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Comment on “Rotational Drag on DNA: A Single Molecule Experiment

Abstract

A Comment on the Letter by Philippe Thomen, Ulrich Bockelmann, and François Heslot, *Phys. Rev. Lett.* 88, 248102 (2002). The authors of the Letter offer a Reply.

Disciplines

Physical Sciences and Mathematics | Physics

Comment on “Rotational drag on DNA: A single molecule experiment” by P. Thomen, U. Bockelmann, and F. Heslot

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(Dated: November 17, 2003)

The authors of Ref. [1] performed an experiment to measure the rotatory drag on double-stranded DNA (see also [2]). They cited as their motivation a theoretical prediction of this drag using the “hybrid rotation” model of Ref. [3]. When comparing their experimental result to the model, however, they used an inaccurate calculation of the model’s prediction. We show here that the hybrid rotation model’s prediction of the torsional drag, in the experimental conditions where Thomen *et al.* compared the model to experiment, is roughly four times the experimental value (not 38000 times as stated in [1]). For comparison, the older speedometer-cable model [4] predicts a value about one tenth the experimental value [5].

The hybrid-rotation model supposes that when a segment of DNA is cranked axially, the resulting motion is a combination of (a) rigid rotation on contour-length scales shorter than some crossover scale L_c , and (b) speedometer-cable (flexing) rotation on scales longer than the crossover (see Fig. 1). This hybrid motion represents a compromise between the large viscous drag of rigid rotation and the elastic-energy barrier to flexing during speedometer-cable motion. The elastic energy of flexing arises because DNA is not a naturally straight rod; it contains fixed natural bends arising from its sequence. The appropriate measure of these natural bends is the “structural persistence length” P , experimentally determined in Ref. [6] to be $P \approx 130$ nm.

The viscous drag per unit length on a thin rod dragged sideways through water [7] is $f = \mu_{\text{drag}} v$, where $\mu_{\text{drag}} = 4\pi\eta/(0.8 + \ln(X/2R))$. Following Ref. [3], we take the cut-off length X to be equal to P , so $\mu_{\text{drag}} = 2.5 \cdot 10^{-3} \text{ J s m}^{-3}$. The rotatory drag on a rigid rod segment of contour length L_c equals $\Delta\tau = \mu_{\text{drag}}\omega L_c \langle r_{\perp}^2 \rangle$ as in Ref. [3], with the mean-square perpendicular displacement from the axis equal to $\langle r_{\perp}^2 \rangle = 2(L_c)^3/(90P)$ [8].

$\Delta\tau$ is the drop in torsional stress across a rod segment of length L_c . We now estimate the torsional barrier to flexing the segment and set it equal to $\Delta\tau$. Because the crossover length will turn out to be shorter than P , we cannot simply assume that the angular deviation from one segment to the next is large, as was appropriate in Ref. [3]. Instead, we assume that the flexing needed to undergo speedometer-cable motion on length scales larger than L_c equals the expected angular deviation θ for a random walk with persistence length P , where $\cos\theta = e^{-L_c/P}$. Following Ref. [3], we estimate the torque needed to flex the segment through this angle as $\tau_{\text{flex}} = \frac{1}{2} \times \frac{\kappa}{2} L_c (\theta/L_c)^2$, where κ is the elastic bend

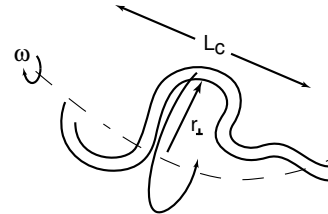


FIG. 1: The hybrid-rotation model. DNA is assumed to flex on length scales longer than L_c , so that the coarse-grained backbone (dashed curve) spins in place.

stiffness of the DNA. We estimate κ from the observed DNA persistence length and P as $\kappa \approx (80 \text{ nm})k_B T$ [3, 6].

Setting $\Delta\tau$ equal to τ_{flex} and choosing the experimental values $\omega = 12600 \text{ s}^{-1}$, $\eta = 10^{-3} \text{ J s m}^{-3}$ yields $L_c = 111 \text{ nm}$ and hence $\Delta\tau = 0.20k_B T$. The torque drop per unit length equals $\Delta\tau/L_c$, and so the total torque needed to crank the DNA is $\tau = \Delta\tau L_{\text{tot}}/L_c$. For $L_{\text{tot}} = 12 \mu\text{m}$, we find $\tau \approx 22k_B T$, about four times the experimental result in Ref. [1]; the speedometer-cable theory predicts $\tau = 4\pi\eta(1 \text{ nm})^2\omega L_{\text{tot}} \approx 0.47k_B T$.

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 - [2] S. Cocco, R. Monasson, and J. F. Marko, *Physical Review E* **66**, 051914 (11 pages) (2002).
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 - [4] C. Levinthal and H. Crane, *Proc. Natl. Acad. Sci. USA* **42**, 436 (1956).
 - [5] In an accompanying Reply, Thomen *et al.* present additional comparisons of theory to experiment showing that the hybrid rotation model diverges from experiment at lower cranking rates. These discrepancies may arise not from the hybrid-rotation model per se, but rather from the additional assumption in [3] that at low speeds a cranked DNA will rotate as a solid spherical body, and.
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 - [7] J. G. de la Torre and V. A. Bloomfield, *Quart. Rev. Biophys.* **14**, 81 (1981), eqns. 73, 77.
 - [8] We cannot use Equation (3) of Ref. [3] because, as noted there, it applies only when L_c is much longer than P . We will see below that instead $L_c \lesssim P$; the formula just given is valid in this regime. The difference in scaling regimes arises because the cranking rate ω used in the comparison to experiment is much greater than that considered in

Ref. [3].