of free energy was discussed and compared with that predicted of the *Gaussian* chain.

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0006-291X/$ - see front matter © 2006 Published by Elsevier Inc.
doi:10.1016/j.bbrc.2006.06.198

Model

The two-dimensional bond fluctuation model (BFM) combined with single-segment Monte Carlo moves was used in our simulation, since the excluded volume effect plays an important role on the static and dynamical properties of confined polymer chain in the lower dimension [18]. Two square lattice spaces with different sizes $R_1 = 30$ and $R_2 = 800$ are connected by a channel of length M. The channel is narrow enough so as to ensure that the polymer chain was stretched out in the channel (Fig. 1). A chain that consists of N monomers is initially placed in the donor square (of size R_1) with one end of it positioned at the pore entrance. In our simulation, the channel and the squares are viewed as hard walls whose only interactions with the chain are steric. The chain is then allowed to reach an equilibrium conformation using the standard Monte Carlo method, but with the constraint that the first monomer, placed at the pore entrance, is fixed. This constraint makes the chain to be kept in the donor space during the relaxation.

Once the chain is in the equilibrium conformation, the first monomer at the pore entrance is released from its constraint and the simulation of the polymer chain moving through the pore begins. In this paper, we put aside the question of how the chain first enters the channel, focusing, instead on the dynamics once one end has been inserted. So, the first monomer is not allowed to go back to the donor space during the translocation.

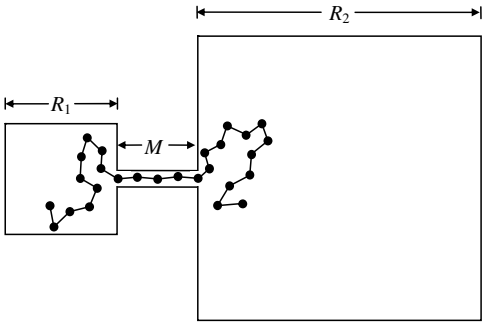

Fig. 1. Schematic representation of a N-monomer polymer in the process of the translocation through a nano-channel of length M from the confinement. The channel is so narrow that the "hairpin" translocation is forbidden.

Results and discussion

The typical motion of the polymer chain viewed in our simulation is as follows. Once the first monomer at the entrance of the pore is loosed, the chain continues to perform its conformational changes inside the donor square. After a certain time, the front end of the chain spills into the channel and quickly arrives at the receipt square. However, this step does not necessarily lead to a successful spontaneous translocation in spite of the fact that the monomer density is higher in the donor. The free energy barrier arising from the losing of chain conformation will pull the chain back into the channel. The chain will undergo back and forth motion if the number of monomers entering the receipt square is smaller than a critical number. The time for the chain consumed in this period to overcome the free energy barrier is the trapping time τ_{trap}. In the end, when enough monomers above the critical numbers are pushed inside the recipient square by a sequence of random events, the chain will spontaneously transport into the receipt square and a successful translocation occurs.

The typical results for the chain length N and channel length M dependences of the trapping time, τ_{trap}, are plotted in Fig. 2. It can be seen that there is a linear relationship between $\log(\tau_{\text{trap}})$ and N

$$\log(\tau_{\text{trap}}) \backsim -N \tag{1}$$

Also, for $\log(\tau_{\text{trap}})$ and M, there is

$$\log(\tau_{\text{trap}}) \backsim M \tag{2}$$

The results can be understood as follows. As N increases, the confinement depresses the conformational entropy of the chain, and hence increases the free energy of the chain in the donor. It takes shorter time for the chain to go over the free energy barrier. While M increases, the peak in the chain's free energy during translocation builds up. More time will be required for the chain to overcome the free energy barrier. The free energy landscapes during polymer translocation are sketched in Fig. 3.

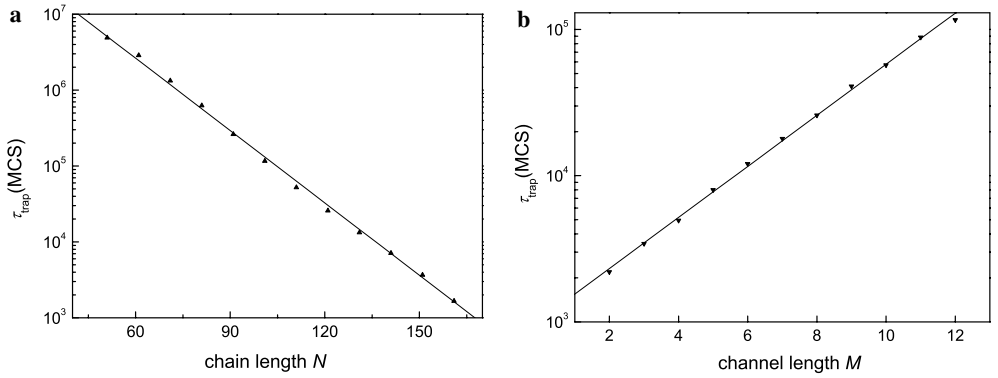

Fig. 2. (a) Average τ_{trap} as a function of the chain length N; (b) average τ_{trap} as a function of the nano-channel length M.

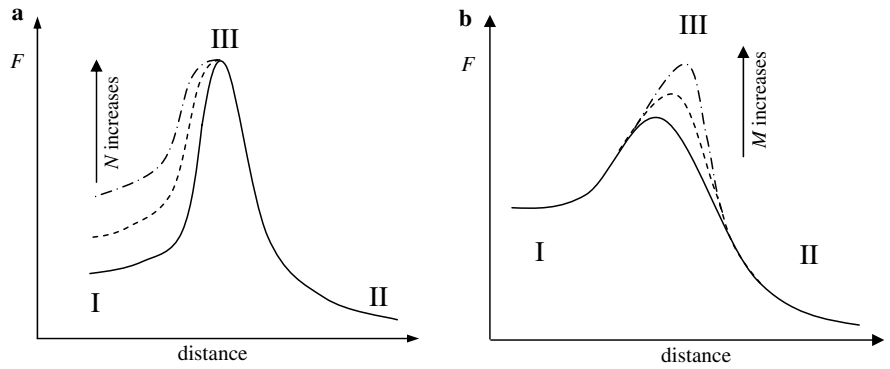

Fig. 3. The free energy barrier of the chain (a) for different chain length N; (b) for different nano-channel length M.

An estimate of the barrier height of free energy can be made based on *Arrhenius* equation. The reaction rate $k(\backsim\tau_{\mathrm{p}}^{-1})$ for the present situation is given by

$$k \backsim \mathrm{e}^{-\frac{\Delta F}{k_{\mathrm{B}}T}} \tag{3}$$

where ΔF is the barrier height; k_{B} and T are Boltzmann constant and absolute temperature, respectively. Combining with Eq. (1) and (2), we have

$$\Delta F \backsim -N \tag{4}$$

and

$$\Delta F \backsim M \tag{5}$$

Therefore, the barrier height of the free energy depends linearly on the polymer chain length N and the channel length M.

It is therefore of interest to compare our simulation results with the prediction for a *Gaussian* chain. Theoretically, one often uses the equation [10,19]

$$-\frac{\partial G_N(r,r')}{\partial N} = -\frac{l^2}{4}\nabla^2 G_N(r,r') \tag{6}$$

with the condition that G_N is zero if r or r' is on the boundary of the square for all values of N to describe a confined *Gaussian* chain. Solving Eq. (6) and combining with ground-state-dominance (GSD) approximation, we can get the free energy expression for the chain in the confinement of size R with m monomers in the nano-channel

$$\frac{F_a(m)}{k_{\mathrm{B}}T} = \frac{N\pi^2 l^2}{2R^2} + m\left(\epsilon - \frac{\pi^2 l^2}{2R^2}\right) + \text{const.} \tag{7}$$

where l is the bond length and $\epsilon = \ln z$, z is the effective coordination number inside the square and $z = 4$ for our situation. The detailed calculations are given in Appendix A. For $l \ll R$, the second term on the right-hand side of Eq. (7) is positive. So, the free energy increases with m varying from 0 to M. The free energy barrier is thus obtained

$$\Delta F_a = F_a(M) - F_a(0) = M\left(\epsilon - \frac{\pi^2 l^2}{2R^2}\right) \backsim M \tag{8}$$

From Eq. (8) one can obtain that the barrier height of the free energy of the *Gaussian* chain is independent of N. It is quite different from the simulation result for the self-avoiding walk chain that the barrier height decreases linearly with N (Eq. 4). This observation suggests that the excluded volume can significantly affect the free energy barrier during polymer translocation. However, for both of them, the barrier height of the free energy increases linearly with M. We count one of the important reasons for this accordance is that the segment of the chain in the nano-channel is considered to be self-avoiding walk both in our simulation and in theoretical calculation.

Conclusions

To summarize, we have studied the translocation of a confined polymer chain through a nano-channel by using two-dimensional lattice BFM combined with single-monomer Monte Carlo moves. We focus on the trapping stage for the chain to overcome the free energy barrier which arises from the loss of the available configurations. For a self-avoiding walk chain, the trapping time, τ_{trap}, decreases exponentially with the chain length N and so, the free energy barrier depends linearly on N. It is quite different with that predicted for the *Gaussian* chain model, in which the energy barrier is independent of N. Therefore, the excluded volume plays an important role on the translocation dynamics. However, for self-avoiding walk and *Gaussian* chain, the barrier height of the free energy both increases linearly with the nano-channel length M. One of the important reasons for this accordance is that the segment of the chain in the nano-channel is considered as self-avoiding walk in both simulation and theoretical calculations. We hope our results can enhance the understanding for complex transport processes in many biological systems.

Appendix A. Details of calculation of free energy of Gaussian chain

In this appendix, we will derive the expression of Eq. (7) for the free energy of a *Gaussian* chain with N monomers in the confinement. We wish to solve the equation

$$-\frac{\partial G_N(r,r')}{\partial N} = -\frac{l^2}{4}\nabla^2 G_N(r,r') \tag{A1}$$

where $G_N(r,r')$ is the probability that the ends of the chain are at r and r'. And, it subjects to the boundary conditions that $G_N = 0$ if r or r' is on the surfaces of the square for all values of N. The solution of Eq. (A1) is

$$\begin{aligned} P_0 &\equiv G_N(r,r') \\ &= \frac{4}{R^2}\sum_{m=1}^{\infty}\sum_{n=1}^{\infty}\sin\left(\frac{m\pi}{R}x'\right)\sin\left(\frac{n\pi}{R}y'\right)\sin\left(\frac{m\pi}{R}x\right)\sin\left(\frac{n\pi}{R}y\right) \\ &\quad\times\exp\left[-(m^2+n^2)\pi^2\left(\frac{Nl^2}{4R^2}\right)\right] \end{aligned} \tag{A2}$$

where R is the dimension of the square. Averaging over all possible locations of r' in the square, we have

$$\begin{aligned} \langle P_1\rangle &\equiv \int_0^R\int_0^R G_N(r,r')\mathrm{d}x'\mathrm{d}y' \\ &= \frac{4}{R^2}\sum_{m=1}^{\infty}\sum_{n=1}^{\infty}\left[\frac{(-1)^{m+1}+1}{m}\right]\left[\frac{(-1)^{n+1}+1}{n}\right]\sin\left(\frac{m\pi}{R}x\right)\sin\left(\frac{n\pi}{R}y\right) \\ &\quad\times\exp\left[-(m^2+n^2)\pi^2\left(\frac{Nl^2}{4R^2}\right)\right] \end{aligned} \tag{A3}$$

If one end of the chain is anchored at a distance a, comparable to l, away from the entrance of the nano-channel, while the other end can be anywhere inside the square, the probability P_a of realizing all configurations follows from Eq. (A3) with $x = R - a$ and $y = R/2$ as

$$\begin{aligned} P_a &= \frac{4}{\pi^2}\sum_{m=1}^{\infty}\sum_{n=1}^{\infty}\left[\frac{(-1)^{m+1}+1}{m}\right]\left[\frac{(-1)^{n+1}+1}{n}\right] \\ &\quad\times\sin\left(\frac{m\pi}{R}a\right)\sin\left(\frac{n\pi}{2}\right)\exp\left[-(m^2+n^2)\pi^2\left(\frac{Nl^2}{4R^2}\right)\right] \end{aligned} \tag{A4}$$

The entropy S_a of the *Gaussian* chain with confinement is given by $S_a = k_B \ln P_a$. Therefore, the free energy of the *Gaussian* chain $F_a(= -TS_a)$ follows from Eq. (A4) as

$$\begin{aligned} \frac{F_a}{k_BT} &= \epsilon - \ln\left[\frac{4}{\pi^2}\sum_{m=1}^{\infty}\sum_{n=1}^{\infty}\left[\frac{(-1)^{m+1}+1}{m}\right]\left[\frac{(-1)^{n+1}+1}{n}\right]\right. \\ &\quad\left.\times\sin\left(\frac{m\pi}{R}a\right)\sin\left(\frac{n\pi}{2}\right)\exp\left[-(m^2+n^2)\pi^2\left(\frac{Nl^2}{2R^2}\right)\right]\right] \end{aligned} \tag{A5}$$

where $\epsilon = \ln z$, z is the effective coordination number inside the square.

The first term in Eq. (A5) is exponentially larger than all subsequent terms as m and n become large. We expect to use the first term to replace this infinite sum (ground-state-dominance approximation). If we make this approximation, F_a becomes

$$\frac{F_a}{k_BT} = \epsilon - \ln\left[\frac{16}{\pi^2}\sin\left(\frac{\pi a}{R}\right)\exp\left(-\pi^2\frac{Nl^2}{2R^2}\right)\right] \tag{A6}$$

Since $a \ll R$, expanding Eq. (A6) in a Taylor's series and neglecting the high-order terms, we obtain the free energy expression for a *Gaussian* chain with one end located at the entrance of the nano-channel

$$\frac{F_a}{k_BT} = \epsilon - \ln\left[\frac{16a}{\pi R}\exp\left(-\pi^2\frac{Nl^2}{2R^2}\right)\right] \tag{A7}$$

If m monomers have inserted into the nano-channel, the free energy of the *Gaussian* chain $F_a(m)$ is

$$\frac{F_a(m)}{k_BT} = \frac{N\pi^2l^2}{2R^2} + m\left(\epsilon - \frac{\pi^2l^2}{2R^2}\right) - \ln\left(\frac{16a}{\pi R}\right) \tag{A8}$$

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