

TRANSLOCATION OF A PROTEIN-LIKE CHAIN THROUGH AN INTERACTING CHANNEL*

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Abstract The effect of channel-protein interaction on the translocation of a protein-like chain through a finite channel under certain electric field was studied by using dynamical Monte Carlo simulations. The interior behavior of chain conformation under different interactions was investigated, such as the number of monomers outside of channel n_{out} , monomers inside of channel n_{in} , mean-square radius of gyration $\langle S^2 \rangle$ and the average energy $\langle U \rangle$. It shows that with strong attractive interaction, the translocation is more difficult than moderate interaction. At the same time, the dependence of translocation time with different interactions shows that moderate repulsive interaction ($\varepsilon_{\text{cp}} = 0.5$) accelerates the translocation. Although the waiting time for successful translocation of $\varepsilon_{\text{cp}} = 1.0$ is the longest, the average translocation time is not very large. It is far smaller than that of $\varepsilon_{\text{cp}} = -1.0$. The probability distributions of translocation time $p(t')$ and the probability distributions of three duration times $p(t_1')$, $p(t_2')$ and $p(t_3')$ were all discussed. Log-normal distributions are found. All these findings will strengthen the understanding of protein translocation.

Keywords: Translocation; Protein-like chain; Dynamical Monte Carlo simulation.

INTRODUCTION

Translocation of biopolymers such as DNA, RNA and proteins across nanopores or channels plays an important role in many biological processes. For example, translocation of DNA and RNA across nuclear pores, DNA packaging into a shell during viral replication, gene swapping through bacterial pili, virus infection of cells, translocation of protein through membrane channels^[1, 2] and translocation of nascent proteins inside the ribosomal tunnel or across the endoplasmic reticulum^[3–6]. Moreover, the translocation processes have various potential technological applications, such as rapid DNA sequencing, gene therapy, controlled drug delivery, etc^[7–9].

In order to understand the physics of the fundamental biological processes, there are a considerable number of theoretical^[10–14] and simulation studies^[15–28]. In the theoretical studies, the translocation process is approximated as a one-dimensional diffusion over a potential barrier and that polymers are in equilibrium during translocation process. Sung and Park^[10] described the process with a Fokker-Planck equation of the probability distribution function of translocation monomers and assumed constant chain diffusivity. Muthukumar^[11, 12], Kong^[13] and Slonkina and Kolomeisky^[14] used the nucleation theory to investigate the translocation problem. The translocation time depends on many factors, such as chemical potential gradient, polymer configuration entropy, diffusion coefficient and the interaction between polymers and pores. In the other hand, a number of simulation studies^[15–28] on the translocation process are explored under an applied external field^[15–21], chemical

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potential gradient^[20, 22], confinement^[23], absorption^[24] and unbiased translocation^[21, 25–28]. In these studies, the dependence of translocation time on polymer chain length is preferentially considered. Additionally, the dependence of translocation time on the simulation temperature and the pore size is also investigated.

However, in these studies, the complicated biological environments and boundary conditions existing in the actual polymer translocation are neglected or seriously simplified. Therefore, the biopolymer translocation had attracted a large number of scientists. As is known, proteins are compact polymers^[29]. Zhang *et al.* have investigated the translocation of compact chains on the simple-cubic lattice by PERM method^[30, 31]. The attractive interaction between the channel and compact polymer is considered. However, repulsive channel is not investigated. In another work, free energy barrier was shown in the study of compact polymers escaping from a small sphere through a hole^[32]. It is in accordance with theoretical study. In the same time, the group also use ODI model and PERM method to simulate protein-like chain escape from a finite channel^[33]. An energy barrier is found in that work. However, no free energy barrier is found. And the influence of channel-protein interaction was not mentioned. Some experiments implied that the interaction might play an important role in the translocation of chain through small pore or narrow channel^[7, 34, 35]. And some simulation also showed the importance of interaction in translocation^[36, 37]. For instance, Luo and his coworkers investigated that a moderate attractive pore-polymer interaction accelerates the translocation of chain^[36]. At weak interaction region, the chain is trapped at the entrance while at strong interaction region, the chain is trapped at the exit of nanopore^[37]. However, translocation time as a function of interaction energy is mainly discussed. Change the point of view, this work concentrates on investigating the interior change of protein-like chain in the process of protein translocation through an interacting channel. And the effect of the channel-protein interaction on the translocation of a protein-like chain is also presented. We use dynamical Monte Carlo method^[39, 40], based on our previous model (modified ODI model)^[40, 41] to study the translocation process.

METHOD OF CALCULATION

In our simulations, the modified ODI model^[40, 41] is used to simulate protein-like chain, which builds on the ODI Model^[42] (Orientation-Dependent Monomer-Monomer Interactions). Within this model, a protein-like chain is schematically viewed as a linear sequence and the chains are constrained by nearest-neighbors on a three-dimensional cubic lattice. And each lattice site can only be occupied by one monomer. The merit of our model is α -helical and β -sheet structures can be taken into account simultaneously. Therefore, the model is much closer to the real protein. In the model, the energy of protein-like chain is assumed to contain four terms:

$$U = \sum_{|i-j| \geq 3} \varepsilon_c \delta(r_{ij} - a) + \sum_{\substack{|i-j| \geq 3 \\ \vec{r}_i + \vec{s}_i = \vec{r}_j}} \varepsilon_b \delta(r_{ij} - a) + \sum_{i=1}^{N-1} A(\vec{s}_i \cdot \vec{s}_{i+1}) + \varepsilon_h n_h \quad (1)$$

where r_{ij} is the distance between monomers i and j . a is the lattice spacing (in fact, $a = 1$ in our calculation). Here $\delta(x) = 1$ for $x = 0$, and $\delta(x) = 0$ for $x \neq 0$. The unit vector $\vec{s}_i$ represents the orientation of monomer, and $(\vec{s}_i \cdot \vec{s}_{i+1})$ is a scalar product of the orientation vectors. ε_c is the energy of one contact. Monomer i and j will form a contact if the two monomers are at adjoining lattice sites while not adjacent along the chain. The first term of Eq. (1) represents the total contact energy of the chain. ε_b corresponds to the hydrogen bonds in topological contacts. Bearing in mind the conditions necessarily for formation of hydrogen bonds, we consider that the values of ε_b is negative if (i) one of the monomers is directed toward the other monomer (e.g., $\vec{r}_i + \vec{s}_i = \vec{r}_j$), and (ii) simultaneously the vectors $\vec{s}_i$ and $\vec{s}_j$ are parallel. In all the other cases, $\varepsilon_b = 0$. In fact, we consider the second term of Eq. (1) to be β -sheet energy. The third term (with $A > 0$), constructed in analogy with the Ising antiferromagnetic spin-spin interaction, describes the orientational dependence of the interaction between nearest-neighbor monomers linked *via* the peptide bonds. Its goal is to reproduce an antiparallel orientation of nearest-neighbor monomers. In the last term, ε_h is the energy of one helix, n_h is the number of helix in the chain, $\varepsilon_h n_h$ represents the total energy of helix. Therefore, the α -helical and β -sheet energy are both considered in the conformational energy. In this paper, we fix $\varepsilon_c = -0.5$, $\varepsilon_b = -0.5$, $A = 0.5$ and $\varepsilon_h = -0.5$ (in units of kT).

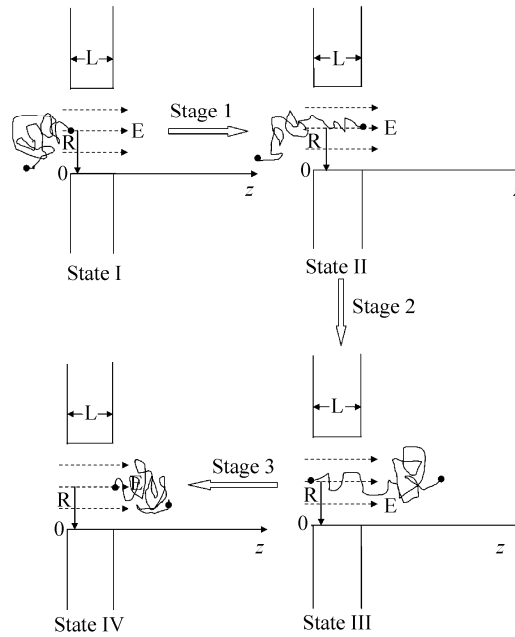


Fig. 1 Three stages of translocation for a protein-like chain through a finite channel from left to right part along z -axis
Here $R = 5$, $L = 5$; Solid filled circles represent the head and the end monomers of the chain.

Figure 1 shows four states of a protein-like chain through a finite channel. The radius of the channel R is 5, and the length of the channel L is 5. The chain length N is 100. The external driving force is modeled as a potential difference which gives rise to an electric field $E = 1.0$. The potential is expressed as^[15]

$$U_e = \begin{cases} 0, & z < 0 \\ -Ez, & 0 \leq z \leq L \\ -EL, & z > L \\ \infty, & \text{otherwise} \end{cases} \quad \text{and} \quad x^2 + y^2 \leq R^2 \quad (2)$$

In this model, the channel walls are impenetrable, and the interaction between the monomer and the walls is expressed as ϵ_{cp} . In this paper, two attractive interaction ($\epsilon_{cp} = -1.0, -0.5$) and two repulsive interaction ($\epsilon_{cp} = 0.5, 1.0$) are investigated. At the same time, no interaction between channel and protein is also studied.

The translocation process consists of three stages^[14], as illustrated in Fig. 1. In the first stage, the protein undergoes translocation from state I where the head of the chain is at the channel entrance and the rest of the chain is out of the channel, to state II where the head is at the channel exit and the rest is at the left. The average duration time τ_1 is defined here. The second stage with duration time τ_2 in the process is from state II to state III where the end of the chain is at the entrance of channel and the rest is at the right. The final stage with duration time τ_3 is the detachment of the chain end from the entrance to the exit and the rest of chain is out of channel. The total translocation time τ is defined as duration time for the three stages. And the results are averaged over 5000 independent runs.

In this paper, dynamical Monte Carlo simulation is performed. Trial moves with a probability of acceptance $\min[e^{-\Delta U / k_B T}, 1]$ are used here, where ΔU is the energy difference between the new and old configurations^[43, 44]. In the study, the translocation time τ is measured in units of Monte Carlo step (MCS). One MCS means the average moves of every monomer at once.

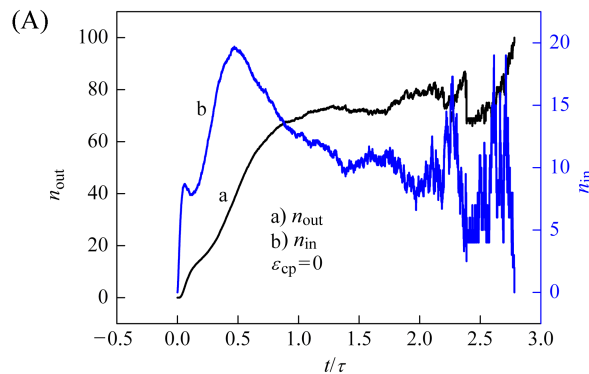
SIMULATION RESULTS AND DISCUSSION

The Interior Change of the Chain in the Translocation Process

In order to understand the different behaviors of a protein-like chain under different interactions, we have studied some interior behaviors during the translocation. Figure 2 gives the number of monomers which are out of the channel n_{out} and the number of monomers which are inside the finite channel n_{in} in the process of translocation. First, from the results of non-interacting channel in Fig. 2(A), it is shown that at translocation time $t/\tau < 1.0$, n_{out} increases fast. While, at $1.0 < t/\tau < 2.4$, n_{out} increases gradually only from 70 to 80. That is, 70% monomers of chain are out of the channel, the folding of chain outside leads the exit of channel crowded, the velocity of n_{out} increasing drops. Therefore, the chain adjusts its conformations to gain a large velocity to cross the channel. At almost $t/\tau = 2.4$, n_{out} rapidly decreases to 70. Then, n_{out} increases fast again, and successfully escape the channel at last. At the same time, the value of n_{in} has two peaks before $t/\tau = 1.0$. Especially at $t/\tau = 0.5$, n_{in} has the maximum number during the translocation. Since there is no interaction between the channel and protein, the appearance of the maximum is certainly due to the interior interaction of protein. When interior interactions act most inside the channel, the monomers inside the channel will take up the possible situation to assemble together. That is why n_{in} has a maximum at $t/\tau = 0.5$. While, with t increasing, in order to continue the translocation, and also because the electric force, the secondary structure inside the channel is destroyed. Thus, n_{in} drops. And the following fluctuations of n_{in} indicate the multiple adjustments of chain conformation in order to pass through the channel successfully.

Figure 2(B) gives the results of n_{out} and n_{in} for attractive ($\varepsilon_{\text{cp}} = -1.0, -0.5$) and repulsive ($\varepsilon_{\text{cp}} = 0.5, 1.0$) channel. It is found that the curves of n_{out} and n_{in} versus t for $\varepsilon_{\text{cp}} = 0.5$ is similar to $\varepsilon_{\text{cp}} = 0$. And it is described in detail above. For $\varepsilon_{\text{cp}} = -0.5$, the translocation is also very favorable. The adjustment of chain conformation is not deep as $\varepsilon_{\text{cp}} = 0$ or $\varepsilon_{\text{cp}} = 0.5$, because the value of n_{out} does not decrease rapidly in the process. It is concluded that weak attractive or repulsive interaction do not affect the translocation process very much.

However, for strong attractive ($\varepsilon_{\text{cp}} = -1.0$) channel, n_{out} first increases fast at the beginning of translocation ($t/\tau < 0.8$), then increases gradually at $0.8 < t/\tau < 3.7$. There exits a speedy decrease of n_{out} to 40, but the value of n_{out} stands around 40 for a long time. It can be found a long plateau in the curves of n_{out} . We think the plateau forms because of the strong attractive interaction with channel and protein. The attractions of monomers with channel surfaces prevent it going out of channel. Therefore, the number of n_{out} keeps for a certain time. However, the interaction of channel and protein is no stronger than the electric field, the chain finally successfully cross through the channel. It is investigated that n_{out} rises quickly to 100 at last, which means the translocation is just over. It is obvious that the translocation time for $\varepsilon_{\text{cp}} = -1.0$ is much larger than that for $\varepsilon_{\text{cp}} = -0.5$ and $\varepsilon_{\text{cp}} = 0.5$. That is because the chain is trapped at the exit. For a strong repulsive channel ($\varepsilon_{\text{cp}} = 1.0$), the curves of n_{out} and n_{in} are quite different from the others considering above. n_{out} first increases to 75 at about $t/\tau = 1.8$, then decreases to 0 at $t/\tau < 4.5$. For an amount of time, n_{out} keeps zero. Till t/τ is equal to about 117.0, the value of n_{out} increases quickly to 100. For the curves of n_{in} , it first increases to about 20, then decreases to zero.



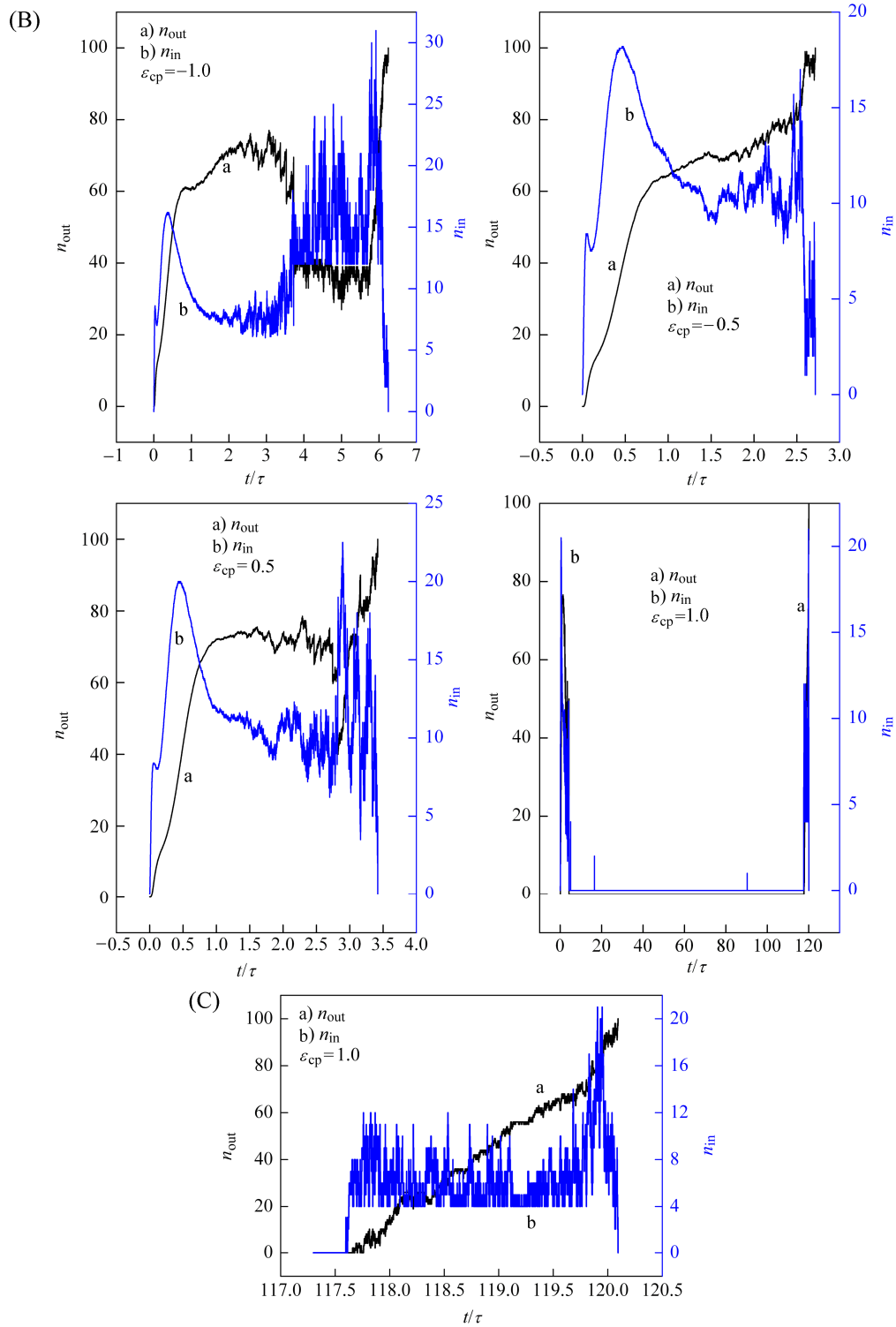


Fig. 2 The number of monomers out of the channel n_{out} and in the channel n_{in} as a function of translocation time t/τ for protein-like chains with no interaction between channel and protein-like chain (A), with different channel-protein interactions $\epsilon_{cp} = -1.0, -0.5, 0.5, 1.0$ respectively (B) and the magnified picture in the range of $117.0 < t/\tau < 120.5$ of $\epsilon_{cp} = 1.0$ (C)

Before the last successful escape, value n_{in} is always zero except two small values which are found in the waiting process. At last, n_{in} increases then drops to zero. This represents the successful translocation. Why is the trend of curves such different from the others? We suggest that for strong repulsive channel, because of electric force, the chain starts to cross the channel. For about $n_{out}=75$, due to strong repulsive interaction between the chain and channel, the exit of the channel is crowded with monomers. And the repulsive interaction turns around to affect the chain to move back. During the process, the repulsive interactions are in existence. Finally the total chain is pulled back to the left space of entrance. Before the final successful translocation, it can be also seen from the figure that there are several trial events. Some short values of n_{in} just represent the trials. In order to explore the final successful translocation, we magnify the range of $117.0 < t/\tau < 120.5$ in the figure of $\varepsilon_{cp} = 1.0$. And the figure is shown in Fig. 2(C). For the final trial, it can be investigated that n_{out} increases from zero to 100 with large velocity. That is shown when the chain has a successful translocation process, the time of the process is not long because the repulsive interaction will accelerate the translocation process. It is also found that value n_{in} increases first, then the value keeps around 4–8 monomers. The number is quite smaller than the other four interactions. Due to the strong repulsive, the monomers in the channel are difficult to form compact secondary structure. Therefore, the monomers inside the channel will not have the compact structure as that of $\varepsilon_{cp} = -1.0, -0.5, 0$ and 0.5 . Finally, as the exit is crowded, the chain has to adjust its conformation. So n_{in} has to increase. When the chain has a suitable conformation, the chain crosses through the channel successfully. Therefore, n_{in} drops to 0 and n_{out} reaches to 100.

Figure 3 show the mean-square radius of gyration $\langle S^2 \rangle$ versus t/τ for $\varepsilon_{cp} = -1.0, -0.5, 0, 0.5$ and 1.0 . For non-interacting channel, $\langle S^2 \rangle$ increases then has a peak before $t/\tau = 1.0$. And it is found that the situation of the peak occurs before the peak of n_{out} . Then at $1.0 < t/\tau < 2.4$, $\langle S^2 \rangle$ has some fluctuations around 20, which are corresponding to the platform of Fig. 2(A). After $t/\tau > 2.4$, the value of $\langle S^2 \rangle$ has a quick increase then drops. It is shown that the structure of the chain becomes looser. However, during the later translocation, the structure becomes compact. From Fig. 3(b), the trend of $\langle S^2 \rangle$ for $\varepsilon_{cp} = 0.5$ is similar to that for $\varepsilon_{cp} = 0$. For moderate attractive interaction ($\varepsilon_{cp} = -0.5$), the peak before $t = 2000$ mcs is also found. However, $\langle S^2 \rangle$ of the protein-like chain does not have the quick increase at the end of translocation. For strong attractive interaction ($\varepsilon_{cp} = -1.0$), the large fluctuation of $\langle S^2 \rangle$ is derived from the strong attractions between channel and chain. For strong repulsive channel ($\varepsilon_{cp} = 1.0$), before the successful translocation, the value of $\langle S^2 \rangle$ has large fluctuations. However, at last, $\langle S^2 \rangle$ increases fast to about 100 and then drops to the natural value. Due to the large repulsive interaction, the chain is relatively flat and the value of $\langle S^2 \rangle$ is relatively large.

We now discuss the change of average energy $\langle U \rangle$ in the translocation process. From Fig. 4(a), it is investigated that average energy decreases firstly. At $1.0 < t/\tau < 2.4$, $\langle U \rangle$ has a slight decrease. Following, there is a sudden increase which is corresponding to Fig. 2(a). The trend of curve for $\varepsilon_{cp} = 0.5$ is similar to Fig. 4(a). However, no obvious mutation of $\langle U \rangle$ is found in $\varepsilon_{cp} = 0.5$. That is also suggested the channel-protein interaction $\varepsilon_{cp} = -0.5$ is suitable to protein translocation cross the channel. However, for strong interactions ($\varepsilon_{cp} = -1.0$ or $\varepsilon_{cp} = 1.0$), $\langle U \rangle$ has a plateau in the translocation process. That is also accordant with the results of n_{out} . For strong attractive channel, $\langle U \rangle$ decreases quickly before $t/\tau = 0.5$. At $0.5 < t/\tau < 3.5$, $\langle U \rangle$ changes little. With an increasement following, the value of $\langle U \rangle$ keeps at about -250 to -200 . The plateau means the adjustment of conformations to across the channel. Lastly, after $t/\tau > 5.7$, $\langle U \rangle$ drops quickly again. However, for strong repulsive channel, $\langle U \rangle$ has a “V” shape at first. The bottom of “V” means there are some monomers out of the channel. The exit is very crowded. At the same time, strong repulsive interaction makes the chain go back to the channel entrance. Then the value of $\langle U \rangle$ increases. The long plateau of $\langle U \rangle$ is corresponding to the waiting time of the chain at the left of entrance to prepare translocation. With the last successful translocation, $\langle U \rangle$ quickly drops. The plateaus occurred in the figures of $\varepsilon_{cp} = -1.0$ and $\varepsilon_{cp} = 1.0$ are not entirely identical.

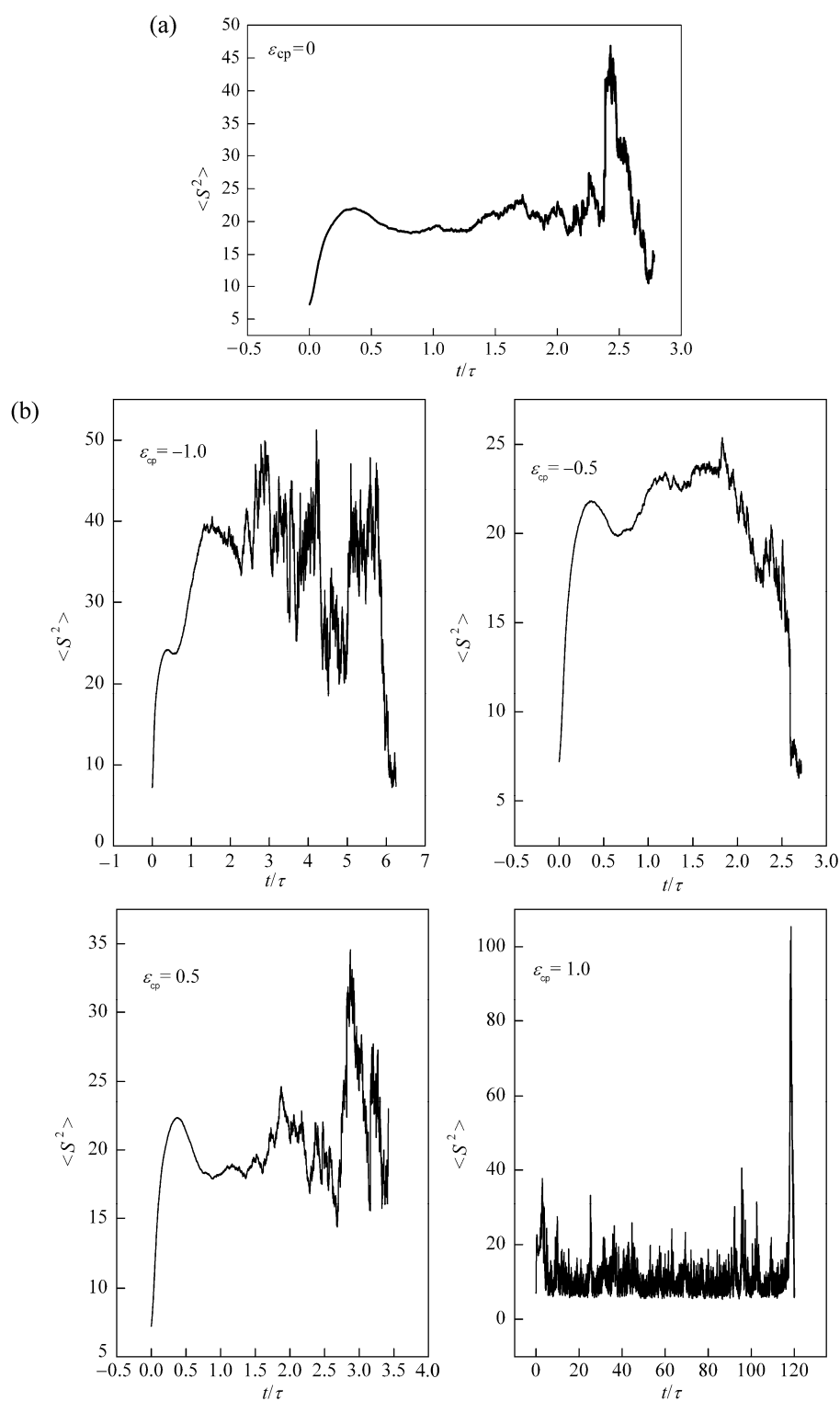


Fig. 3 The mean-square displacement $\langle S^2 \rangle$ as a function of translocation time t/τ for protein-like chains with no interaction between channel and protein-like chain (a) and with different channel-protein interactions $\epsilon_{cp} = -1.0, -0.5, 0.5, 1.0$, respectively (b)

Combined with the results of Fig. 2, it is easy to find that the former plateau of $\varepsilon_{cp} = -1.0$ means a waiting stage during translocation. Parts of the chain are out of the channel. However, the later plateau of $\varepsilon_{cp} = 1.0$ corresponds to the waiting time of the chain to have a successful translocation, and the chain is all at the left of the exit.

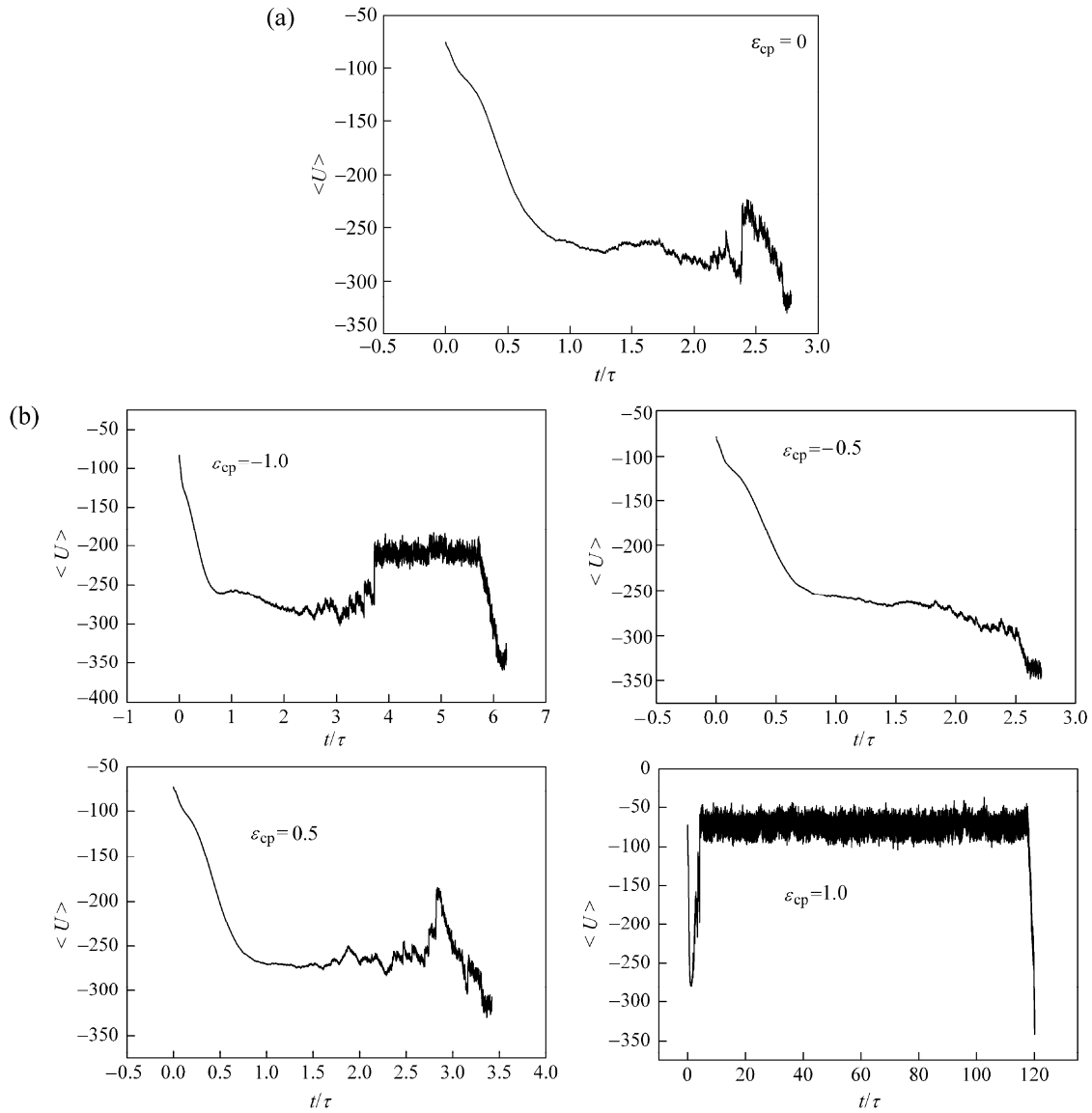


Fig. 4 Average energy $\langle U \rangle$ as a function of translocation time t/τ for protein-like chains with no interaction between channel and protein-like chain (a) and with different channel-protein interactions $\varepsilon_{cp} = -1.0, -0.5, 0.5, 1.0$, respectively (b)

Translocation Time for Different Interacting Channels

The dependences of the average translocation time τ , the duration time τ_1 , τ_2 , τ_3 of the three stages with different channel-protein interaction ε_{cp} are presented in Fig. 5. It is found the behavior of τ_2 is similar to that of the average translocation time τ . For the five interactions $\varepsilon_{cp} = -1.0, -0.5, 0, 0.5$ and 1.0 , translocation time τ and duration time of the second stage τ_2 has a minimum at a repulsive interaction $\varepsilon_{cp} = 0.5$. While for more repulsive channel ($\varepsilon_{cp} = 1.0$), the translocation time τ and τ_2 both are slightly larger than those of $\varepsilon_{cp} = 0.5$. However, for

attractive and non-interacting channels, translocation times τ and τ_2 are all larger than those of $\varepsilon_{cp} = 0.5$ and they increase with the increase of the attractive strength. τ_1 is the average duration time of stage 1 and τ_3 is the average duration time of stage 3 which are described in Fig. 1. These two stages spend less time than the second stage. Therefore, the total translocation time τ is mainly determined by τ_2 . At the same time, we find the duration time τ_1 of $\varepsilon_{cp} = 1.0$ is relatively larger than that of the other four interactions. The reason maybe that repulsive channel will prevent the chain into the channel. However, the duration time τ_3 is just reversed. The average time of the final stage τ_3 of $\varepsilon_{cp} = -1.0$ is larger than that of the others. When the tail of the chain cross through the channel, attractive interaction of channel and protein will draw back the chain, and the time for the escape stage will be longer.

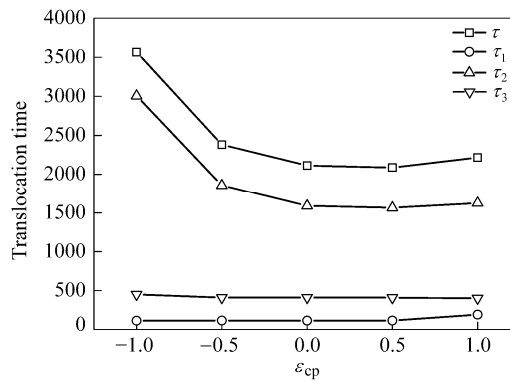


Fig. 5 The dependences of the average total translocation time τ and the duration time τ_1 , τ_2 , τ_3 of the three stages on the channel-protein interaction ε_{cp}

The Probability Distribution of Translocation Time $p(t')$

Probability distributions $p(t')$ of translocation time t' are counted for non-interacting channel ($\varepsilon_{cp} = 0$), attractive channels ($\varepsilon_{cp} = -0.5, -1.0$) and repulsive channels ($\varepsilon_{cp} = 0.5, 1.0$), respectively. Figure 6 (a) gives the probability distributions $p(t')$ versus $\ln t'$ for $N = 100$. For convenience, the variable $t' = t/\tau$ is introduced and x-coordinate variable is $\ln t'$. Where τ is the total translocation time of protein through the finite channel. It is found that the distribution $p(t')$ approaches a log-normal distribution type as

$$p(t') = \frac{1}{\sqrt{2\pi}\sigma'} \exp\left[-\frac{(\ln t' - \mu)^2}{2\sigma'^2}\right] \quad (3)$$

Here μ and σ are parameters determining the distribution. For non-interacting channel ($\varepsilon_{cp} = 0$), $\mu = -0.10$ and $\sigma = 0.52$. For $\varepsilon_{cp} = -1.0, -0.5, 0.5$ and 1.0 , the probability distributions is log-normal distribution with different parameters $\mu = -0.28, \sigma = 0.56, \mu = -0.15, \sigma = 0.56, \mu = -0.09, \sigma = 0.50$ and $\mu = -0.11, \sigma = 0.51$ respectively. It shows that the mean value μ of attractive channel has deviation from zero rather than non-interacting channel and repulsive channel. Standard deviation σ is smaller for attractive channel than that for repulsive channel. The small picture on top left corner shows t_p' with different interactions. t_p' is corresponding to the maximum value of the curves. It is found that t_p' for $\varepsilon_{cp} = 0.5$ is the largest.

The probability distributions of duration times for the three stages $t_1' = t_1/\tau_1$, $t_2' = t_2/\tau_2$ and $t_3' = t_3/\tau_3$ are presented in Figs. 6(b), 6(c) and 6(d) respectively. Log-normal distributions are all found in the five interactions. The mean of the distribution of $\varepsilon_{cp} = 1.0$ is smaller than that of the others. The mean value μ is $-0.27, -0.33, -0.29, -0.28$ and -0.87 for $\varepsilon_{cp} = -1.0, -0.5, 0, 0.5$ and 1.0 . While the standard deviation σ is very close, which are $0.87, 0.88, 0.88, 0.87$ and 0.87 for the five interactions. It means the first stage of the translocation can not well distinguish the channel type. The probability of $t_2' = t_2/\tau_2$ is similar to the total time probability in Fig. 6(a). The mean value increases as $-0.37, -0.25, -0.19, -0.17$ and -0.15 when the interaction from attractive to

repulsive. And the deviation σ is 0.74, 0.75, 0.72, 0.71 and 0.72. The last distribution $p(t_3')$ is not clear as $p(t_2')$ and $p(t_1')$. The value of μ is $-0.65, -0.51, -0.49, -0.47$ and -0.45 of $\varepsilon_{cp} = -1.0, -0.5, 0, 0.5$ and 1.0 respectively. And the corresponding standard deviation σ is 1.81, 1.58, 1.47, 1.44 and 1.38.

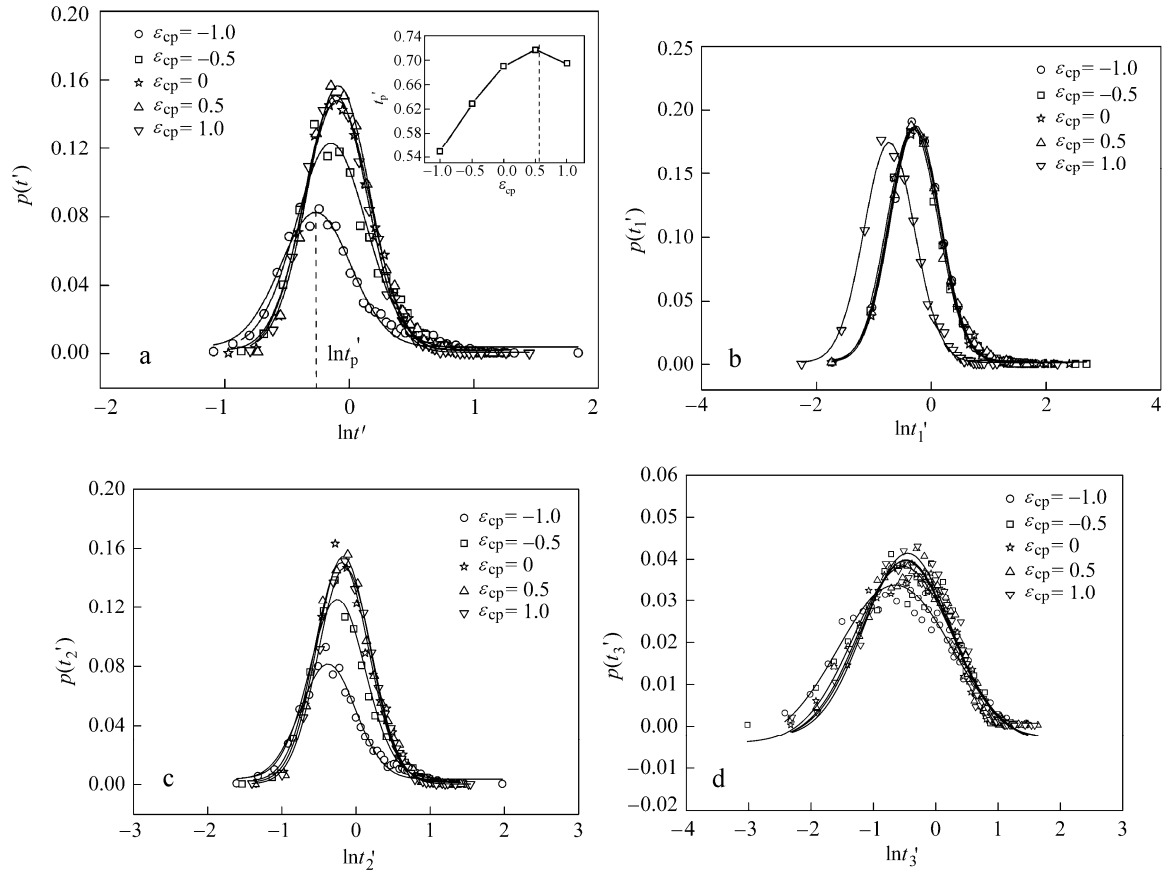


Fig. 6 Probability distribution of total translocation time $p(t')$ (a) and probability distribution of translocation time for three stages $p(t_1')$ (b), $p(t_2')$ (c) and $p(t_3')$ (d), respectively ($t' = t/\tau$, $t_1' = t_1/\tau_1$, $t_2' = t_2/\tau_2$ and $t_3' = t_3/\tau_3$)

τ is average total translocation time; τ_1 , τ_2 and τ_3 are average duration times in each stage in Fig. 1;

The solid curves are log-normal distribution functions of different channel-protein interactions ε_{cp} .

CONCLUSIONS

We have investigated the translocation of protein-like chain through an interacting channel by using dynamical Monte Carlo method. Effect of interaction of channel and protein-like chain on the translocation process is discussed. The results show that with weak interactions ($\varepsilon_{cp} = -0.5$ and 0.5) the translocation is smoothly. While for large attractive interaction ($\varepsilon_{cp} = -1.0$), There is a period of time for the chain waiting for crossing the channel successfully. And for large repulsive interaction ($\varepsilon_{cp} = 1.0$), the waiting time for successful translocation is quite long. These findings are studied with the calculation of n_{out} , n_{in} , $\langle S^2 \rangle$, $\langle U \rangle$ in the process of translocation. At the same time, the average translocation time τ of $\varepsilon_{cp} = 0.5$ has a minimum value, it is smaller than that of $\varepsilon_{cp} = -1.0, -0.5, 0$ and 1.0 . And the time of $\varepsilon_{cp} = -1.0$ is the largest. Since we divide the translocation process into three stages, the duration time of stage 2 τ_2 has the similar trend to τ . While the time τ_1 of $\varepsilon_{cp} = 1.0$ is the largest, and the time τ_3 of $\varepsilon_{cp} = -1.0$ is the largest. The probability distributions of translocation time $p(t')$ and the probability distributions of three duration times $p(t_1')$, $p(t_2')$ and $p(t_3')$ are all discussed. Log-

normal distributions are found. The results are in agreement with the former conclusions. Lastly, the maximum time t_p' of probability distribution $p(t')$ with different interactions shows that t_p' has a peak at $\varepsilon_{cp} = 0.5$. It is also proved that the channel-protein interaction $\varepsilon_{cp} = 0.5$ is the proper interaction for this model. It gives us an important guidance to our future research work.

However, many questions remain unanswered. We will focus on in the future about the effect of the channel length, the channel radius, electric strength and so on. All these works will deepen the understanding of protein translocation.

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