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Single-strand DNA molecule translocation through nanoelectrode gaps

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Abstract
Molecular dynamics simulations were performed to investigate the translocation of single-strand DNA through nanoscale electrode gaps under the action of a constant driving force. The application behind this theoretical study is a proposal to use nanoelectrodes as a screening gap as part of a rapid genomic sequencing device. Preliminary results from a series of simulations using various gap widths and driving forces suggest that the narrowest electrode gap that a single-strand DNA can pass is $\sim$1.5 nm. The minimum force required to initiate the translocation within nanoseconds is $\sim$0.3 nN. Simulations using DNA segments of various lengths indicate that the minimum initiation force is insensitive to the length of DNA. However, the average threading velocity of DNA varies appreciably from short to long DNA segments. We attribute such variation to the different nature of drag force experienced by the short and long DNA segments in the environment. It is found that DNA molecules deform significantly to fit in the shape of the nanogap during the translocation.

1. Introduction
Recently, we proposed a novel technique for detecting single molecules rapidly on a massive scale. The method uses a nanoelectrode gap as a screen and the identity of a molecule (or residue) could be recognized when it threads the gap by measuring the molecule-specific conductance property \cite{1, 2}. This technique is proposed as one of the next-generation DNA sequencing tools \cite{3}. The idea is that when a DNA molecule translocates through the nanogap, its sequence could be measured base by base as if one were looking through a strip of movie film. Theoretically, it has the potential to perform DNA sequencing at a rate thousands of times faster than the current technology, which is based on Sanger’s ‘dideoxy’ protocol \cite{4}.

However, before the proposed technique can be experimentally realized, there are a few fundamental questions that can be addressed by theoretical modeling. One of the primary concerns is the distinguishability of the conductance properties of the four types of nucleotides (A, C, G, T) that are comprised of DNA. Several first-principles studies have been performed on this topic and the conclusion is still under debate \cite{5–7}.

Several other fundamental questions on the design of the proposed device are within the regime of investigation through classical molecular dynamics (MD) modeling. The first question is how narrow the nanoelectrode gap should be fabricated. Previous simulations on the translocation of DNA through nanopores indicate that a single-strand DNA (ssDNA) segment can be driven through a pore with diameter of less than 2 nm \cite{8, 9}. In the device we propose, a narrow gap is preferred because it allows a better control of base-by-base translocation. If the gap is too wide, DNA molecules may pass the gap in folded conformation and the conductance characteristics due to each base would be indistinguishable. On the other hand, the gap should be wide enough to allow the DNA segment to go through smoothly. Therefore, it is crucial to know the limits of the nanogap width that an ssDNA can be driven through.

The second issue is the minimum force required to drive the DNA molecule through the nanogap. An electric field is usually utilized in experiments to drive the DNA molecules due to the net charge on each nucleotide. One recent experimental study indicates that a field as low as 24 mV nm$^{-1}$ is sufficient to drive an ssDNA segment through a 1.8 nm protein pore (alpha-hemolysin) \cite{10}. However, it is unclear about the
minimum force required to force an ssDNA through a metallic nanogap in aqueous environment.

Lastly, the conformation of nucleotides confined between the gap is important input information for the calculation of the conductance characteristics of different types of nucleotides using the first-principles simulations. MD modeling can provide such information on an atomistic level.

A variety of experimental and theoretical investigations on using an electric field to drive biopolymers through nanopores of various shapes have been performed in recent years [8, 11–22]. These studies have shown that it is possible to deliver a DNA molecule and drive it through nanopores using voltage bias. However, the fundamental questions we mentioned above still remain largely open for the particular systems we are interested in. In this paper we present some of our preliminary MD results on ssDNA translocation through nanogaps. We attempt to answer the following basic questions: (1) What is the limiting gap width for a single-strand DNA to go through with a mechanical pulling force? (2) What is the minimum force required in order to pull/push the DNA through the gap? (3) What conformational change is experienced by the DNA during the translocation?

2. Simulation method

The single-strand DNA simulated in this study consists of 4–20 bases. The head-to-tail length of DNA ranges from 1.2 to 8.0 nm. The relatively short DNA segments were chosen due to considerations of computational complexity. We chose the simple form of single-type nucleotide polymers. In real applications DNA segments with mixed type of nucleotides are often used and the properties of random sequence DNA would be different from those of single-type nucleotides. Simulations of long DNA segments with random sequence will be reported in a subsequent paper. In this study most of the simulation were performed with the ssDNA of poly-C, and several simulations were also performed with poly-T, poly-G, or poly-A. Single-strand DNA segments were derived by splitting the double helices created using the utility software NUCGEN included in the AMBER packages [23].

The nanogap is composed of two FCC (face-centred cubic) nanoelectrodes, one of platinum and one of gold. Each nanoelectrode has a dimension of 2 nm by 2 nm by 3 nm. The nominal gap widths simulated were 1.0, 1.5, and 2.0 nm. We define the nominal gap width as the distance between the centers of the constriction atoms in each electrode. If the van der Waals radii of the atoms comprising the electrodes are taken into account, the effective gap width accessible to the solvent molecules is about 0.3 nm narrower than the nominal gap widths. In a typical simulation, the DNA and the electrodes were solvated in a TIP3P [24] water box consisting of about 21,000 water molecules. The initial size of the simulation box is about 11 nm by 7 nm by 9 nm. Periodic boundary conditions are applied in all three directions. Na+ counter ions are introduced to electrically neutralize the system.

The DNA and ions were modeled by the AMBER force field 1999 version [23]. The gold and platinum atoms in the electrodes were modeled by the universal force field potentials [25]. The Lennard-Jones interaction between different species were calculated by the standard Lorentz–Berthelot mixing rules with a 0.9 nm spherical cutoff without long-range corrections. The TIP3P water model was chosen, based on previous simulation works [26, 27]. The particle-mesh Ewald method with a fourth-order interpolation and direct space summation tolerance of $10^{-6}$ was applied to evaluate the electrostatic interactions.

Molecular dynamics simulations were performed within the constant-pressure (1 bar) and constant-temperature (300 K) ensemble [28]. The NAMD [29] software package was employed to integrate the equations of motion. The electrode atoms were kept fixed throughout the simulations. A typical simulation run included 10,000 steps of energy minimization using a conjugate gradient algorithm, followed by gradual heating from 0 to 300 K in 3 picoseconds (ps), 5 ps of molecular dynamics solvent relaxation, 100 ps of constraint-free equilibration, and 3–15 ns of production. A time step of 2 fs was used. The SHAKE [30] algorithm was applied to constrain the bonds involving hydrogen atoms. The structural configurations were collected every 1 ps for subsequent analysis. Visualizations and trajectory analysis were performed using the VMD software package [31].

3. Results and discussion

3.1. Minimum width of the electrode gap

We have performed simulations of translocation of ssDNA through nanogaps under the influence of mechanical pulling force. Pulling the ssDNA by a mechanical force is an idealized concept that is hard to achieve in experiments. But obviously mechanical pulling is more efficient than the electric field commonly used in experiments to drive the DNA towards a target location because mechanical force can be focused specifically on the atoms or residues of interest. By modeling the idealized ‘pulled’ translocation we can obtain reliable information on the minimum gap width that ssDNA can thread.

The nominal gap widths we tried were 1.0–2.0 nm, corresponding to effective gap widths of about 0.7–1.7 nm, after taking into account the excluded volume due to repulsive solution–electrode interactions. In our simulations the ssDNA was initially placed near the gap, with the axis of the DNA parallel to the gap channel and the 3’ end towards the center of the gap entrance. The closest distance between the end base ring and the entrance is about 0.3 nm. Mechanical force ranging from $f = 0.2$ nanoNewton (nN) to 0.9 nN were applied to the base near the entrance (1/3 $f$ is applied to atoms C2, C4, and C6 in the base ring respectively) along the gap channel direction. We note that such a pulling strategy focuses the force on one end of the DNA segment and was proved to be most efficient. We also tried applying the pulling forces on the negatively charged oxygen atom in the phosphate group, or distributing the force evenly on the backbones, which turned out to be not as efficient.

The series of ‘pulling’ simulations indicate that the minimum gap width an ssDNA can be forced through is about 1.5 nm (gap width hereafter refers to the nominal width if not stated specifically). We failed to thread the ssDNA through the 1.0 nm gap even with the pulling force increased beyond 1.0 nN. In this case, the DNA segment sticks at the entrance
and never enters the gap. Using a short ssDNA segment (for example, ssDNA with only four nucleotides) did not help. One extreme trial was made by carefully inserting the end-base tip of the ssDNA into the gap before applying the pulling force. Under such an artificial setup, an ssDNA molecule can be occasionally pulled through the 1.0 nm gap. However, such a critical requirement (i.e., having the base tip pre-inserted in the gap) is essentially impractical in experiments. Therefore, we conclude that forcing an ssDNA through a rigid 1.0 nm metallic gap is unlikely in practice.

On the other hand, we found that an ssDNA molecule can be pulled through a 1.5 nm electrode gap without much difficulty. A pulling force of 0.3 nN on the end base is sufficient to facilitate the translocation within 3 ns. One typical pulled translocation of ssDNA through the 1.5 nm gap is illustrated in the simulation snapshots shown in figure 1.

In contrast to the results from mechanical pulling, simulations using an electric field as the driving force indicate that forcing an ssDNA through the 1.5 nm gap by voltage bias is difficult to achieve if the DNA end is not placed inside the gap initially. Increasing the driving voltage does not help. In particular, it is very difficult to push the end of the ssDNA into the gap entrance by the electric field due to the floppy nature of the ssDNA molecules. In mechanical pulling, the force is focused on the DNA end and it can efficiently guide the ssDNA into the gap. But the driving force from an electric field is evenly distributed along the DNA backbone and is much less effective in driving the ssDNA into the narrow entrance.

In order to thread the ssDNA by electrophoresis, it is necessary to place part of the DNA segment inside the gap at the beginning, or use a funnel-shaped nanopore instead of the abrupt entrance, as shown in previous simulation work [9]. Once the ssDNA is pre-positioned in the 1.5 nm gap entrance, our simulations indicate that it can thread the gap driven by a transmembrane voltage (the thickness of the electrode membrane is 2 nm) as low as 120 mV. But we did not observe any clear translocation within a simulation time of 15 ns if the transmembrane voltage is below 120 mV.

We notice that the minimum gap width (∼1.5 nm, effective width ∼1.2 nm) estimated in this work is in qualitative agreement with previous simulation work on DNA translocation through a silicon nitride pore [9, 16]. Further simulations with wider electrode gaps show that ssDNA molecules can go through a 2.0 nm gap smoothly when high enough transmembrane voltage (for example, 400 mV) is applied in the appropriate direction with the ssDNA initially placed near (not inside) the gap entrance.

3.2. Minimum force required for translocation

Searching for the minimum driving force required for ssDNA translocation through the gap was conducted by performing simulations with various pulling forces. One set of results for ssDNA polyC10 threading a 1.5 nm gap is shown in figure 2. At $t = 0$ the ssDNA head is 0.3 nm away from the gap entrance, but no part of it is inside the gap. The pulling force was applied at $t = 40$ ps. As shown in figure 2, translocation of ssDNA through the gap is successful as long as $f \geq 0.3$ nN. However, no translocation was observed within 15 ns if $f \leq 0.2$ nN. Therefore, we estimate the minimum pulling/driving force needed for the initiation of translocation within nanoseconds is in the range 0.2–0.3 nN. An interesting finding is that the minimum force ($f_{\text{min}}$) required to initiate a translocation does not depend on the length of the ssDNA. Simulations were carried out using ssDNA segments consisting of 4–20 nucleotides, but the value of $f_{\text{min}}$ estimated is consistently ∼0.3 nN. This suggests that a minimum force is required to overcome an energy barrier before the translocation is initiated. This energy barrier seems insensitive to the length of DNA used. We also found that a pulling force as low as 0.1 nN is sufficient to maintain the translocation process once the ssDNA enters the gap and the translocation is initiated.

We should point out that our simulations were performed for relatively short ssDNA (tens of nucleotides) in a short period of time. It is not clear if the same conclusion can be drawn for a much longer ssDNA over a timescale far beyond nanoseconds.

Although the minimum force needed to initiate the translocation seems independent of the DNA length, under the influence of a constant force, the average translocation velocities of DNA segments depend strongly on their lengths.

Figure 1. The process of pulling a piece of single-strand nucleotides through the 1.5 nm electrode gap. The ssDNA consists of 10 cytosine. Force is applied to the base ring of the DNA head group. The direction of the force is shown by the arrow.

Figure 2. Translocation of the ssDNA (polyC10) through a gap of 1.5 nm under the influence of different pulling forces: (a) $f = 0.9$ nN; (b) $f = 0.6$ nN; (c) $f = 0.4$ nN; (d) $f = 0.3$ nN; (e) $f = 0.2$ nN, as labeled in the figure. $\Delta y$ is the separation between the center of mass of the ssDNA and the geometric center of the gap along the force direction. Two dashed lines confine the region of the gap. Solid lines are the trajectories of the ssDNA center of mass.
where

\[ \text{the translocation.} \]

the gap. It is used in the analysis instead of the actual
by the time required for the ssDNA center of mass to pass
\[ \text{defined as the thickness of the gap membrane (2 nm) divided} \]

\[ \text{A} \]

order polyC 4

(figure 4), which is different from that for polyC 10 and polyC 20

\[ \text{dependence patterns of} \]

\[ \langle \text{figure 3}. \rangle \]

\[ \text{after the process is initiated. The average velocity} \]

\[ \langle \text{v} \rangle \]

\[ \text{varies for ssDNA with different lengths. The average} \]

\[ \text{velocities,} \]

\[ \langle \text{v} \rangle \]

\[ \text{for polyC 10 and polyC 20 as a function of the} \]

\[ \text{pulling force are shown in figure 3, and for polyC 4 in} \]

\[ \text{figure 4. Under the influence of the same} \]

\[ \text{f,} \]

\[ \langle \text{v} \rangle \]

\[ \text{follows the order polyC 4} \]

\[ \text{> polyC 10} \]

\[ \text{> polyC 20, as expected. But the} \]

\[ \text{dependence patterns of} \]

\[ \langle \text{v} \rangle \]

\[ \text{on} \]

\[ \text{f for polyC 4 is roughly linear} \]

\[ \text{figure 4), which is different from that for polyC 10 and polyC 20} \]

\[ \text{(figure 3).} \]

We attribute such differences to the different nature of
\[ \text{drag force exerted from the environment on the short and long} \]

\[ \text{ssDNA segments. The drag force on a body moving in a fluid} \]

\[ \text{medium is given by} \]

\[ \text{f}_0 = \frac{1}{2} C_d A \rho v^2, \]

\[ \text{where} \]

\[ f_0 \]

\[ \text{is the drag force;} \]

\[ C_d \]

\[ \text{is the dimensionless drag coefficient;} \]

\[ A \]

\[ \text{is the cross-sectional area perpendicular to the} \]

moving direction; \( \rho \) is the density of the fluid; and \( v \) is the

\[ \text{moving velocity of the body relative to the medium. Usually} \]

\[ \text{the drag coefficient} \]

\[ C_d \]

\[ \text{depends on the velocity of the body, viscosity of the fluid,} \]

\[ \text{the roughness of the body’s surface, etc. The} \]

\[ \text{Reynolds number} \]

\[ (Re) \]

\[ \text{has been found to be useful in} \]

\[ \text{characterizing} \]

\[ C_d \]

\[ \text{[32],} \]

\[ Re = \frac{L \rho v}{\eta}, \]

\[ \text{where} \]

\[ L \]

\[ \text{is the characteristic length of the body along the} \]

\[ \text{moving direction, such as the length of ssDNA; and} \]

\[ \eta \]

\[ \text{is the dynamic viscosity of the fluid. For small values of} \]

\[ Re \]

\[ (Re < 1), \]

\[ C_d \]

\[ \text{is inversely proportional to the velocity} \]

\[ v. \]

\[ \text{This simplifies equation (1) to} \]

\[ f_0 \approx k v, \]

\[ \text{if we assume that} \]

\[ A, \]

\[ \rho \]

\[ \text{are constants.} \]

\[ \text{For ssDNA with 4–20 bases,} \]

\[ L \approx 1.2–8 \text{ nm. The density} \]

\[ \text{of water is} \]

\[ 1 \text{ g cm}^{-3}, \]

\[ \text{and the dynamic viscosity of water at} \]

\[ 300 \text{ K is} \]

\[ 0.89 \text{ mPa s. The translocation velocity} \]

\[ v \]

\[ \text{is in the range} \]

\[ 0.02–0.3 \text{ for the systems studied. Then with} \]

\[ \text{equation (3), the acceleration of ssDNA under the influence} \]

\[ \text{of pulling force} \]

\[ f \]

\[ \text{and drag force} \]

\[ f_0 \]

\[ \text{is given as} \]

\[ \frac{dv}{dt} = \frac{f - f_0}{m} = \frac{f - kv}{m}, \]

\[ \text{where} \]

\[ m \]

\[ \text{is the mass of ssDNA,} \]

\[ m = 1.2, 2.9, 5.8 \text{ kDa for} \]

\[ \text{polyC}_4, \]

\[ \text{polyC}_{10}, \]

\[ \text{and polyC}_{20}, \]

\[ \text{respectively. Equation (4) gives the relationship between} \]

\[ v \]

\[ \text{and} \]

\[ t \]

\[ \text{as} \]

\[ f - (f - kv_0)e^{-\frac{kt}{m}} = kv = k \frac{dy}{dt}, \]

\[ \text{where the boundary condition,} \]

\[ v(t_0) = v_0, \]

\[ \text{is conveniently} \]

\[ \text{defined as the velocity of ssDNA when it enters the gap at time} \]

\[ t_0. \]

\[ y \]

\[ \text{is the coordinate of the ssDNA center along the force} \]

\[ \text{direction. Equation (5) further gives the dependence of} \]

\[ y \]

\[ \text{on} \]

\[ t \]

\[ \text{as} \]

\[ k(y - y_0) = f(t - t_0) + \frac{m}{k}(f - kv_0)[e^{-\frac{kt}{m}} - 1], \]

\[ \text{with} \]

\[ y(t_0) = y_0. \]

\[ \text{If we define} \]

\[ v \]

\[ \text{as} \]

\[ \langle v \rangle = \frac{y_1 - y_0}{t_1 - t_0}, \]

\[ \text{where} \]

\[ y_1 \]

\[ \text{corresponds to the exit of ssDNA from the gap at} \]

\[ t_1, \]

\[ \text{then equation (6) gives the theoretical estimate of} \]

\[ \langle v \rangle \]:

\[ \langle v \rangle = \frac{f}{k} + \frac{m(f - kv_0)}{k^2(t_1 - t_0)} \left[ e^{-\frac{kt_0}{m}} - 1 \right]. \]

\[ \text{The values of} \]

\[ f \]

\[ \text{and} \]

\[ m \]

\[ \text{are given,} \]

\[ v_0, t_0, \]

\[ \text{and} \]

\[ t_1 \]

\[ \text{can be calculated from simulation data, so the only unknown} \]

\[ \text{parameter in} \]

\[ \text{equation (8) is the drag coefficient} \]

\[ k. \]

\[ \text{From equation (8) we see that} \]

\[ \langle v \rangle \]

\[ \text{is made up of two parts:} \]

\[ \text{the linear contribution in the first term and the nonlinear second} \]

Figure 3. The average translocation velocities of the ssDNA polyC 10 (diamonds) and polyC 20 (filled circles) as a function of pulling force.

Figure 4. The average translocation velocities of the ssDNA polyC 4 as a function of pulling force.
For polyC4, the linear contribution dominates, and the nonlinear term can be approximated as a constant. That is,

\[ \langle v \rangle \approx \frac{f}{k} + C. \]  

(9)

The slope in figure 4 gives an estimate of \( k \), which is about 2.5 × 10^{-12} \text{ N s m}^{-1}. The mass of ssDNA, \( m \), is about 2–10 × 10^{-24} \text{ kg} for polyC4 to polyC20. The translocation time for ssDNA through the gap, \( t_1 - t_0 \), is about 0.02 (polyC4) to 0.05 (polyC20) ns as calculated from simulations. With the assumption that \( k \) is constant, \( -k(t_1 - t_0)/m \) equals about −25 for polyC4 and about −12.5 for polyC20. This implies that the exponential term in the brackets in equation (8) can be neglected. Equation (8) becomes

\[ \langle v \rangle = \frac{f}{k} - \frac{m(f - kv_0)}{k^2(t_1 - t_0)}. \]  

(10)

Equations (7) and (10) give

\[ \langle v \rangle = \frac{f}{k} - \frac{m(f - kv_0)}{k^2 \Delta y}, \]  

(11)

with \( \Delta y = y_1 - y_0 = 2 \text{ nm} \). Correlations of \( \langle v \rangle \) to \( f \) using equations (11) and (9) are plotted as the lines in figures 3 and 4. It can be seen that the theoretical correlations agree qualitatively with the simulated data in the region \( f = 0.4–0.9 \text{ nN} \).

One major difference between the short and long ssDNA studied in this work is the shape difference. The polyC4 ssDNA segment is about 1.2 nm in both length and width, much like a ball, while polyC10 and polyC20 are rope-shaped. Therefore, pulling the polyC4 segment in solution is similar to pulling a ball in a fluid. No significant deformation was observed. On the other hand, significant deformation was observed for polyC10 and polyC20 during the translocation. As illustrated in figure 5, the head-to-tail length of the polyC10 segment, \( l \), almost doubled during the translocation. The stretch of long ssDNA during the process requires energy. This energy penalty consumed part of the pulling work and possibly resulted in the nonlinear behavior in the translocation velocities for polyC10 and polyC20 compared with that observed for polyC4.

The minimum electric field required to initiate the translocation of ssDNA can be estimated based on the minimum force calculated from the simulation. The minimum force to initiate the translocation is \( \sim 0.3 \text{ nN} \), corresponding to driving a polyC10 using a voltage of 400 mV across the 2 nm membrane. In other words, a 400 mV voltage is necessary to initiate the translocation for the system within nanoseconds. The actual strength of the field required could be higher than 400 mV because of the inefficiency of the electric field compared to the mechanical pulling. Once the process is begun and the DNA is inside the gap, a voltage of 120 mV is strong enough to maintain the translocation and push the DNA through the gap within nanoseconds, as mentioned earlier. We noticed that the minimum voltage (400 mV for initiating and 120 mV for maintaining the translocation) determined from our simulations is higher than those demonstrated in recent experimental studies. Meller et al demonstrated that ssDNA can be driven through a 1.8 nm α-HL (α-hemolysin) using a voltage of 70–300 mV along a 5 nm long pore [11]. They also showed that a transmembrane potential as small as 20 mV can strongly bias the escape of a DNA segment from the 1.8 nm protein pore [10].

The inconsistency between our simulation results and experimental observations could be attributed to a number of factors. (1) The nanogap in our simulation is rigid instead of the soft protein α- HL pore used in the experiment. It is possible that the protein pore was deformed from its native form during the translocation due to interaction from the ssDNA. Theoretically the electrode atoms contacting the ssDNA may also experience restructuring during the translocation. But in our simulations the electrode atoms are treated as rigid. Information on how such a factor impacts the translocation could be investigated by including the flexibility of the electrode atoms in the simulation. (2) The temperature in our simulations is 300 K, while the experimental temperatures in Meller et al’s work are 275 and 288 K. Usually the activity of biomolecules is strongly influenced by the temperature change, but it is not clear how such temperature difference will affect the system we studied. (3) The accuracy of simulation results depends on the realism of the force field employed. In this study we used the widely accepted AMBER and UFF potentials to model the interaction between biopolymers and the electrodes. However, the image charge effects between the charged particles and the electrode surfaces were not included. Exclusion of image charge interaction may result in the overestimate of the initiation force required because the image charge interaction may increase the adsorbing probability between the DNA and gap entrance, and thus promote the initialization of translocation. This concern will be discussed in a subsequent paper [33]. (4) Last but not the least, our simulations were limited to a timescale of ~ns, which will not be long enough to catch an event that may happen at a timescale significantly longer than nanoseconds.

### 3.3. Conformation of DNA during the translocation

We found that an ssDNA molecule would adjust its conformation during its translocation through the gap. The relative geometry between the bases and the nanogap changes so that the ssDNA molecule can fit the shape of the gap. One example is shown in figure 6, for the ssDNA polyC10 threading a 1.5 nm gap under the influence of mechanical pulling force.
The solid curve represents the cosine of the angle between the gap inner surface and an arbitrarily selected base plane. The dashed curve shows the separation between the selected base and the gap along the translocation direction, $\Delta y = y_{\text{gap}} - y_{\text{DNA}}$, where $y_{\text{gap}}$ is the $y$-coordinate of the gap center, and $y_{\text{DNA}}$ is the $y$-coordinate of the center of mass of the selected base on the ssDNA. The trajectory (dashed curve) confined between two dashed horizontal lines $-1 \text{ nm} < \Delta y < 1 \text{ nm}$ corresponds to the region when the base passes the gap. It can be seen that the angle between the gap surface and the base plane changes dramatically to about $0^\circ$ ($\cos \theta \approx 1$) when the base enters the gap. In contrast, the angle is essentially random either before the base enters or after it exits the gap.

The deformation of ssDNA observed from this work is consistent with a previous finding in modeling of ssDNA either before the base enters or after it exits the gap. In contrast, the angle is essentially random when the bases are outside the gap. However, for a wider gap, ssDNA can thread it without sacrificing too much of its native conformations. This implies that very precise gap fabrication will be needed in order to control the DNA orientation. Relatively speaking, controlling the orientation of a double-strand DNA inside a gap could be easier than controlling that of ssDNA because a double-strand DNA behaves more like a robust stick rather than a floppy rope as ssDNA does.

4. Conclusions

We modeled the translocation of single-strand DNA segments through a nanoelectrode gap with various widths. Our simulations of pulling the ssDNA segments using mechanical force indicate that the minimum gap width ssDNA can pass is $\sim 1.5 \text{ nm}$ (effective width $\sim 1.2 \text{ nm}$). Simulations using varying pulling forces suggest that there is an energy barrier for initiating the translocation. The minimum force required to initiate the translocation of ssDNA within nanoseconds is in the range $0.2$–$0.3 \text{ nN}$, and is insensitive to the length of ssDNA. Once the translocation starts, the force from an electric field as small as $60 \text{ mV nm}^{-1}$ is sufficient to maintain the process. Under the influence of constant driving force, the average translocation velocities of DNA molecules depend strongly on the length of the ssDNA segments.

DNA molecules adjust their relative orientation when they pass the gap. In particular, when an ssDNA segment passes a narrow gap, the bases change their orientations to a parallel position to the inner surface of gap, in contrast to their random orientations when the bases are outside the gap. Although the simulations in this work were based on an idealized setup and relatively short timescales, the results provide useful information on development of the proposed device for fast genome sequencing.

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