Intrachain Dynamics of Large dsDNA Confined to Slitlike Channels

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(Received 30 August 2012; published 8 February 2013)

Hydrodynamic interactions (HI) between particles within bounded domains has become a field of intense research because of its importance in colloidal sciences [1], polymer physics [2], and microfluidic applications. In free solution, long range solvent flow induced by particle motion decays as 1/r, and the cooperative motion between particles is described by the Oseen-Burger tensor. If one confines the particle to a cylindrical pore (quasi-1D confinement) then the far field flow brought about by particle motion decays exponentially at lengths beyond the channel width. Hence, motion between particles due to solvent flow is decorrelated, and HI is said to be screened at lengths greater than the channel width [2,3]. However, many micro- or nanofluidic devices are more precisely described as quasi-2D or slit-like. Unlike the pore geometry, particle motion in slits induces a far field dipolar flow (Hele-Shaw flow) [4] which decays algebraically as 1/r^2. Tlusty demonstrated that screening in an isotropic quasi-2D system is possible because the angular average over the disturbance velocity results in a many-body cancellation of HI [5]. Unlike exponential velocity decay in pores, there is no apparent screening length associated with the algebraic far field velocity decay in slits [6] and produces much uncertainty when developing theories of internal mechanics of confined polymers.

Traditionally, blob theory has been the foundation for describing intrachain dynamics of DNA confined to slitlike channels [7,8]. In this theory, dynamic lengths are naturally separated into lengths shorter and longer than the channel height h by assuming the polymer is composed of a string of blobs, each with diameter h. Expanding on work by Balducci et al. [9], Hsieh et al. [10] carefully examined each individual assumption of blob theory and concluded that HI between blobs is screened when dsDNA is confined to slits but that intrablob HI was weaker than proposed by blob theory (i.e., blobs are partial draining). Strychalski et al. [11] arrived at a similar conclusion when analyzing their results for DNA diffusion in slits. Lin et al. compared the diffusion of circular and linear λ-DNA within slit channels [12]. They concluded that complete screening within a polymer coil occurs only when h ≪ R_g, bulk; however, they fail to appreciate that contributions from HI vary at different lengths within the molecule. A more recent study by Lin et al. [13] maintains this viewpoint. Consider, for instance, how one determines the strength of intrachain HI using blob scaling for in-plane diffusivity, D. The original theory assumes

\[ D \sim N^{-1} h^{2/3} \]

The assumption of screening between blobs gives rise to the N^{-1} factor and has been validated in previous experiments [9–12]. But, diffusivity power law dependence on h is a convolution of assumptions for the intrablob HI and chain static properties. Thus, experimental deviations from the original scaling cause uncertainty in regards to the nature of intrachain hydrodynamics. Moreover, this indirect method of measuring intrachain hydrodynamic interactions does not capture some of the underlying physics.

Here, we explore cooperative dynamics within single DNA molecules in slitlike channels using a two-point density correlation function [14]. This method allows us to isolate intrachain dynamics without varying channel height or molecular weight. It is shown that HI become decorrelated at length scales proportional to the channel height. This, to our knowledge, is the first time experiments have directly shown the existence of an effective HI screening length within slit channels. We are able to demonstrate that, for typical channel heights and solvent conditions, blobs are indeed partially draining. They are not Zimm-like, as is assumed in original blob theory. The degree of blob draining is shown to be dependent on the segmental concentration within individual blobs and hence is directly related to buffer conditions.

Equilibrium dynamics of λ-DNA (48,502 kbp, New England Biolabs) were studied in slit channels with heights...
in the range from 90 nm to 2 μm. The DNA samples were stained with YOYO-1 intercalating dye (Invitrogen) at 4 base pair per dye molecule and were immersed in a buffer of 1.5 × TBE (270 mM Tris base, 270 mM boric acid, and 6 mM EDTA) with 4% β-mercaptoethanol (BME, Cabiochem) and 0.1% (w/v) poly(vinylpyrrolidone) (Polysciences). YOYO-1 dye locally untwists the double helix causing the contour length to increase from ≈ 15 to 22 μm; however, the intrinsic persistence length has been shown to be weakly dependent on the dye staining ratio [15]. The buffer viscosity was measured as μ = 1.14 cP, and the ionic strength was estimated to be 56.9 mM. An external dc power source was used to electrophorese DNA into channels and subsequently turned off until the molecules reached thermal equilibrium. Fluorescence excitation was then turned on and video was captured using a Hamamatsu EB-CCD camera (model 7190-43) at a rate of 30 frames per sec. The point spread function of our optical system has a half-width maximum of 440 nm which allows us to resolve two point correlations at a distance of 220 nm. See Supplemental Material [16] for additional details.

The intensity distribution relative to the center of mass for our 2D images, \(I(\mathbf{r}, t)\), is related to the density covariance function by

\[
C(\mathbf{r}_1, \mathbf{r}_2, \delta t) = \langle \delta I(\mathbf{r}_1, t)\delta I(\mathbf{r}_2, t + \delta t) \rangle,
\]

where \(\mathbf{r}_1\) and \(\mathbf{r}_2\) are position vectors relative to the center of mass and \(\langle \cdot \rangle\) indicates an ensemble-averaged quantity. Figure 1 shows example 2D images of λ-DNA molecules in a 560 nm tall slit and the resulting \(\langle I(\mathbf{r})\rangle\). The dynamic structure factor is related to a lower-dimensional projection of the function

\[
S(r, \delta t) = \sum_{\mathbf{R}} \sum_{\delta t} C(\mathbf{R} + r, \mathbf{R}, \delta t),
\]

where \(r = |\mathbf{r}|\) and \(\theta\) defines orientation of the vector \(\mathbf{r} = r[\cos(\theta)\mathbf{e}_x + \sin(\theta)\mathbf{e}_y]\). The summations are taken over all \(\theta\) and position vectors, \(\mathbf{R}\), within the image.

The function \(C(\mathbf{r}_1, \mathbf{r}_2, \delta t)\) is not dominated by center-of-mass translation at long times, and, therefore, it is an excellent basis for measuring intramolecular dynamic response. Naturally, an important question is what are the limitations of this technique? We are limited by our optics to correlated motion on lengths larger than \(r > 220\) nm. Additionally, we are only able to measure long-time internal mechanics for \(r > 33\) ms. Thus, motions dominated by stretching modes and hydrodynamics are readily observed while dynamics from bending undulations of dsDNA are not (bending mode length, \(r_{\text{bend}} \sim 2l_p \sim 100\) nm and characteristic time, \(\tau_{\text{bend}} \sim 10^{-3}\) s). When \(S(r, \delta t)\) is matched to a stretched exponential such as \(S(r, \delta t) \propto \exp[-(\delta t/\tau_r)^\beta]\), the stretching exponent \(\beta\) provides information about intracoil HI. From the de Gennes’ dynamic light scattering models we expect \(\beta_{\text{Rouse}} = 1/2\) [17,18] for no HI and \(\beta_{\text{Zimm}} = 2/3\) [18,19] for strong HI coupling.

Figure 2 shows the measured \(\beta\) as a function of varying distance within λ-DNA under different degrees of confinement. The shaded gray area represents our optical resolution limit and the horizontal dashed lines indicate the Zimm and Rouse limits. A slit height of 2 μm weakly confines λ-DNA (\(R_g,\text{bulk} = 0.65\) μm) and, therefore, is close to the free solution state. From this, one observes that Rouse modes dominate the short distance dynamics and Zimm behavior is prominent at long distances (\(r > 1\) μm). This is in accord with results from Cohen [14] and Shusterman [20] and demonstrates that HI dominates the longest-time modes of λ-DNA near equilibrium. We find at the strongest confinement conditions (\(h = 90\) nm) the molecule exhibits purely Rouse-like dynamics suggesting complete screening of HI between DNA segments. Bakajin et al. [21] made use of electrophoretic force to stretch dsDNA in slit channels and, via numerical modeling, implicitly showed negligible contribution of HI at a channel height of 90 nm. At this height only one Kuhn segment is within a blob of size \(h = 2l_p = 100\) nm. Therefore, the friction along individual Kuhn segments dominates, and one observes Rouse dynamics.

The moderate confinement channels (\(h = 1\) μm and 560 nm) provide more insight about the intrachain HI in slits. The distance varying \(\beta\) curves show Rouse behavior at short distances and a sub-Zimm \(\beta\) peak at intermediate lengths. The apex is associated with the characteristic length for the onset of HI screening and is directly related.  

![Figure 1](color online). Schematic of our analysis method for extracting HI information within λ-DNA confined to a 560 nm tall slit channel. (a) Example of an instantaneous 2D image with intensity \(I(t)\), the time average of all images \(\langle I \rangle\) and visual representation of the instantaneous intensity perturbation from the average, \(I(t) - \langle I \rangle\). The red arrows represent the position vectors in \(S(r, \delta t) = \sum_{\mathbf{R}} \sum_{\delta t} C(\mathbf{R} + r, \mathbf{R} + \delta t)\) and the circle indicates the continuous integration over all \(\theta\). The analysis is done for all time-varying images such as those in (b). Afterwards, we perform a nonlinear regression with a stretched exponential \(S(r, \delta t) \propto \exp[-(\delta t/\tau_r)^\beta]\) as shown in (c).
The strength of the dynamic interactions between two test particles in an unconfined Stokes flow may approximately be expressed as $E = \int H(r)g(r)dr$ [2], where $H(r)$ is the solvent velocity decay and $g(r)$ is the segmental pair correlation. To the first order, the pair correlation can be approximated by the segmental concentration, $g(r) \sim c$. Increasing polymer concentration magnifies the strength of HI within the DNA coil. The most direct method to alter the segmental concentration is to modulate the intrachain electrostatic screening between segments by varying the salt concentration. In Figure 4 we show results for experimentally, this involves changing the segmental concentration, to modulate the intrachain electrostatic screening between segments by varying the salt concentration. In Figure 4 we show results for
measured β of T4 DNA confined to a 1 μm tall slit in three different buffers 1.5, 0.1, and 0.02 × TBE with ionic strengths of 56.9, 5.3, and 1.5 mM, respectively.

Reducing the salt concentration enhances the excluded volume between segments thereby reducing the intrablob concentration. Consider an effective draining parameter, $h_{\text{drain}} = N_{\text{blob}} \frac{\gamma}{(12 \pi^3)^{1/2} \eta R}$, for a blob [23]. We assume the blob size is equal to the channel height $R = h/2$, and the drag on each segment can be estimated as $\gamma = 6 \pi \eta \frac{l_p}{\ln(2l_p/d)}$ ($l_p$ = persistence length) [24]. The hydrodynamic width, $d = 2.76$ nm, is chosen to match free solution chain mobilities [25]. Modulation of the excluded volume changes the number of segments within the blob $N_{\text{blob}} = h^{5/3} w^{-1/3} l_p^{4/3} / 2$ ($w$ is the excluded volume segment width). Both $l_p$ and $w$ increase with decreasing ionic strength [26] (see Supplemental Material [16]). For $h_{\text{drain}} \ll 1$ HI is weak, and for $h_{\text{drain}} \gg 1$ HI is strong. Using this definition of the draining parameter we find the blob draining to be $h_{\text{drain}} = 1.85, 1.06, and 0.72$ for blobs of size $R = h/2 = 0.5 \mu m$ in 1.5, 0.1, and 0.02 × TBE buffers, respectively. This indicates an increase in blob draining and is directly seen in Fig. 4. Long range, $r > h$, dynamics of confined DNA remain Rouse-like irrespective of ionic strength. Naturally, at the low salt limit, the intrachain concentration will be low enough to cause short length, $r < h$, dynamics to be fully Rouse, and, therefore, HI will be completely negligible within the confined coil.

In this Letter, we measured length dependent hydrodynamic cooperativity within single DNA molecules confined to slits. By isolating HI effects, we were able to show a HI screening length within slit channels that is proportional to the channel height. dsDNA has long served as a model polymer, but there has been recent suggestion that intrachain hydrodynamics will not dominate global chain dynamics for molecules of similar size to λ-DNA [27]. Here, we have shown that deviations in the current literature from blob theory can be explained by an insufficient length of contour composing each blob [10], and that, for moderate ionic conditions, the HI is dominant in blobs of radius $R = 1 \mu m$. These observations are of practical importance to microfluidic assays for DNA and bring to light the complexities of quasi-2D hydrodynamic flow fields in polymer physics.

This work was supported by NSF Grant No. 0852235 and the MIT-Singapore Alliance for Technology and Research (SMART).

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