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Abstract

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Disciplines

Physical Sciences and Mathematics | Physics

Transport of Torsional Stress in DNA

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Abstract

It is well known that transcription can induce torsional stress in DNA, affecting the activity of nearby genes or even inducing structural transitions in the DNA duplex. It has long been assumed that the generation of significant torsional stress requires the DNA to be anchored, forming a limited topological domain, since otherwise it would spin almost freely about its axis. Previous estimates of the rotational drag have, however, neglected the role of small natural bends in the helix backbone. We show how these bends can increase the drag *several thousandfold* relative to prior estimates, allowing significant torsional stress even in linear, unanchored DNA. The model helps explain several puzzling experimental results on structural transitions induced by transcription of DNA.

1 Introduction and Summary

DNA can be regarded as a linear repository of sequence information, or as a chemical compound subject to various modifications (*e.g.* methylation), and each of these viewpoints is important for understanding some aspects of gene function and regulation. However, many other important processes require an appreciation of DNA as a *physical elastic object in a viscous environment*. For example, the action-at-a-distance between eukaryotic promoters and their enhancers involves an effective concentration of bound enhancer units depending on both torsional and bend rigidity of DNA.

While the equilibrium statistical mechanics of stiff macromolecules such as DNA is a classical topic (see *e.g.* [1]), still the *nonequilibrium transport* properties of such molecules remains incomplete, in part due to the experimental difficulty of probing those properties. In particular, Liu and Wang proposed that the *transport of torsional stress (torque)* along DNA during transcription could play a role in gene regulation (the “twin supercoiled domain model”) [2]. Transcription causes axial rotation of the transcribed DNA relative to the transcribing polymerase. If free rotation is hindered in some way, a resulting torsional stress will propagate down the DNA, destabilizing (or overstabilizing) the double helix structure at some distant point. The resulting “topological coupling” between nearby genes has been observed in several experiments (see Sect. 2 below).

Liu and Wang assumed a simple mechanism for the transport of torsional stress, following Levinthal and Crane¹ [3]. In a viscous medium a straight infinite rod meets a frictional resistance to axial rotation given by

$$\tau = \mu_{\text{spin}}\omega L \tag{1}$$

Here the torque τ (with dimensions of energy) depends on the rotation rate ω (radians/sec) and length L *via* a friction constant μ_{spin} . A simple calculation [4] gives $\mu_{\text{spin}} = 4\pi\eta R^2 \approx 1.3 \cdot 10^{-15}$ dyn-sec, where $R \approx 1$ nm is the rod radius and $\eta = 0.01$ erg sec cm⁻³ is the viscosity of water. Other authors give slightly different prefactors [5].

Liu and Wang pointed out that the torsional friction constant μ_{spin} appearing in eqn. (1) is extremely small due to the factor of R^2 , and so they concluded that no significant torsional stress was possible in DNA of reasonable length without some additional physical anchoring. Absent such anchoring, both linear (open) and circular (plasmid) DNA would *spin in place*, like a plumber’s snake [3]. For concreteness we will consider below the example of a linear DNA of length 3.5 kbp (1200 nm), rotated at its end with angular frequency $\omega = 60$ radians/sec; a related case is a 7 kbp construct, linear or circular, rotated near its center. In either case formula (1) gives a maximum torsional stress $\tau \approx 9 \cdot 10^{-18}$ dyn cm. Since the torque needed to denature DNA locally is several thousand times greater (see below), Liu and Wang’s conclusion seems to be safe.

The analysis of this paper was motivated by several experimental observations which defy the familiar analysis just summarized (Sect. 2 below). A variety of assays, both in living cells

¹Levinthal and Crane’s “speedometer-cable” motion will be called “plumber’s snake” motion, or “spinning” motion, in the present paper.

and *in vitro*, have found significant torsional stress following transcription at a single promoter on unanchored DNA constructs. All these experiments are sensitive to topoisomerase, pointing to the role of torsional stress. The estimates given above imply that such large stresses are impossible.

To resolve this paradox, the analysis in Sects. 3–4 below will show that the classical formula (1) can be very misleading: it *vastly underestimates the torsional stress on the DNA duplex near the transcribing polymerase*. The discussion rests on the observation that DNA is a heteropolymer, *i.e.* it is naturally bent on length scales longer than its persistence length of about 50 nm. For a curved molecule to spin in place without dragging sideways through the surrounding medium, as assumed in formula (1), requires constant *flexing*. The natural bends resist this flexing, forcing the molecule to translate through the fluid and greatly increasing the viscous drag through the surrounding water. (Fig. 1*d* below summarizes the model.) This enhanced drag indeed explains the large observed torsional stress near the point of transcription.

2 Experiments

2.1 General

This section briefly reviews a few of the relevant experimental results, focusing on *in vitro* assays. Sect. 3 below describes our physical model.

RNA polymerases are efficient motors: for example, *E. Coli* RNAP can generate forces of up to 20 pN against an opposing load [6]. When the same mechanical energy is expended against a *torsional* load, it corresponds to a torque of 20 pN·0.34 nm/step divided by 2π radians for every 10.5 steps, or 10^{-13} dyn cm, more than enough to induce structural transitions in DNA. The speed of transcription ranges from 50 nt/sec in eukaryotes to twice as great for T7 [7]. The corresponding rotational driving rates are then $\omega = 30$ and 60 radians/sec, respectively.

The actual torsional stress during transcription need not, however, attain the maximal value just given. Liu and Wang’s twin supercoiled domain model rests on the observation that torsional stress will only build up if *a)* the polymerase itself is prevented from counterrotating about the DNA template, and *b)* a suitable *torsional load* opposes the rotation of the DNA at a point sufficiently close to the cranking polymerase. The present paper is concerned mainly with point *(b)*, but for completeness we first digress to discuss *(a)*.

Anchoring at the transcribing polymerase A number of effects can prevent counterrotation of the polymerase. For example, in eukaryotes the polymerase may be physically attached to the nuclear matrix. Even without a rigid attachment, the eukaryotic polymerase holoenzyme is physically quite large and thus offers a large hydrodynamic drag to rotation. Similarly in prokaryotes, the nascent RNA transcript can begin translation before it is fully transcribed, leading effectively to a large complex consisting of polymerase, transcript and ribosome. Liu and Wang proposed a particularly attractive possibility: if the emerging protein is membrane-bound (for example, the tetracycline-resistance *tet* gene product), it can anchor its ribosome to the cell membrane [2]. Many experiments have shown that translation of *tet* greatly increases twin-supercoil domain effects (see [8, and references therein]).

The above mechanisms operate only *in vivo*. Remarkably, twin-supercoiled domain effects have also been observed in a number of *in vitro* assays, where no cellular machinery exists (see Sect. 2.2 below). At least three mechanisms can nevertheless create significant drag opposing counterrotation of the polymerase: *i*) polymerase has been found to create a tight loop in the DNA, greatly increasing its effective hydrodynamic radius and hence the drag for counterrotation [9]; *ii*) the nascent RNA transcript itself will create some hydrodynamic drag to rotation [2]; *iii*) under the conditions of most experiments (*e.g.* [10]) polymerase is present at concentrations leading to batteries of simultaneously-transcribing complexes. To relieve torsional stress, all active complexes would have to counterrotate simultaneously, with a drag proportional to their total number.

Anchoring elsewhere Thus, even *in vitro*, transcription can effectively lead to the cranking of DNA by a nearly immobilized polymerase. As mentioned in point (*b*) above, however, cranking at one point still does not suffice to create torsional stress: DNA rotation must be effectively hindered somewhere else as well, since otherwise both linear and circular DNA would simply spin freely in place at the driving rate ω .

As in point (*a*), many mechanisms can anchor DNA in the crowded cellular environment. For example, in eukaryotes a DNA-binding protein could tie the DNA onto some part of the nuclear matrix. Another possibility, envisioned by Liu and Wang and implemented in several experiments, is to bind a second polymerase to the DNA and rely on its resistance to rotation as in (*a*) above. The second polymerase can either be stalled or actively transcribing in the opposite (divergent) sense from the first.

Once again, however, the clearest results come from the *in vitro* assays mentioned earlier, in which only a single promoter is active on a circular [10, 11, 12, 13, 14] or even linear (L. B. Rothman-Denes, unpublished results; D. Levens, unpublished results) template. In these experiments the only known hindrance to free spinning motion is the torsional hydrodynamic drag. If DNA were effectively a simple, straight, rod of diameter 2 nm, then the estimate in equation (1) would apply, and we could confidently predict that transcription would generate negligible torsional stress. Since the experiments contradict this expectation, we must modify the naïve physical picture of the transport of torsional stress in DNA.

2.2 Experimental results

In vitro Tsao *et al.* made a circular plasmid with only one promoter actively transcribing [10]. They assayed transient torsional stress in the wake of polymerase by allowing topoisomerase I to selectively eliminate negative supercoils, then measuring the remaining degree of positive supercoiling via 2d electrophoresis. They found that transcription induces a degree of supercoiling “much bigger than expected” and concluded that “it is possible that the degree of supercoiling generated by transcription is underestimated in the theoretical calculation” of [2].

Dröge and Nordheim assayed torsional stress in a 3 kbp circular plasmid using the B-Z structural transition [11]. They concluded that “Interestingly our results suggest that diffusion rate of transcription-induced superhelical twists must be relatively slow compared to their generation, and that under *in vitro* conditions localized transient supercoiling can reach unexpectedly high levels.” Similarly Dröge later found that transcription can induce site-specific recombination *in vitro* [12]. Here the conclusion is that transcription created local torsional stress, in turn driving local writhing and bringing recombination sites into synapsis. Wang and Dröge later extended these experiments and called attention to the fact that torsional strain remains localized in a gradient region close to the polymerase, instead of spreading rapidly around the plasmid and cancelling at the antipodal point [14].

Drolet, Bi, and Liu studied the reciprocal effects of topoisomerase I and gyrase [13], assaying with 1d electrophoresis. The result of interest to the present paper is that they found that membrane anchoring via the nascent TetA protein was not necessary for transcription-induced supercoiling, in contrast to earlier *in vivo* studies.

Finally, Rothman-Denes *et al.* and Levens *et al.* (unpublished results) have used *linear* (open) 2300 nm templates including a T7 RNA polymerase promoter near the center. Tran-

scription from this promoter by T7 RNA polymerase generates torsional stress. Rothman-Denes *et al.* used the activity of a bacteriophage N4 early promoter as a stress reporter. This promoter is inactive in its unstressed state and activated through cruciform extrusion at a superhelical density $\sigma_{\text{crit}} = -0.03$ [15], corresponding to a torsional stress of $\tau_{\text{crit}} \approx 7 \cdot 10^{-14}$ dyn cm, consistent with the estimate given above². Levens *et al.* instead used an element of the human *c-myc* gene, which interacts with single-stranded DNA binding proteins, and measured unwinding using potassium permanganate, which reacts with single-stranded tracts. The results of both sets of experiments suggest that structural transitions are induced by T7 RNA polymerase transcription. Thus it again appears that *transcription of linear DNA can create torsional stress several thousand times greater than that predicted by the classical formula (1)*.

In vivo As mentioned above, *in vivo* experiments are harder to interpret, but nevertheless we mention a few illustrative results to show the very general character of the frictional-drag paradox.

Rahmouni and Wells used a circular 6.3 kb plasmid, reporting its torsional stress via the B-Z structural transition [20, 21]. They concluded that “the diffusion of supercoils must be slower than was originally predicted [in [2]]”.

Lilley and collaborators have carried out an extensive series of experiments reviewed in [8]. Their conclusion that an “as yet unidentified topological barrier should exist” may point to the same surprisingly large rotational drag argued for in the *in vitro* experiments above. In later work they also found that the transcribing polymerase need not be physically anchored, reinforcing the argument in point (a) of section 2.1 above [22, 23].

Turning finally to experiments in eukaryotes, we mention only two experiments of Dunaway and coworkers. Dunaway and Ostrander sought to eliminate any anchoring of their DNA template by injecting linear DNA with no subsequences known to associate with the nuclear architecture into *Xenopus* oocytes [24]. They injected an exogenous (bacterial) polymerase into their oocytes and ensured that its promoter was the only spontaneously-transcribing promoter on their template. They also used *linear* templates, reducing the likelihood of any entanglement effects. Using 3.6–4.5 kb templates with a ribosomal RNA promoter to report torsional stress,

²We estimate that about 30% of the superhelical density goes into twisting the double helix (and the rest into the mean writhe) [16]. Multiplying $0.3\sigma_{\text{crit}}$ by the microscopic twist stiffness $Ck_{\text{B}}T \approx 4.5 \cdot 10^{-19}$ erg cm [17] and the relaxed Link density $2\pi/(10.5 \text{ bp} \cdot 0.34 \text{ nm/bp})$ gives the above estimate for τ_{crit} . Direct physical manipulation on stretched DNA gives similar results [18, 19].

they concluded that “localized, transient domains of supercoiling” could occur in open DNA, trapping significant torsional stress. Similarly, later work by Krebs and Dunaway concluded that “The viscous drag against a large DNA molecule is apparently sufficient to prevent transcription-generated supercoils from diffusing rapidly off the end of the DNA, so DNA length creates a topological domain” [25]. Once again this conclusion is remarkable, in that it contravenes the estimates in Sect. 1 above.

3 Physical picture

As described in Sect. 1, the surprising physical aspect of the experiment is the buildup of torsional stress in the DNA, when nothing seems to prevent the molecule from spinning almost freely in place. Apparently the simple physical model of a uniform elastic rod in a viscous fluid has left out some crucial effect. One may at this point be tempted to abandon simple physical models altogether, pointing to the many specific biochemical features of real DNA which they omit. But the elastic rod model successfully describes many detailed features of DNA stretching and fluorescence-depolarization experiments, including effects of torsional stress (*e.g.* [26, 17]). Moreover, the surprising observed behavior is generic and robust, not specific to a particular situation, suggesting that the model needs only some simple new ingredient in order to capture the observed behavior.

In this section we argue that augmenting the elastic rod model by including the *natural bends* in the DNA duplex dramatically changes the transport of torsional stress. The strength of these bends has been independently measured; it is not a new free parameter. Their effect on the *equilibrium* properties of DNA coils has long been recognized. In this section and the next we instead study their effects *far* from equilibrium.

3.1 Need for spin-locking

Imagine a given segment of an elastic rod (modeling a twist-storing polymer such as DNA) as contained in a black box with only the two ends of the rod accessible. Cranking one end about its axis amounts to *injecting a conserved quantity*, “linking number” (or Lk), into the rod.³ We

³Strictly speaking Lk is well defined only for a closed loop. Nevertheless, the *change* in Lk in an open segment with fixed end is well defined, and must vanish, whatever happens inside the black box. Rotating one end about its axis thus injects a conserved quantity.

can schematically think of linking number as taking one of five pathways away from the cranking site:

1. Lk can be elastically stored as *twist* in the rod: the rod segment can rotate about its axis by an amount which depends on position along the rod;
2. Lk can be elastically stored as *writhe*: the rod can begin to supercoil;
3. Lk can be transported by *spinning* (plumber's-snake) motion, emerging at the far end with no net change in the rod state;
4. Lk can be transported by *rigid rotation* (crankshaft motion) of the whole segment about some axis;
5. Lk can be *lost* via the action of topoisomerase.

We are interested in steady-state transport, in the absence of topoisomerase, and so we consider only the competition between pathways #3 and #4.

This picture allows a more precise summary of the paradox reviewed in Sects. 1–2 above. The steady transport of injected Lk will meet with resistance in the form of effective frictional constants μ_{spin} for spinning and μ_{rigid} for rigid rotation, and hence a total frictional constant $\mu_{\text{tot}} = (\mu_{\text{spin}}^{-1} + \mu_{\text{rigid}}^{-1})^{-1}$. But we have seen that experimentally μ_{tot} is much larger than the theoretically expected value of μ_{spin} . No matter how large μ_{rigid} may be, it cannot resolve this paradox. In particular the well-known coupling between torsional stress and writhing motion (see *e.g.* [27, 28] and references therein) is of no help, since the problem is precisely that there is little torsional stress.

What is needed is a way to *shut down* pathway #3, *i.e.* to *lock* the spin degree of freedom, at least partially.

The fact that a uniform rod is never actually straight on length scales beyond its bend-persistence length A does not help, either.⁴ Spinning creates no long-range hydrodynamic

⁴Even in the absence of thermal motion, a naturally-straight rod will bend when cranked fast enough, executing a hybrid of rigid rotation and spinning [29]. Wolgemuth *et al.* found, however, that for the parameters of interest to us here the Lk transport is dominated by spinning, exactly as argued above. The ease of spinning relative to translation of the rod through the fluid can alternately be understood from the point of view of Brownian fluctuations: a thin, axially-symmetric object receives random thermal kicks from the surrounding fluid, but these deliver very little torque due to the small rod radius R . By the general relation between diffusion and friction [30], we again obtain a rotational friction constant suppressed by powers of R , consistent with formula (1).

interaction, since the fluid velocity field falls off on the scale of the rod diameter $R = 1$ nm [4]. Since A is much larger than R , the straight rod approximation is adequate [31]. Certainly the spinning in place of a thermally-bent but naturally-straight rod requires continuous flexing of the rod, as the direction of curvature rotates in the material frame of the rod, but the elastic cost of a bend in a cylindrical rod depends only on the magnitude, not the direction, of the curvature, and this does not change: such a rod has no energetic barrier to spinning.

To summarize, the naïve equation (1) will be accurate, and torsional stresses will be small, unless some sort of locking mechanism *inhibits free spinning* of linear DNA in solution. To find such a mechanism, we must now introduce some new element of realism into our description of DNA.

3.2 Natural bends

As mentioned in Sect. 1, the key ingredient missing so far from our model is the natural curvature of the DNA duplex. Immense effort has been focused on predicting the precise conformation of a DNA tract given its basepair sequence, using molecular modeling, oligomer crystallography, and NMR, among other techniques. Fortunately, for our problem it suffices to characterize the *average* effect of curvature over hundreds of basepairs. For such purposes a very simple phenomenological approach suffices.

Natural DNA is a stack of similar but nonidentical subunits, arranged in an order which is fixed but random for our purposes. It is crucial that even though these bends are random, their effects do not average to zero on length scales much longer than one base-pair. Instead, the minimum-energy conformation of such a stack may be regarded as a distorted helix whose backbone follows a random walk, with a *structural persistence length* P . Note that P is a purely geometrical parameter, having nothing to do with the mechanical bend stiffness κ_{bend} of DNA nor the thermal energy $k_{\text{B}}T$. Instead P reflects the *information content* in a piece of DNA.

Just as in the straight case, bent (natural) DNA can also be deformed *away* from its minimum-energy state at some enthalpic cost characterized by a bend stiffness κ_{bend} , with units energy-length. Since fluctuations are controlled by the thermal energy $k_{\text{B}}T$, we define the *bend length* $A = \kappa_{\text{bend}}/k_{\text{B}}T$. The combined effect of thermal and natural bends then makes DNA a random coil with total persistence length⁵ $A_{\text{tot}} = (A^{-1} + P^{-1})^{-1}$ [34]. Under physiological

⁵Some authors call P the “static persistence length” and A the “dynamic persistence length”. Schellman and Harvey verified Trifonov *et al.*’s heuristic derivation of this formula within a number of detailed models [32]. Since

conditions A_{tot} has the familiar value of 50 nm. Experiments on artificial, naturally-straight DNA make it possible to determine A and P separately, yielding $A \approx 80$ nm and $P \approx 130$ nm [35].⁶

3.3 Hybrid motion

We wish to explore the consequences of the natural bends introduced in the previous subsection for the transport of torsional stress in DNA. Before doing any calculations, it is worthwhile to formulate some intuitive expectations, based on four increasingly realistic cartoons for the steady-state motion of a cranked DNA segment of contour length ℓ (Fig. 1a–d).

As noted in Sect. 1, a straight, rigid segment (Fig. 1a) would encounter a torsional drag per unit length $\mu_{\text{spin}}\omega$, or a net drop in torsional stress between the ends of $\mu_{\text{spin}}\omega\ell$, with friction constant μ_{spin} given below eqn (1). We argued in Sect. 3.1 that the case of a naturally-straight but semiflexible segment is similar (Fig. 1b).

Matters change considerably when we introduce natural bends. If the rod were perfectly rigid (Fig. 1c), it would have to execute crankshaft motion; individual rod elements would then drag sideways through the fluid. We will see below that as ℓ increases, the corresponding drag per unit length would increase without bound. On long enough scales, then, we may expect that any realistic molecule cannot be regarded as infinitely stiff.

At the other extreme, we could imagine the naturally-bent rod spinning in place. This however would mean that every joint periodically bends *oppositely* to its preferred conformation. The corresponding elastic energy cost creates a barrier to this motion.

We will argue that in fact a real, semiflexible heteropolymer chooses a compromise between these extremes of motion, selecting a *crossover scale* L_C and executing a hybrid motion (Fig. 1d). On length scales shorter than L_C this motion is nearly rigid, since as just argued an activation barrier resists flexing. On longer length scales the motion must cross over to spinning, since as just argued rigid (crankshaft) motion meets a large viscous drag on long scales.

$P^{-1} < A^{-1}$ we can regard the bend disorder as smaller than the thermal disorder. In this case Trifonov’s formula also gives the effective persistence length measured by fitting DNA stretching experiments to the naïve worm-like chain model [33].

⁶ Though Bednar *et al.* did not estimate the uncertainty in their determination of P [35], it may well be large. They note, however, that their direct experimental determination agrees with the model-dependent prediction of Bolshoy *et al.* [36].

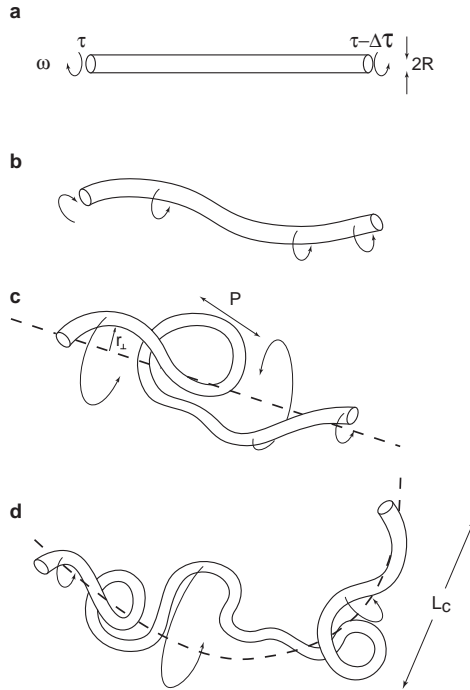


Figure 1: Four increasingly realistic models of cranked DNA motion. *a*) Straight, rigid rod, assumed in the derivation of the naïve formula eqn. (1). *b*) Naturally-straight but thermally-bent rod. *c*) Naturally-bent, rigid rod. *d*) Hybrid motion of a naturally-bent, semiflexible rod. The rod rotates rigidly on length scales shorter than L_C while flexing on scales longer than L_C .

We must now justify these intuitive ideas and obtain a numerical estimate for the crucial crossover scale L_C . Since L_C will turn out to be significantly longer than the basepair step size, we will conclude that the spinning (plumber’s-snake) motion is effectively locked, as we argued was necessary in Sect. 3.1.

4 Scaling Analysis

We must now justify and quantify the expectations sketched in Sect. 3.

4.1 Spin-locking

Consider first the hypothetical case of a perfectly rigid, naturally-bent rod (Fig. 1c). The viscous force per length f on a straight rod much longer than its radius R , dragged sideways through a viscous medium, is [5]

$$f \equiv \mu_{\text{drag}} v = \frac{4\pi\eta}{0.8 + \ln(X/2R)} v \quad (2)$$

where v is the speed and X is the rod length. Our polymer is of course *not* straight on length scales beyond its structural persistence length P , so we substitute P for the long-scale cutoff X in eqn. (2). Since the dependence on X is weak this is a reasonable approximation.⁷ Taking $P = 130$ nm and $R = 1$ nm then gives $\mu_{\text{drag}} \approx 2.5 \cdot 10^{-2}$ erg sec cm⁻³.

Suppose we crank a rod segment of arc length ℓ , which then rotates rigidly about an axis. Each element of the rod then moves through fluid at a speed $v = r_{\perp}\omega$, where r_{\perp} is the distance from the rod element to the rotation axis (Fig. 1c). Multiplying the moment arm r_{\perp} times the drag force, eqn. (2), and integrating over the curve yields the torque drop $\Delta\tau = \mu_{\text{drag}}\omega\ell\langle r_{\perp}^2 \rangle$ across the segment. Here $\langle r_{\perp}^2 \rangle$ is the average of r_{\perp}^2 along the rod segment.

Each rod segment of course has a different sequence, and hence a different preferred shape. Each segment will therefore have a different value of $\langle r_{\perp}^2 \rangle$. Fortunately, we are interested in the sum of the torque drops across many segments, each with a different, random, sequence. Thus we may replace $\langle r_{\perp}^2 \rangle$ by its *ensemble average* over sequences, which we will call $\langle\langle r_{\perp}^2 \rangle\rangle$. This average has a simple form: eqn. 7.31 of Ref. [1] gives $\langle\langle \mathbf{r}_{\perp}^2 \rangle\rangle = \ell P/9$, and hence

$$\Delta\tau = \mu_{\text{drag}}\omega\ell^2 P/9 \quad (3)$$

In the language of Sect. 3.1, we have just estimated the drag torque $\mu_{\text{rigid}}\omega\ell$, finding $\mu_{\text{rigid}} \approx \mu_{\text{drag}}\ell P/9$. Indeed we see that the drag per unit length grows with ℓ , as suggested in Sect. 3.3 above. Formula (3) is valid when the segment length ℓ is longer than P , an assumption whose self-consistency we will check below.

We can now relax the artificial assumption of a perfectly rigid rod and thus pass from Fig. 1c to the more realistic Fig. 1d. Suppose that a long polymer has been subdivided into segments of length ℓ , each approximately executing rigid rotation about a different axis. The axes will all be different, since we are assuming that ℓ is longer than the structural persistence length P . To

⁷A rod pulled at some angle other than 90° to its tangent will have a drag given by eqn. (2) with a slightly different prefactor; we will neglect this difference and use eqn. (2) in all cases.

join these segments smoothly as they rotate, each segment therefore needs to flex. On average, each segment must periodically bend one end relative to the other by about 90° . The least costly conformational change which accomplishes this is to spread the bending strain uniformly along the entire segment length ℓ ; we can then estimate the elastic bending-energy cost as ⁸

$$\frac{\ell \kappa_{\text{bend}}}{2} \left(\frac{\pi}{2\ell} \right)^2 \quad (4)$$

This energy barrier becomes small for large ℓ , just the opposite trend to that of eqn. (3). The physical reason for this behavior is that we do not insist on ironing out every small kink in the rotating rod's shape; the rod segment can satisfy the imposed conditions on its ends by deforming only a fraction of its many intrinsic bends.

The bending energy needed to crank the segment through an angle θ is roughly eqn. (4) times $\frac{1}{2}(1 - \cos \theta)$; the torque needed to increase θ is then the derivative of this formula, $\frac{1}{2} \sin \theta$. Thus the driving torque needed to overcome the bending-energy barrier turn through a complete revolution is just one half of eqn. (4). The crossover length L_C is then the value of ℓ at which the viscous torque drop, eqn. (3), just balances this critical value:

$$\mu_{\text{drag}} \omega L_C^2 P / 9 = \frac{k_B T}{2} \frac{A}{L_C} \frac{\pi^2}{8} \quad (5)$$

Substituting the numerical values we find $L_C \approx 450$ nm for T7 RNAP, and slightly larger for other, slower, polymerases.

Our crossover length has indeed proven to be longer than the structural persistence length P , so the assumption $\ell > P$ made above is self-consistent. Indeed, L_C has proven to be about 1.4 kbp. In our illustrative example of a 7 kbp DNA construct cranked at the midpoint, we see that intrinsic bends shut down spinning motion almost completely: *the naïve model of Sect. 1 does not describe the true motion at all*. We must now see what this implies for the overall torsional stress on the construct.

4.2 Hydrodynamic interactions

In contrast to spinning in place, dragging a thin rod sideways sets up a long-range flow field. Now that we know that spinning is effectively forbidden, we must therefore study the possibility of long-range hydrodynamic interactions between rod segments.

⁸Natural DNA can have localized regions of reduced bend stiffness. These flexible tracts will not significantly affect this estimate unless they are spaced more closely than the length scale L_C found below.

The theory of polymer dynamics tells us that a short random coil dragged through fluid can be viewed as a set of thin-rod elements moving independently in a motionless background (the “free-draining” case), but a long coil instead moves as a *solid spherical object*, due to hydrodynamic interactions [37]. The crossover between these two regimes is controlled by the dimensionless parameter $Q \equiv \sqrt{\frac{L}{A_{\text{tot}}}} \frac{\mu_{\text{drag}}}{\eta}$. Free draining corresponds to the case $Q \ll 1$. For our illustrative example of a coil of length $L = 2300$ nm and total persistence length $A_{\text{tot}} = 50$ nm, we get $Q = 17$, interactions are important, and the coil moves as a solid sphere.

The viscous drag torque on such a coil is $\tau = \mu_{\text{coil}}\omega L$, where $\mu_{\text{coil}} = \frac{4}{9}\sqrt{3\pi^3 LA^3} \cdot 1.26\eta$ (see §31 of [1]). Dividing this torque equally between the upstream and downstream halves of the construct, we find the estimated torsional stress on either side of the cranking point to be $\omega \cdot 1.0 \cdot 10^{-15}$ dyn cm sec. Taking $\omega = 60$ radian/sec then gives a torsional stress of $6 \cdot 10^{-14}$ dyn cm, comparable to the value quoted in Sect. 2 as necessary to induce structural transitions and *about seven thousand times greater than the naïve estimate* given below eqn. (1).

4.3 Relation to prior theoretical work

The viewpoint taken in this paper can be regarded as a synthesis of two established threads.

Fluid-mechanics work One of these threads studies the deterministic dynamics of externally driven (*i.e.* far from equilibrium) rods in a viscous environment. For example, Garcia de la Torre and Bloomfield studied the effects of a *single, permanent, large-angle* bend on viscous drag [5], obtaining precise versions of some of the formulæ given above. Individual large-angle bends caused by DNA-binding factors may well be present *in vivo*, but our point here is that a *statistical distribution* of *small, finite-stiffness* bends still leads to dramatic effects.

Several authors have studied the interplay between shape and twist in the dynamics of *naturally straight, flexible* rods in a viscous medium [38, 39, 40, 29], again obtaining precise formulæ for situations simpler than that studied here. It would be very interesting to incorporate intrinsic bends into their formalism.

Finally, Marko has proposed that the *impulsive* (jumpy) action of RNA polymerase can lead to *transient* torsional stresses greater than predicted by the naïve formula, eqn. (1) [41]. The range of this enhancement, however, depends on the time scale of each step and may be too short to explain the observed phenomena. Experimental measurement of this time scale will be needed to assess this proposed mechanism.

Simulation work A second thread is the extensively studied problem of the *equilibrium fluctuations* of a polymer, particularly the diffusive torsional motion of DNA as measured in fluorescence experiments. Most of this work used Monte Carlo or Brownian dynamics numerical simulation techniques; most did not introduce long-range hydrodynamic interactions as we did in Sect. 4.2 above.

Fujimoto and Schurr noted that fitting experimental fluorescence polarization anisotropy data to a model of intrinsically-straight DNA yielded an effective hydrodynamic radius which increased with increasing segment length [42]. They suggested the possibility that this effect could be caused by permanent or long-lived bends in DNA.

Collini *et al.* took up the same problem [28], explicitly introducing intrinsic bends. Their physical model, however, was the crankshaft motion of a perfectly rigid, zig-zag shape. The zig-zag shape introduces structure on *one* length scale. A major point of the scaling analysis in Sect. 4 above, however, was that the minimum-energy conformation of natural DNA is actually a random coil, and random walks have structure on *all* length scales. A second key point of our analysis was that DNA is *not* infinitely stiff, leading to the crossover phenomenon found in Sect. 4.1.

Schurr *et al.* distinguished between “phase-locked bends”, equivalent to the natural bends in the present work, and “non-phase-locked bends” including the thermal bends of the present work.⁹ They verified using Monte Carlo simulation that in the absence of natural bends, the torsional drag on a thermally-bent rod is the same as that for a straight rod, as argued physically in Sect. 3.1 above. Schurr *et al.* went on to anticipate the hybrid motion studied in the present work, proposing that “beyond some length the degree of global phase locking should decrease, as the motion approaches that of a wobbly eccentric speedometer cable, and the effective hydrodynamic radius should reach a plateau value, which is possibly 1.2 nm. The available evidence indicates that this radius is independent of length for $L > 60$ nm” [31]. The authors did not, however, present a model incorporating random natural-bend disorder.

The present work predicts instead that the response of DNA to external cranking is controlled by an effective drag constant that does not saturate until $L > L_C$. The crossover scale L_C depends on the transcription rate via eqn. (5) and is typically hundreds of nanometers; the

⁹Another example of a non-phase-locked bend could be a universal joint: a bend maintaining fixed polar angle but free to swivel in the azimuthal direction. Schurr *et al.* also distinguish between slowly- and rapidly-relaxing bends. The present work assumes that the large external applied torsional stress (absent in the equilibrium situation studied in [31]) suffices to overcome any kinetic barriers to elastic deformation of the DNA duplex.

saturation value of the effective hydrodynamic radius is then much greater than 1.2 nm. The driven situation of interest here is not, however, the same as the equilibrium situation studied in [31].

Finally, A. Maggs has independently shown that in a naturally-straight, thermally-bent rod twist relaxation follows the same diffusive law as in a rigid straight rod, out to extremely long scales (over 2 kbp) (A. Maggs, unpublished results). Beyond this scale Maggs found that pathway #2 in Sect. 3.1 above begins to affect twist relaxation, leading to an interesting new scaling relation.

5 Conclusion

The analysis of this paper rests upon a surprising fact from slender-body viscous hydrodynamics. The drag torque for spinning a thin rod behaves reasonably as one decreases the rod radius R : it is proportional to R^2 . In surprising contrast, the drag force for pulling such a rod *sideways* is practically independent of R (eqn. (2) above). The only length scale available to set the rotational drag for rigid crankshaft motion is then the radius of curvature of the rod. But a randomly-bent rod has structure on every length scale, and so the drag torque per length increases without bound for longer segments until the crossover condition, eqn. (5), is met. Since the crossover scale L_C proves to be long, cranked DNA is effectively spin-locked on scales shorter than at least 1 kbp. This observation explains why the naïve formula, eqn. (1), is inapplicable, eliminating the paradox described in Sect. 1.

The transport of torsional stress may enter in many cell processes. While this paper has stressed its possible role in gene regulation, torsional stress has recently been assigned a role in the disassembly of nucleosomes in front of an advancing polymerase complex (*e.g.* [43, 44]), in chromatin remodeling (*e.g.* [45]), and in the action of enzymes on DNA (*e.g.* [46]). The ideas of this paper may be relevant to these problems too, though of course in eukaryotes the phenomenon described here may be preempted by the effects of higher-order chromatin structure. Direct manipulation of single DNA molecules sometimes involves cranking as well (*e.g.* [47]).

The simple scaling analysis used in this paper makes some testable predictions. The key claim has been that intrinsic bends can have a huge effect on the transport of torsional stress along DNA. For example, synthetic DNA engineered to be less bent than natural sequences [35] will have longer crossover scale L_C (eqn. (5)), and hence should support less torsional stress for

a given length. Shortening a linear template below L_C should also sharply reduce the overall drag coefficient. More generally, none of the experimental papers cited earlier made quantitative estimates of the effective torsional friction constant needed to explain their results. One could imagine an *in vitro* experiment using local stress reporters (*e.g.* the B-Z structural transition), inserted at various positions, to get the full torsional stress profile, in space and time, as function of transcription rate. Even a limited subset of this quantitative information would yield insight into the mechanisms of torsional stress transport.

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