Diffusion of supercoiled DNA and the effect of base-flipping by Brownian dynamics

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Abstract: We have evaluated the diffusion constant of a ladder-like model of supercoiled DNA (see figure) in solution through Brownian dynamics with both hydrodynamic and excluded volume effects. After twisting the ladder we connect the ends so that its linking number \( L_k \) is conserved. We found that the diffusion constant is a linear function of \( L_k \). In order to study the effect of base-flipping we disconnect the FENE spring potential that connects one of the pairs. The diffusion constant of the model with base-flipping becomes smaller especially when we take into account the angle potential.

1. Introduction

We make a ladder-like model (see above figure) of supercoiled DNA. We connect the ends of the ladder after twisting it. The linking number \( L_k \) is conserved for the model. With the model, we investigate the relation between the diffusion constant and the linking number. We have evaluated the diffusion constants of the model in solution by Brownian dynamics with both hydrodynamic and excluded volume effects. We found that the diffusion is a linear function of \( L_k \). Randall et al suggest that one of the hydrogen bond that connects the base-pairs may disappear in all atom simulations of underwound DNA. It is called “base-flipping”. We examine the effect of base-flipping on diffusion. We disconnect the FENE spring potential that connects one of the pairs. The diffusion constant becomes smaller when we assume base-flipping. The diffusion constant becomes much smaller when we employ the angle potential.
2. Results

Figs 1 and 2 show the graphs of the diffusion constant and the squared gyration radius versus linking number $L_k$ fitted with $a+bL_k$ where $a$ and $b$ are fitting parameters. We found that the diffusion constant and the squared gyration radius are linear functions of $L_k$. The diffusion constant should be small for the model with large squared gyration radius.

![Graphs showing diffusion constant and squared gyration radius versus linking number.](image)

We evaluated the diffusion and squared gyration radius when we disconnect the FENE spring potential that connects one of base-pairs (we call the model $bf=1$). We call the model with no base-flipping “nbf”. The diffusion constant and squared gyration radius of $bf=1$ model become smaller than those of the nbf model. Figs 3 and 4 show the diffusion constant and the squared gyration radius versus the $L_k$ under the angle potential. The squared gyration radii of both models are almost the same. The difference of diffusion constants between the two models becomes larger than that of the model with no angle potential.

![Graphs showing diffusion constant and squared gyration radius versus linking number under angle potential.](image)

3. Conclusions

We make the ladder-like model where the linking number is conserved. We evaluated the diffusion constant against linking number $L_k$. We examined the effect of base-flipping and found that the diffusion constant becomes smaller for the model with base-flipping.

References


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