Effects of nucleoid proteins on DNA repression loop formation in *Escherichia coli*

Nicole A. Becker¹, Jason D. Kahn² and L. James Maher III¹,*

¹Department of Biochemistry and Molecular Biology, Mayo Clinic College of Medicine, 200 First St SW, Rochester, MN 55905 and ²Department of Chemistry and Biochemistry, University of Maryland, College Park, MD 20742-2021, USA

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**ABSTRACT**

The intrinsic stiffness of DNA limits its ability to be bent and twisted over short lengths, but such deformations are required for gene regulation. One classic paradigm is DNA looping in the regulation of the *Escherichia coli* lac operon. Lac repressor protein binds simultaneously to two operator sequences flanking the lac promoter. Analysis of the length dependence of looping-dependent repression of the lac operon provides insight into DNA deformation energetics within cells. The apparent flexibility of DNA is greater in vivo than in vitro, possibly because of host proteins that bind DNA and induce sites of flexure. Here we test DNA looping in bacterial strains lacking the nucleoid proteins HU, IHF or H-NS. We confirm that deletion of HU inhibits looping and that quantitative modeling suggests residual looping in the induced operon. Deletion of IHF has little effect. Remarkably, DNA looping is strongly enhanced in the absence of H-NS, and an explanatory model is proposed. Chloroquine titration, psoralen crosslinking and supercoiling-sensitive reporter assays show that the effects of nucleoid proteins on looping are not correlated with their effects on either total or unrestrained supercoiling. These results suggest that host nucleoid proteins can directly facilitate or inhibit DNA looping in bacteria.

**INTRODUCTION**

DNA looping has been proposed as a fundamental mechanism for action at a distance in the control of gene expression and DNA recombination [reviewed in (1)]. It is of interest to understand whether the intrinsic physical properties of DNA are consistent with DNA looping constrained only through protein binding at the ends of the loop, or if looping also requires the action of proteins that enhance the apparent flexibility of the intervening DNA. There is active debate over the best model for describing local DNA stiffness, including recent controversial results on the probability of large bends in short pieces of DNA (2–6). However, it is clear from in vitro experiments that DNA strongly resists bending and twisting over distances shorter than its ~150 bp persistence length. For example, the efficiency of in vitro recombination using the *Hin* invertasome system falls dramatically as the length of DNA looped between recombination sites is reduced below one persistence length (7). That this effect is due to bending stiffness is confirmed by the observation that restriction fragments shorter than ~200 bp are poor substrates for cyclization by DNA ligase (8). Both reactions involve contact between distant DNA sites, and their rates are both increased dramatically when sequence-non-specific architectural proteins (bacterial HU or eukaryotic HMGB proteins, respectively) are present. Architectural binding proteins are sequence-specific or non-specific proteins whose main functions appear to be reshaping DNA and/or changing its apparent stiffness (9–20). Despite considerable study, it remains unclear whether these proteins function to increase apparent flexibility by creating static bends at various locations or by inducing flexible DNA kinking. The lifetimes of many such complexes on unperturbed DNA are unknown.

Both prokaryotes and eukaryotes must dramatically compact their genomic DNA while maintaining access of the genetic material to replication, transcription and repair machinery. If it were rigid, the 4.5 × 10⁶ bp *E. coli* chromosome would form a circle 1.5 mm in circumference. The intrinsic flexibility of DNA should allow spontaneous collapse only to a volume of ~200 μm³ (i.e. ~400 times larger than the *Escherichia coli* nucleoid). Thus, significant further DNA compaction must be achieved in vivo (21). Proteins can facilitate this additional compaction using binding-free energy available from protein/DNA interactions. Genome compaction in eukaryotes is achieved by the spooling of DNA onto histone octamers and packing of the resulting nucleosomes into 30 nm and higher-order
fibers. Packaged prokaryotic DNA lacks defined structures analogous to nucleosomes. Rather, six key nucleoid proteins assemble with the bacterial chromosome (21–23). These proteins include (in decreasing order of abundance during exponential growth): factor for inversion stimulation (Fis), heat-unstable nucleoid protein (HU), integration host factor (IHF), histone-like, nucleoid-structuring protein (H-NS), suppressor of td mutant phenotype A (StpA) and DNA-binding protein from starved cells (Dps). The present work focuses on HU, IHF and H-NS.

HU is a heterodimer of 90-residue (9.2 kDa) HU-1 and HU-2 subunits encoded by the E. coli hupA and hupB genes, respectively (22,24). HU binds DNA without sequence specificity, but has been reported to bind with greater avidity to pre-bent or kinked DNA (25–28), consistent with expectations for a DNA-bending protein. HU accumulates to ~25,000 dimers per cell during exponential growth, and it has been proposed that the protein functions in many processes including DNA replication, transcriptional repression and recombination (23). HU facilitates formation of a DNA repression loop in the gal operon, where the protein reportedly binds a specific sequence in the loop (29). Analysis of co-crystals of HU and DNA show sharp and variable DNA bending around the protein (30).

The integration host factor IHF, named for its role in phage λ integration, binds specific asymmetric DNA sites (WATCAANNNTTTR; W, A or T; N, any base; R, A or G) as a heterodimer (31,32), bending DNA by 160°. IHF and HU monomers share ~30% sequence identity and are related in both structure and function (20,31,33). The IHFα (99 aa, 11.2 kDa) and IHFβ (94 aa, 10.7 kDa) subunits are ~30% identical to each other (and to HU monomers) and are encoded by the E. coli himA and himD genes, respectively. Unlike HU, which can form either homodimers or heterodimers, IHF is isolated from cells only as a heterodimer, and IHFβ homodimers can only be produced at high subunit concentration in vitro. Such IHFβ homodimers bind DNA with 100 lower affinity than heterodimers, and IHFα homodimers are even less stable; thus, the removal of only the IHFα subunit in our experiments should eliminate all DNA-binding activity (34). Cells contain ~10,000 IHF dimers during exponential growth (23). Gene array profiling indicates that the expression of at least 100 genes is altered upon deletion of IHF, with 46 of the genes containing putative IHF-binding sites (35).

H-NS homodimers (137 aa, 15.4 kDa), the product of the E. coli hns gene, also accumulate to ~10,000 dimers per cell (21,36,37). The protein is believed to oligomerize into higher-order complexes via a coiled-coil domain (23,38,39). The protein C-terminus binds DNA, appearing to prefer A/T-rich or curved DNA. H-NS acts as a transcriptional repressor or silencer, with an H-NS-deficient strain showing increased expression of the heat-stable nucleoid protein (HU), histone-like, nucleoid-structuring protein (H-NS), suppressor of td mutant phenotype A (StpA) and DNA-binding protein from starved cells (Dps). The present work focuses on HU, IHF and H-NS.

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We have developed an experimental system for measuring DNA flexibility in living E. coli cells and have used it to determine whether proteins play important roles in enhancing the apparent flexibility of DNA. The system, shown schematically in Figure 1, is based on classic studies of DNA looping in repression of the E. coli lac operon, where the Lac repressor tetramer (circles) fills the high-affinity O sym operator, but repression by looping to the O 2 operator depends on the properties of the intervening DNA. Looping is disfavored by the energetic costs of twisting and bending DNA. Spacings that position operators on opposite faces of the DNA helix are unfavorable for repression loops because of the requirement for DNA twisting. (C) Spacings that position operators on the same face of DNA are favorable for repression loop formation.

Figure 1. In vivo DNA looping assay. (A) Arrangement of strong (O sym) and weak (O 2) lac operators (rectangles) flanking the lac promoter (P) upstream of the lacZ reporter gene. Operator spacing was systematically varied from 63 to 91 bp in individual strains. The binding face recognized by repressor tetramer is indicated by shading. (B) The Lac repressor tetramer (circles) fills the high-affinity O sym operator, but repression by looping to the O 2 operator depends on the properties of the intervening DNA. Looping is disfavored by the energetic costs of twisting and bending DNA. Spacings that position operators on opposite faces of the DNA helix are unfavorable for repression loops because of the requirement for DNA twisting. (C) Spacings that position operators on the same face of DNA are favorable for repression loop formation.
single copy on an F′ episome. Host strains with or without the genes encoding architectural DNA-binding proteins are used; they all express wild-type levels of the wild-type bidentate Lac repressor tetramer (49). The development of this system and its application to flexibility induced by the rat HMG-B protein have been described in detail (49).

Measurement of the degree of promoter repression as a function of operator separation provides information about the longitudinal and torsional bending properties of DNA in vivo. Control experiments using IPTG (a stable allolactose analog) reveal the behavior of the system when the affinity of repressor for DNA has been dramatically reduced. Previous characterization of this system for loop lengths of 63–91 bp revealed that (i) DNA twisting rather than bending is the major obstacle to DNA looping; (ii) weak repression loops are still detected in the presence of saturating concentrations of IPTG; (iii) deletion of the E. coli architectural protein HU dramatically destabilizes repression loops; (iv) replacement of E. coli HU with heterologous mammalian HMGB proteins can partially rescue DNA looping and (v) the effect of HU loss on DNA looping does not result from changes in DNA supercoiling (49). The key conclusion of these experiments was that the sequence-non-specific HU protein is required to stabilize small repression loops in E. coli.

These data as well as the original length-dependence work of Müller-Hill (48) have been analyzed recently by others, using several different formalisms (50). In one analysis (50) it was concluded that the bending properties of DNA in cells lacking HU match those measured in vitro, but other work has used Lac operon looping to support the existence of surprisingly easily bent DNA (1). An earlier rod mechanics model of the loop suggested that the repressor conformation changes depending on the supercoiling environment (51), in agreement with earlier experiments (52). The additional repression peaks caused by weak loops formed by the presence of IPTG-bound repression [conclusion (ii) above] have been identified in the Müller-Hill data set (48,53). Clearly, more experimental work is needed to clarify the loop geometry, the dependence of DNA flexibility on architectural proteins, and the effects of supercoiling.

The present study explores how the loss of HU and other E. coli nucleoid proteins affects DNA looping. We have confirmed and extended our earlier results. The most surprising new finding is that H-NS acts to destabilize rather than stabilize small loops. Changes in either total or unrestrained superhelicity do not appear to explain the effects of architectural proteins on DNA looping.

### MATERIALS AND METHODS

#### Bacterial strains and gene disruption

E. coli strains bearing gene disruptions are described in Table 1. The *hupA* and *hupB* genes were disrupted in parental E. coli strain FW102 (54) as described (49,55). Disruption of the *himD* gene (encoding the IHFβ subunit) was accomplished by gene-targeted recombination with a kanamycin selectable marker (complementary sequence in bold) amplified with primer pair LJM-2485 5′-A7TCAGCA CGACGT GTAGTG TCAGTG GTCGAC and LJM-2486 5′-AGCACCTG GTAGTG TCAGTG GTCGAC. Disruption of the *hupA* gene similarly involved recombination with a selectable marker (complementary sequence in bold) amplified with primer pair LJM-2477 5′-TA2G3CTCTAT2ACTAC4A2CA3C2AC4A2TATA2GT3 GTGTAG2CTG2AGCTGCT2C and LJM-2478 5′-AT9TC2GC2GCT2CG2AT4A2GCA2GTGCA2TCTACA T2C2G4ATC2GTCGAC. In each case, the integrated selectable marker was removed in a second step involving recombination between FRT sites as described (55).

Genotypes of all deletion strains and the presence of looping assay episomes were confirmed by diagnostic PCR amplification following conjugation and selection.

#### In vivo DNA looping assay

DNA looping constructs were based on plasmid pJ992, created by modifications of pFW11-null (54) as previously described (49). Constructs contained a strong distal O2 sym operator and a weak proximal O2 operator. The O2 operator normally present within the lacZ coding region was destroyed by site-directed mutagenesis (49). A construct with a proximal O2 but lacking upstream O2 sym was used as a normalization control. Test promoters did not contain CAP-binding sites. lacZ looping constructs were placed on the single copy F128 episome by homologous recombination between the constructed plasmids and bacterial episome. F128 carries the lacI gene producing wild type levels of repressor. Bacterial conjugation and selections were carried out as previously described (54). After mating and selection, correct recombinants were confirmed by PCR amplification.

#### Reporter assay

All chemicals were obtained from Sigma (St Louis, MO, USA). lacZ expression was measured by a liquid β-galactosidase colorimetric enzyme assay as

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>Designation</th>
<th>Comment</th>
</tr>
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<tbody>
<tr>
<td>FW102a</td>
<td>StrepR derivative of CSH142 [araD(gpt-lac)]</td>
<td>WT</td>
<td>Loss of both HU-1 and HU-2 subunits of HU heterodimer</td>
</tr>
<tr>
<td>BL643</td>
<td>FW102 ΔhupA ΔhupB</td>
<td>ΔHU</td>
<td>Loss of H-NS homodimer</td>
</tr>
<tr>
<td>BL706</td>
<td>FW102 Δhns</td>
<td>ΔH-NS</td>
<td>Loss of IHFβ subunit of IHF heterodimer. IHFβ homodimers are not stable.</td>
</tr>
<tr>
<td>BL707</td>
<td>FW102 ΔhimD</td>
<td>ΔIHF</td>
<td></td>
</tr>
</tbody>
</table>

*aFW102 was the kind gift of F. Whipple. BL strains were created for this study.*

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*Downloaded from https://academic.oup.com/nar/article/35/12/3988/1143420 by guest on 06 March 2022*
described (56). The assay was modified as follows to increase efficiency: cultures were grown in 1.1 ml LB/antibiotic in 96-well plates (2 ml capacity per well) with shaking (250 rpm) at 37°C. Subcultures (1.1 ml of media) were then inoculated with 30 μl of overnight culture in the presence or absence of 2 mM IPTG. Subcultures were grown with shaking at 37°C until OD_{600} reached ~0.3. For samples with low β-galactosidase activity, 800 μl of bacterial culture was assayed after centrifugation and resuspension in 1 ml Z-buffer (60 mM Na_{2}HPO_{4}, 40 mM NaH_{2}PO_{4}, pH 7.0, 10 mM KCl, 1 mM MgSO_{4}, 50 mM β-mercaptoethanol). For samples with high levels of β-galactosidase activity, 100 μl of bacterial culture was diluted with 900 μl of Z-buffer before analysis. Cells were lysed by addition of 50 μl chloroform and 25 μl 0.1% SDS, followed by repeated pipetting (10–12 times) with a 12 channel pipettor. Samples were equilibrated at 30°C for 5 min, followed by the addition of 200 μl of 4 mg/ml O-nitrophenylpyranogalactoside (ONPG) in Z-buffer. Incubation at 30°C continued with accurate timing until OD_{420} reached ~0.5. Reactions were stopped with 500 μl 1 M Na_{2}CO_{3} and the reaction time was recorded. Cell debris was pelleted by centrifugation of the 96-well box for 10 min at 4000 × g. Three hundred and fifty microliters of cleared samples were transferred to 96-well plates. Sample OD readings were measured on a Molecular Devices SpectraMax 340 microtiter plate reader. β-galactosidase activity (E) was calculated according to:

$$E = \frac{1000 \left(\text{OD}_{420} - 1.75(\text{OD}_{550})\right)}{r \cdot v \cdot \text{OD}_{600}}$$

where OD\(_x\) refers to optical density at wavelength \(x\), \(t\) is the reaction time (min) and \(v\) is the assay culture volume (ml). Assays were performed with a total of six colonies from each independent strain repeated on two different days.

**Looping data analysis and modeling**

The enhancement of repression due to specific DNA looping is expressed in terms of the normalized expression parameter \(E'\), according to:

$$E' = \frac{E_{\text{OsymO2}}}{E_{O2}}$$

where \(E_{\text{OsymO2}}\) is the raw β-galactosidase activity (induced or uninduced) from test constructs with both O\(\text{sym}\) and O\(2\) operators, and \(E_{O2}\) is the corresponding raw β-galactosidase activity (induced or uninduced) from test constructs with only the proximal O\(2\) operator. Note that Equation 2 is corrected from the original report (49).

The conventional repression ratio, \(RR\), is given by

$$RR = \frac{E_{+\text{IPTG}}}{E_{-\text{IPTG}}}$$

where \(E\) is the raw β-galactosidase activity under the indicated conditions.

A previously described statistical weights/DNA mechanics model (49) was used for simultaneous fitting of experimental \(E\) and \(RR\) data to expressions for the distribution of possible states of the O\(2\) operator under repressed and induced conditions. The experimentally derived fraction of O\(2\) that is bound by repressor (\(\tau_{\text{bound}}\)) is modeled as a function of DNA spacer length \(\langle sp \rangle\) with five adjustable parameters: the optimal operator spacing in bp \(\langle sp_{\text{optimal}}\rangle\), the DNA helical repeat \(\langle hr \rangle\), the apparent torsional modulus of the DNA loop \(\langle C_{\text{app}}\rangle\), the equilibrium constant for specific O\(\text{sym}\)–O\(2\) loop formation when operators are perfectly phased \(\langle K_{\text{max}}\rangle\) and an equilibrium constant for non-specific loop \(\langle K_{\text{NSL}}\rangle\). The \(K_{\text{NSL}}\) term describes all forms of O\(\text{sym}\)-dependent enhanced binding to O\(2\) other than the specific loop; for example, it could include looping between O\(\text{sym}\) and a pseudoperator overlapping O\(2\), or enhanced O\(2\) binding via sliding or hopping from O\(\text{sym}\).

**Assay of total supercoiling**

The total linking number deficit of plasmid DNA isolated from cells (500 ng) was assayed by separating topoisomers on multiple agarose gels at different concentrations of chloroquine (49,57). Electrophoresis was performed at 2 V/cm for ~18 h in 1X TAE buffer (45 mM Tris-acetate and 1 mM EDTA) through 0.8% agarose gels containing 0–10 μg/ml chloroquine. Gels were then stained with 5 μg/ml ethidium bromide until bands were barely visible, nicked for 30 s with long-wave UV irradiation, and then stained for an additional 30 min prior to photography. This procedure assures that the ethidium bromide binds equivalently to the different topoisomers.

**Assays of unrestrained supercoiling**

Trimethylpsoralen (TMP; Sigma) photo-crosslinking of plasmid DNA followed by Southern analysis was performed with modifications of a published method (58). Briefly, bacterial strains containing plasmid pJ992 (49) were subcultured and grown to mid-log phase, A\(_{600}\) ~ 0.6, typically in 5 ml of LB medium containing antibiotics. Cultures were pelleted by centrifugation at 3000 × g for 10 min, washed in M\(9 \) salts (56) and resuspended in M\(9 \) salts at 1/10 of the original volume, all at 4°C. TMP treatment and the initial steps of DNA harvesting were performed in the dark at 4°C unless otherwise indicated. An ethanol-saturated solution of TMP (5 μl) was added to 500 μl cell culture in a 6-well plate and allowed to equilibrate for 5 min. Samples were irradiated for various times using long-wavelength UV light (~366 nm) delivered from a hand-held (Mineralight) lamp at an intensity of 0.6 mW/cm². To compensate for TMP autoinactivation, additional TMP was added every 10 min (59). Cells were then lysed and DNA harvested as previously described (58). DNA was digested with XmiI to yield an ~950 bp restriction fragment from plasmid pJ992. A sample (5 μg) of the total resulting DNA was denatured in 100 mM NaOH by treatment for 2 min at 55°C followed by acid neutralization, and electrophoresed on a 1.2% agarose gel at 3 V/cm (60). DNA was transferred to a Nytran membrane (Whatman) using an alkaline transfer system following the manufacturer’s recommended protocol. After UV cross-linking to the membrane this method...
We first collected expression data for the full set of operator spacings using recombinant F’ episomes carried in our standard laboratory strain of *E. coli* (FW102, labeled ‘WT’). Data are shown in Figure 2A. The upper panel displays the conventional repression ratio (RR), while the lower panel shows normalized expression (*E*) both in the absence and presence of 2 mM IPTG as inducer. Data points were analyzed by a statistical weights/DNA mechanics model (49) with simultaneous fitting to *RR* and *E* data. The full data set is given in Supplementary Tables S1 and S2, and curve fit parameter estimates are provided in Table 2. Since our previous work, we introduced assay modifications that allow more rapid data collection and therefore more simultaneous measurements directly comparing different strains and conditions. The changes in assay timing, however, resulted in slightly higher measurements of gene expression for the most tightly repressed WT strains. Even so, the fit parameters in Table 2 for WT cells are quite similar to the previous report (49). The value for *K*_max is slightly smaller reflecting less-efficient peak repression and the value of *K*_NSL is slightly larger to compensate for the largely unchanged level of out-of-phase repression. All data reported here are new and were collected using the same methodology.

The repression ratio data for WT cells are characterized by periodic oscillation, with peaks (maximal repression) corresponding to alignment of operators on the same DNA face separated by integral multiples of the helical repeat of the DNA. As previously noted (49), the oscillation pattern contains secondary peaks, and it also appears to be damped as DNA length increases. The origin of this unexpected complexity is revealed by plotting the *E* data from both induced and uninduced WT cells (Figure 2A, lower panel). It is clear that under both conditions reporter expression oscillates with the DNA helical repeat, but that the oscillations are not precisely in phase. This is evidence for weak looping by Lac repressor even under conditions of induction at saturating IPTG concentrations. Optimal operator spacing differs by ~0.5 bp and the helical repeat differs by ~0.9 bp when loops are fit under induced versus uninduced conditions (Table 2). The complex peak structure of the repression ratio curve reflects dephasing (due to the helical repeat difference) between the uninduced and induced *E* data rather than a spacing-dependent change in DNA looping energy. The apparent overall damping in the repression ratio is also due to dephasing, as well as to broadening of the torsional oscillations as the length increases. It does, however, appear that points at longer DNA length tend to fall slightly below the fit curves, suggesting a weak effect of longitudinal flexibility. This lack of a strong dependence of optimal loop probability on DNA length for such small DNA segments suggests enhanced apparent DNA longitudinal flexibility *in vivo*; if the loop-free energy were controlled by the *in vitro* DNA elastic bending energy, we would have observed much more dramatic length dependence. The low fit value of the apparent DNA torsional modulus (*C*_app; Table 2) suggests a similar increase in apparent torsional flexibility.
DNA looping in the absence of HU, IHF or H-NS

Analysis of the ΔHU E. coli strain (Figure 2B) substantiates previous observations that loss of HU substantially disables looping (49). The observed ~3-fold effects of genetic background on promoter strength are factored out of both repression ratio (upper panel) and $E'$ data (lower panel), so Figure 2 reflects specific effects on DNA loop stability. Loss of HU protein causes a global ~3-fold decrease in estimated equilibrium constants for specific and non-specific loop formation ($K_{\text{max}}$ and $K_{\text{NSL}}$, Table 2). Notably, induced lacZ expression shows almost no residual operator phase dependence (Figure 2B, lower panel, filled circles), suggesting that the putative loop formed by IPTG-bound repressor requires HU for stability. The optimal operator spacing for uninduced DNA looping is ~2bp shorter in the absence of HU, suggesting a change in the optimum repression loop geometry, a reorganization of the DNA domain, or a change in the local supercoiling status in the absence of this nucleoid protein. Destabilization of DNA looping in the absence of HU could imply a direct, sequence-non-specific but possibly structure-specific binding of HU to looped DNA, as is seen for the related Gal

![Figure 2. Dependence of DNA looping on nucleoid proteins. $RR$ (upper panels) and $E'$ (lower panels) parameters were calculated as described in ‘Materials and Methods’ section. Closed and open symbols in lower panels reflect data obtained in the presence and absence of IPTG, respectively. Mean and standard deviation reflect assays from six different colonies repeated on two different days. Panels (A–D) show expression data reflecting DNA looping in (A) WT E. coli, (B) cells lacking HU, (C) cells lacking IHF and (D) cells lacking H-NS. Each new data set is shown as mean with standard deviations. Least squares curve fits (red) are based on the statistical weights/DNA mechanics model with simultaneous fitting to $RR$ and $E'$ data. The fits to the WT data from A are replicated in panels B–D in gray with thin lines, for comparison. Shading between uninduced and induced WT $E'$ fits (lower panels) is to facilitate comparison.](https://academic.oup.com/nar/article/35/12/3988/1143420)

**Table 2.** Fitting parameters from statistical weights/DNA mechanics model of DNA looping$^{a,b}$

<table>
<thead>
<tr>
<th>Strain</th>
<th>$s_{p_{\text{optimal}}}$ (bp)$^a$</th>
<th>$C_{\text{app}}$ ($\times 10^{-19}$ erg cm)$^4$</th>
<th>$hr$ (bp/turn)$^5$</th>
<th>$K_{\text{max}}$$^c$</th>
<th>$K_{\text{NSL}}$$^g,b$</th>
</tr>
</thead>
<tbody>
<tr>
<td>IPTG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WT</td>
<td>78.7 ± 0.2</td>
<td>79.2 ± 0.3</td>
<td>0.73 ± 0.14</td>
<td>1.16 ± 0.52</td>
<td>11.6 ± 0.3</td>
</tr>
<tr>
<td>ΔHU</td>
<td>76.9 ± 0.6</td>
<td>78.6 ± 0.7</td>
<td>0.68 ± 0.11</td>
<td>0.33 ± 0.08</td>
<td>11.1 ± 0.3</td>
</tr>
<tr>
<td>ΔIHF</td>
<td>78.8 ± 0.5</td>
<td>80.3 ± 0.5</td>
<td>0.40 ± 0.07</td>
<td>0.67 ± 0.33</td>
<td>12.4 ± 0.7</td>
</tr>
<tr>
<td>ΔH-NS</td>
<td>77.0 ± 0.2</td>
<td>79.0 ± 1.3</td>
<td>0.69 ± 0.09</td>
<td>1.38 ± 0.60</td>
<td>11.4 ± 0.3</td>
</tr>
</tbody>
</table>

$^a$The indicated error range are the 95% confidence limits from Matlab.
$^b$The fits are to $E_{-\text{IPTG}}, E_{+\text{IPTG}},$ and $RR$ simultaneously.
$^c$Operator spacing (center-to-center) nearest 80 bp for optimal DNA loop stability.
$^d$Apparent torsional rigidity of the protein/DNA loop (compare with value for DNA in vitro: 2.3–3 $\times 10^{-19}$ erg cm).
$^e$DNA helical repeat (bp/turn).
$^f$The fits are to $E_{-\text{IPTG}}, E_{+\text{IPTG}}$ and $RR$ simultaneously.
$^{g}$Specific DNA loop$^h$[free operator] for the most stable loop at the cellular [LacI], assumed to be constant.
$^{h}$Specific DNA loop$^i$[non-specific DNA loops][free operator].
$^i$Parentheses indicate an unreliable parameter estimate (large error).
Role of unrestrained negative supercoiling in DNA looping

Perturbations in the normal complement of nucleoid proteins could influence the stabilities of repression loops by direct and/or indirect mechanisms. For example, direct loop stabilization could occur if architectural proteins bind within the DNA loop so as to introduce at least transient favorable bends or sites of flexibility. Indirect effects on DNA looping could result from local changes in superhelical strain or superhelix geometry caused by the absence of a nucleoid protein. To differentiate among explanations invoking superhelical writhe, twist strain and protein binding, it is important to have measurements of restrained supercoiling (due to DNA wrapping on protein surfaces), and unrestrained supercoiling, which creates actual mechanical twisting strain (63). The total DNA linking number deficit is the sum of these two components. Restained supercoiling could be important in creating a DNA geometry favorable or unfavorable for looping, whereas unrestrained supercoiling has the potential to drive the compaction of naked DNA, facilitating formation of the repression loop. Enhancement of DNA looping by supercoiling has been reported in vitro (64–66) and in vivo (29).

To determine whether direct or indirect mechanisms better explain the effects of nucleoid proteins on DNA looping, we independently measured both total and unrestrained negative supercoiling in WT, ΔHU, ΔIHF and ΔH-NS E. coli strains using several methods. Total supercoiling was monitored by assessing plasmid topoisomer distributions after extraction from cells, using electrophoretic separation of topoisomers in agarose gels containing different concentrations of the intercalating agent chloroquine. The concentration of chloroquine required to alter DNA twist sufficiently to eliminate negative supercoils (thereby maximally reducing plasmid electrophoretic mobility) is directly related to the initial negative superhelical density of the extracted plasmid. Figure 3 and Table 3 show the results when plasmids from WT, ΔHU, ΔIHF and ΔH-NS strains were electrophoresed in the presence of 1, 2, 3, 5, 7 or 9 μg/ml chloroquine. Plasmid topoisomer mobility decreased over this chloroquine concentration range, demonstrating that all plasmid populations were initially negatively supercoiled. Importantly, however, the degree of total negative supercoiling depended on the complement of nucleoid proteins. Inspection of the electrophoresis series showed that total negative supercoiling was indistinguishable in WT and ΔH-NS strains. In contrast, total negative supercoiling was strongly reduced in ΔHU cells but strongly increased in ΔIHF relative to WT (this is most clear Figure 3, 7 μg/ml chloroquine). The result for ΔHU cells confirms our previous observations (49).

As discussed earlier, the chloroquine titration method assays total supercoiling, reflecting the in vivo sum of restrained and unrestrained supercoiling of plasmids in the cell. Because unrestrained supercoiling generates local twisting strain, while restrained supercoiling does not, it was important to determine if levels of unrestrained supercoiling follow the same trends as those seen in Figure 3.
Figure 3. Effects of nucleoid proteins on DNA supercoiling. (A) Effects on total supercoiling. The superhelical strain in plasmid pJ1035 isolated from the indicated E. coli strains was measured by electrophoresis in the presence of the indicated concentrations of the weak intercalator chloroquine, as described in ‘Materials and Methods’ section. Negatively supercoiled plasmid DNA (high mobility) is relaxed by increasing binding of chloroquine over this range of concentrations. (B) Unrestrained superhelical strain is measured by the rate of psoralen crosslinking of plasmid DNA. The Southern blot distinguishes ssDNA and rapidly renaturing dsDNA. Native (lane 1) and denatured (lane 2) markers are shown. Cross-linked (ds) and non-cross-linked (ss) mobilities are indicated. Samples were analyzed after 5, 10, 15, 20 or 25 min of exposure to TMP in WT (lanes 3–7), ΔHU (lanes 8–12), ΔH-NS (lanes 13–17) and ΔIHF (lanes 18–22) cells. (C) Quantitation of data from panel B after subtraction of local background signal. WT: filled circles; ΔHU: open squares; ΔH-NS: open circles; ΔIHF: filled squares. The percentages indicated are the slopes fit by linear regression relative to the WT slope.
One biochemical approach to the measurement of unrestrained supercoiling in vivo was developed for eukaryotic cells. It is based on the enhanced binding and photocrosslinking of intercalating psoralen derivatives to DNA under unrestrained superhelical strain (67). We adapted this approach to monitor changes in superhelical strain in prokaryotes. The assay measures changes in the rate of trimethylpsoralen (TMP) crosslinking of plasmid pJ992. The extent of psoralen cross-linking was measured by plasmid isolation, restriction digestion, denaturation, electrophoresis and Southern blotting to measure the extent of crosslink-enabled rapid dsDNA renaturation. Sample autoradiograms are shown in Figure 3B, and the results of image quantitation are given in Figure 3C and Table 3. These data show that levels of unrestrained negative supercoiling were similar for WT and ΔH-NS strains, while negative supercoiling in the WT and ΔH-NS strains was increased relative to WT (Table 3). These results generally track with measured levels of total supercoiling except for the ΔH-NS strain.

We found the TMP crosslinking assay to be technically challenging and only moderately reproducible for the present purpose. We therefore performed a more direct bioassay that has recently been reported for the measurement of unrestrained supercoiling in bacteria (61). This assay exploits the fact that the promoters driving expression of DNA gyrase (gyrA) and topoisomerase I (topA) are oppositely responsive to local levels of unrestrained negative supercoiling. The gyrA promoter is repressed by high unrestrained negative supercoiling and activated when unrestrained negative supercoiling is low. In contrast, the promoter cluster driving topA is activated by high unrestrained negative supercoiling and repressed when unrestrained negative supercoiling is low. This intuitively reasonable relationship supports bacterial supercoiling homeostasis. By placing reporter genes downstream from these promoters (Figure 4) in separate plasmid constructs or in the bacterial assay episome itself, the ratio of topA:gyrA reporter activities can be used to monitor unrestrained negative supercoiling in vivo. This assay approach was applied to WT, ΔHU, ΔHIF, and ΔH-NS strains with reporter promoters either carried on high or low-copy number plasmids of different sizes or integrated into the large F episome, providing the results shown in Table 3. As seen for total supercoiling, the extent of unrestrained negative supercoiling was found to be very similar for WT and ΔH-NS strains, independent of the DNA construct carrying the reporters. This result was completely reproducible, though it does not agree with a previous report that loss of H-NS caused a modest increase in negative supercoiling (58). In contrast, the diagnostic Qsc ratio for ΔHU cells depended on the location of the reporter genes. For plasmids, the Qsc ratios were significantly less than the WT ratio, but the Qsc value was more variable and somewhat increased versus WT when assayed in the F episome (Table 3). The basis for context-dependent changes in the unrestrained negative supercoiling in the absence of HU protein is unknown. The data in Table 3 also show that unrestrained negative supercoiling was consistently and significantly higher in ΔIHF cells, with the diagnostic Qsc ratio 2- to 4-fold higher that observed for WT cells; for ΔIHF cells the results of all supercoiling assays are concordant.

Three important conclusions can be drawn from these supercoiling assays. First, the promoter activity bioassays of unrestrained supercoiling in the test strains parallel the results of total supercoiling assays. In general it appears

### Table 3. DNA supercoiling

<table>
<thead>
<tr>
<th>Strain</th>
<th>Total negative supercoiling</th>
<th>Unrestrained negative supercoiling</th>
<th>Unrestrained negative supercoiling</th>
<th>Qsc index b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(chloroquine titration)</td>
<td>(%) of control</td>
<td>(Qsc index)</td>
<td>% of control</td>
</tr>
<tr>
<td>WT WT level (reference)</td>
<td>100°</td>
<td>2.1 ± 0.2 d</td>
<td>100 ± 9 d</td>
<td>3.1 ± 0.5 c</td>
</tr>
<tr>
<td>ΔHU Noticeable decrease</td>
<td>90°</td>
<td>3.0 ± 0.3 e</td>
<td>100 ± 9 e</td>
<td>3.1 ± 0.5 c</td>
</tr>
<tr>
<td>ΔH-NS Slight decrease</td>
<td>330°</td>
<td>0.7 ± 0.1 c</td>
<td>34 ± 5 c</td>
<td>2.0 ± 0.3 c</td>
</tr>
<tr>
<td>ΔHIF Large increase</td>
<td>560°</td>
<td>5.9 ± 2.5 c</td>
<td>190 ± 73 c</td>
<td>2.6 ± 0.2 c</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.2 ± 0.1 c</td>
<td>102 ± 6 e</td>
<td>3.2 ± 0.3 c</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4.6 ± 0.2 d</td>
<td>220 ± 7 d</td>
<td>13.7 ± 1.2 c</td>
</tr>
<tr>
<td></td>
<td></td>
<td>12.7 ± 2.3 e</td>
<td>405 ± 73 c</td>
<td>10.2 ± 4.3 e</td>
</tr>
</tbody>
</table>

bCalculated as described in ‘Materials and Methods’ section based on rate of psoralen cross-linking or topA: gyrA ratios of reporter gene expression, where the promoters are inversely responsive to local unrestrained superhelical tension.

cQuotient of supercoiling, defined as topA: gyrA reporter ratio after normalization for cell density as described in ‘Materials and Methods’ section.

dBased on reactivity of plasmid pJ992.

eBased on topA: gyrA reporter ratio in large plasmids pJ1345 and pJ1346.

fBased on topA: gyrA reporter ratio in small plasmids pJ1454 and pJ1456.

gBased on topA: gyrA reporter ratio in the bacterial F episome.
that a fairly constant fraction of total supercoiling is due to unrestrained supercoiling in vivo. Second, unrestrained supercoiling estimates from supercoiling-dependent promoters generally do not depend on whether the promoter-reporters are present on plasmids or episomes. Third, and most importantly here, the effects of eliminating different nucleoid proteins on repression loop stability cannot be explained simply by invoking perturbations in local unrestrained supercoiling. Comparison of the data in Table 3 and Figure 2 reveal no correlation between repression loop stability and levels of unrestrained negative supercoiling in the different genetic backgrounds tested. In particular, ΔH-NS cells showed strongly enhanced DNA looping but had a level of negative DNA supercoiling that was similar to WT cells (Table 3). The ΔIHF cells showed strongly increased unrestrained negative supercoiling but little change in DNA looping (Table 3). The ΔHU cells have only slightly decreased negative supercoiling but show substantial changes in loop stability and character. These results suggest that the observed changes in looping are not caused by indirect supercoiling effects. This conclusion also supports our previous observation that DNA looping was not reduced when total negative supercoiling in E. coli was reduced using the gyrase inhibitor Norfloxacin (49).

Model for enhanced DNA looping in the absence of H-NS

The data in Figure 2 indicate that loss of the H-NS protein enhances the formation of the experimental DNA loop in living E. coli. The data in Figure 3 and Table 3 show that this effect does not involve changes in DNA supercoiling. How might the loss of H-NS facilitate DNA looping? Single molecule experiments have shown that H-NS, like other DNA-binding proteins (68,69), can either endow flexibility (at low binding densities) or stiffness (at high binding densities) (24,42). If H-NS concentrations were sufficient to drive high protein occupation of the repression loop, DNA stiffening might antagonize looping, but this seems unlikely, as exponentially growing cells are thought to contain only about one H-NS dimer per 1400 bp of DNA (21,70). Another model to explain H-NS inhibition of DNA looping is based on the observation that H-NS dimers have two DNA-binding domains and can bridge between DNA duplexes (21,43). Such cross-linking could inhibit DNA looping by the mechanism shown in Figure 5. Looping requires the shortening of a segment of DNA and would be inhibited if DNA segments are cross-linked by H-NS proteins and not free to slide past one another in the crowded nucleoid.

SUMMARY AND IMPLICATIONS

We have adapted classic work on the lac operon (45–48) to develop a system for studying in vivo DNA flexibility. Regulatory elements from the lac operon have been organized into a series of episomal constructs in which reporter gene repression is highly dependent on the stability of a small DNA loop between operators. We previously used this system to show that DNA twist inflexibility limits looping in vivo, while optimal loop stabilities are independent of DNA length over the range 63–91 bp (49). We also demonstrated weak DNA looping by Lac repressor even when saturated by IPTG, and showed evidence that loss of the nucleoid protein HU destabilized repression loops. The present experiments confirm and extend these conclusions. We demonstrate
that the simple statistical weights/DNA mechanics model used here can capture the observed experimental variations and suggest underlying physical interpretations. It has not been necessary to include explicit consideration of DNA bending persistence length changes or alternative loop shapes, but the lack of a DNA length effect and the calculated values of the torsional modulus confirm that the apparent effective flexibility of DNA in vivo is much greater than would be expected from in vitro experiments.

The structure and composition of the bacterial nucleoid is ill-defined, and much remains to be learned regarding the roles of major nucleoid proteins. In one proposed classification (21), nucleoid proteins are characterized as DNA bridging factors (H-NS, SMC, Lrp) or DNA bending factors (HU, IHF, Fis). Our study used DNA loop stabilization as a probe of the effects of HU, IHF and H-NS proteins on properties of the E. coli nucleoid. We conclude that loss of the sequence-non-specific DNA bending factor HU strongly destabilizes a repression loop, while loss of the sequence-specific bending factor IHF has much less effect. In contrast, loss of the DNA bridging factor H-NS from the nucleoid facilitates DNA looping. We show that the effects of these gene disruptions on DNA looping do not generally correlate with their effects on negative DNA supercoiling in the host. Therefore we interpret the DNA looping phenotypes of HU, IHF and H-NS deletion strains as evidence for direct protein–DNA interactions that alter the apparent physical properties of the looped DNA. We cannot rule out that DNA looping effects observed upon removing nucleoid proteins could have more complex origins. For example, mutant strains may express altered levels of the remaining nucleoid proteins and/or other factors related to apparent DNA flexibility (39). The different effects on DNA looping of HUF versus HU loss may be due to the lower abundance of IHF or to higher non-sequence-dependent DNA binding by HU in the DNA loop. Future studies will investigate whether IHF and HU participate in the experimental repression loop. The strong enhancement of DNA looping upon deletion of H-NS is surprising, and the mechanism remains unknown. It remains possible that the loss of H-NS might simply reduce competition for important HU sites near the DNA loop, but we suggest that loop stabilization is due to inhibition of DNA slithering. Comparisons among other bending and bridging proteins should resolve this issue.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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**Conflict of interest statement.** None declared.

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