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Quantitative determination of linking number differences between circular polynucleosomes and histone H1-bound circular polynucleosomes

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ABSTRACT

With the aim of discovering contribution of histone H1 to linking number changes of DNA, determination of linking number differences between histone H1-free circular polynucleosomes and histone H1-bound circular polynucleosomes was carried out during our investigations. Our results showed that on average, binding of ~11.5 histone H1 molecules causes one linking number change in circular polynucleosomes in the presence of 1.5 mM spermidine. When concentrations of spermidine decreases or increases, these linking number differences decrease significantly. It is therefore evident that linking number changes caused by histone H1 are spermidine concentration-dependent.

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As highly abundant proteins in the eukaryotic cells, histones can be divided into core histones (H2A, H2B, H3 and H4) and linker histones (H1/H5) respectively according to their relative positions in nucleosomes.[1,2] Two copies of each of H2A, H2B, H3 and H4 histones constitute histone octamers that display disc-like overall shape.[3] In the co-existence of histone octamers and plasmid DNA, circular polynucleosomes will form, which are the assemblies of repeating unites of nucleosome core particles and linker DNA.[4–6] It was demonstrated in our previous investigations that negative DNA supercoiling was generated by these circular polynucleosomes upon addition of histone H1, which led to their formation of highly compact structural aggregates.[6] Our further studies showed that negative supercoils in these circular polynucleosomes could arise because binding of histone H1 to nucleosomes forced two arms of DNA to adopt right-handed positive supercoils along the surfaces of nucleosomes (Fig. 1).[7] With the intention of knowing linking number changes of DNA that are caused by binding of histone H1 to nucleosomes, new studies on histone H1-bound circular polynucleosomes were carried out in our lab recently. Here we report that in the presence of 1.5 mM spermidine, binding of one histone H1 protein molecule leads to the increase of linking number *ca.* +0.09 in circular polynucleosomes. In addition, when spermidine concentrations either decreased or increased, contribution of histone H1 to linking number changes decreased. In the absence of spermidine or in the presence of 5 mM spermidine, the effect of histone H1 on linking number changes of circular polynucleosomes dropped significantly. It is therefore evident that linking number differences between circular polynucleosomes and histone H1-bound circular polynucleosomes are spermidine concentration-dependent.

Fig. 2a depicts our preparations of (i) nick-containing circular polynucleosome (Structure 3) and (ii) nick-containing histone H1-bound circular polynucleosome (Structure 4) starting with pBR322 (Structure 1). This 4361 base-pair plasmid DNA contains a single 5′-GCTCTTCN*-3′/3′-CGAGAAGN-5′ site in its circular sequence, which is the recognition site of nicking endonuclease, Nt.BspQI. Nt.BspQI was accordingly incubated with pBR322 in our studies for generating a nick site in its circular entity (Structure 2). As shown in Lane 3 in Fig. 2b, rates of mobility shifts of Structure 2 was slower than that of Structure 1 (Lane 2), which is the sign that nick sites were produced in this plasmid DNA. Core histones (H2A, H2B, H3.1, and H4) were incubated next with Structure 2 and the resultant products did not show any mobility in the gel (Lane 4 in Fig. 2b). This non-migratable nature of the band in Lane 4 in Fig. 2b is evident that extremely high molecular weight DNA-protein complexes (Structure 3) were formed. Histone H1-bound polynucleosomes (Structure 4) was subsequently prepared in our studies by incubating Structure 3 with histone H1 (Step 3 in Fig. 2a). Similar to Structure 3 (Lane 4 in Fig. 2b), Structure 4

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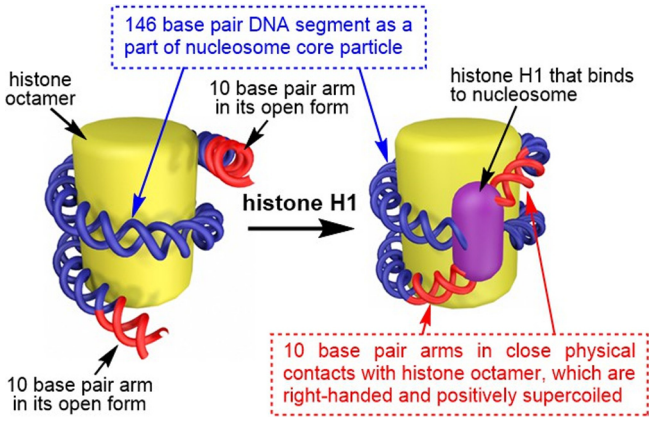


Fig. 1. Illustration of right-handed positive DNA supercoils in the two arm DNA segments that are affiliated with binding of histone H1 to a nucleosome.[7]

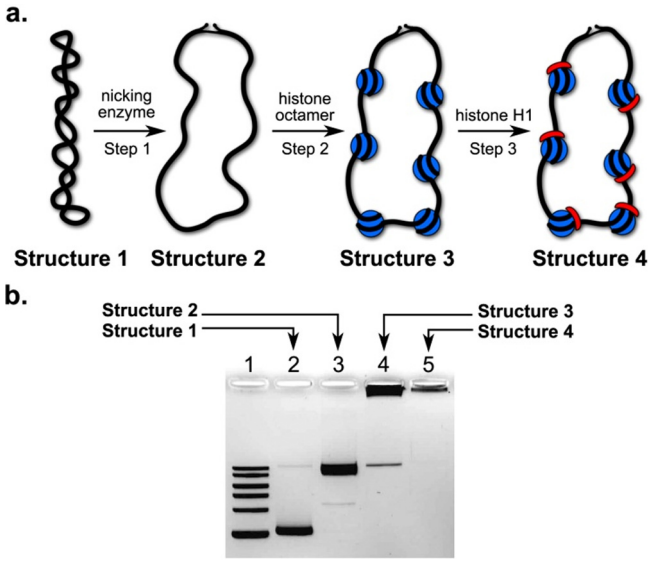


Fig. 2. (a) Illustration of our synthetic routes toward nick-containing histone H1-free polynucleosomes (Structure 3) and nick-containing histone H1-bound polynucleosomes (Structure 4). (b) Agarose gel electrophoretic analysis of Structure 3 and Structure 4. Lane 1, 1 kb DNA molecular weight marker; Lane 2, pBR322 (Structure 1); Lane 3, reaction products (Structure 2) of Nt.BspQI (nicking endonuclease) with pBR322; Lane 4, products (Structure 3) generated from mixtures of Structure 2 and histone octamers; Lane 5, products (Structure 4) generated from mixtures of Structure 3 and histone H1 (detailed descriptions about the sample preparations are given in Supporting Information).

(Fig. 2a) did not display any mobility shift (Lane 5 in Fig. 2b) as a result of formation of pBR322 complexes with histone octamers and histone H1.

With the aim of determining contribution of histone H1 to linking number changes in polynucleosomes, Structure 6 and Structure 8 were prepared in our studies starting with Structure 3 and Structure 4 (Route 1 and Route 2 in Fig. 3a). The nick sites in Structure 3 and Structure 4 were accordingly covalently sealed through using DNA ligase in our studies in the presence of 1.5 mM spermidine (Lane 4 and Lane 5 in Fig. 3b). Proteinase K hydrolysis on the resultant Structure 5 and Structure 6 were carried out next to remove histone proteins from plasmid DNA molecules to form Structure 7 and Structure 8 respectively (Lane 6 and Lane 7 in Fig. 3b). In theory, if histone H1 could contribute to linking number changes of circular DNA in polynucleosomes, linking number difference between Structure 6 and Structure 8 should exist.

If plasmid DNA molecules of identical sequences possess different linking numbers, on the other hand, they are defined as "DNA topological isomers".[8,9] In order to make the distribution patterns of topological isomers of plasmid DNA clearly visible, Shure et al. successfully developed a special agarose gel-based method previously, in which chloroquine molecules were used as DNA intercalating agents. This method reported by Shure et al. was accordingly used in our studies for analyzing distribution patterns of topological isomers in Structure 6 and Structure 8 respectively. As seen in Lane 3 and Lane 4 in Fig. 4a, band distributions emerged in our agarose gel electrophoresis of Structure 6 and Structure 8, as it occurred in all of the previously reported chloroquine-based examination on DNA topological isomers.[10–12] Intensities of these bands in relation to their distances of migration in Lane 3 (Structure 6) and Lane 4 (Structure 8) in Fig. 4a were subsequently measured in our investigation (Fig. 4b and d) through using densitometry methods as reported previously.[13–15] Because relative amounts of each types of DNA topological isomers obtained upon actions of (i) type I topoisomerase,[16,17] (ii) type II topoisomerase,[16,18] and (iii) DNA ligase[14] obey Gaussian distributions,[14,16–18] Gauss fit was performed next in our studies on the data shown in Fig. 4b and d through using the same approaches as those reported by Vetcher et al.[14] for the purpose of generating Gaussian representation of linking number distributions of our DNA topological isomers in Structure 6 (Fig. 4c) and Structure 8 (Fig. 4e) respectively. Our obtained mean values of ΔLk ($\Delta Lk = Lk - Lk_0$, where Lk is the linking number of supercoiled plasmid DNA and Lk_0 is the one in its relax form[8]) in (i) Structure 6 and (ii) Structure 8 derived from the Gaussian distributions in Fig. 4c and e are (i) −5.89 and (ii) −5.38 while the difference between these two mean values is +0.51 [(−5.38) − (−5.89) = +0.51]. The value of +0.51 is the linking number contributed by histone H1 molecules that bound to Structure 8 because supercoils in Structure 8 were contributed by both histone octamers and histone H1 while those in Structure 6 was caused by histone octamers alone. In addition, since Structure 8 (i) possesses 5.89 histone octamers in its structure, and (ii) holds the same quantity of histone octamers as Structure 6, there should be 5.89 histone octamers on average in Structure 8. Consequently, there should be 5.89 histone H1 molecules that bound to nucleosomes in Structure 8. As a result, each histone H1 protein molecule contributes to changes of linking number is +0.09 (+0.51/5.89 = +0.09), which signifies that binding of 11.5 (5.89/0.51 = 11.5) histone H1 molecules produces one linking number change in circular polynucleosomes.

Besides the examinations shown in Fig. 4 that were conducted in the presence of 1.5 mM spermidine, studies of effects of lower concentrations of spermidine was carried out as well during our investigations. As shown in Figs. 1 and 2 in Ref. 19, differences of mean values of linking numbers of DNA topological isomers between histone H1-free polynucleosomes and histone H1-bound polynucleosomes are +0.27 and +0.03 in the presence of 0.75 mM and 0 mM spermidine respectively. These results indicate that differences of linking numbers between (i) histone H1-bound and (ii) histone H1-free polynucleosomes decreased with the decrease of spermidine concentrations. This decrease is consistent with our previous observations that at lower concentrations of spermidine and in the absence of spermidine, nucleosomes tended to adopt their arm-closed forms (Assembly 1 in Column 1 in Fig. 5b).[7] More specifically, since the two arm DNA segments already exist in their arm-closed forms in the absence of spermidine in Assembly 1, binding of histone H1 to nucleosomes (Assembly 2 in Column 1 in Fig. 5b) will have little effects on the conformational changes of nucleosomes.

With the aim of knowing how increase of spermidine concentration affects differences of linking numbers of DNA topological isomers between histone H1-free polynucleosomes and histone

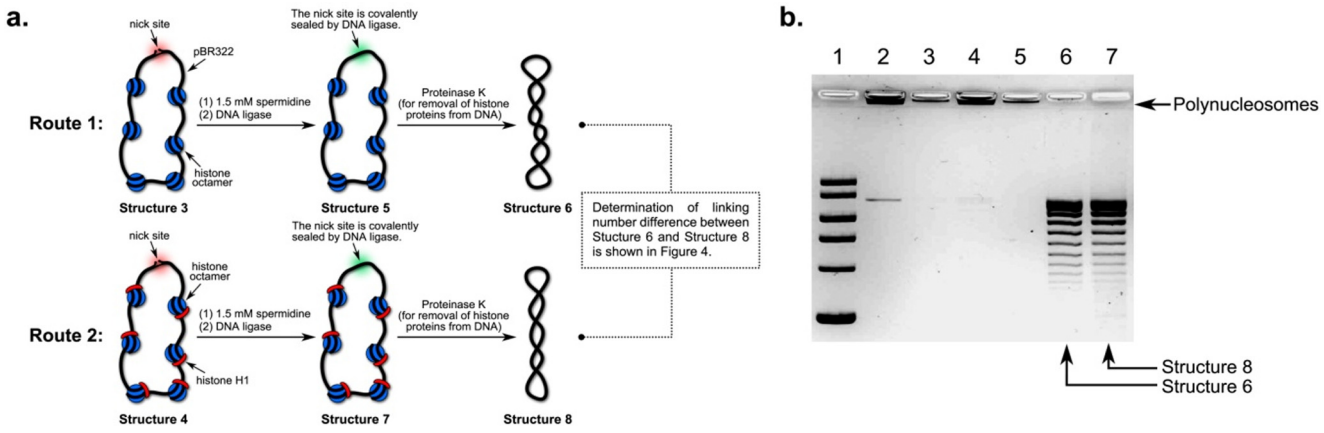


Fig. 3. (a) Illustration of our synthetic routes toward Structure 6 and Structure 8 starting with nick-containing histone H1-free polynucleosomes (Structure 3) and nick-containing histone H1-bound polynucleosomes (Structure 4) separately. (b) Electrophoretic analysis of Structure 6 and Structure 8 as well as their precursors. Lane 1, 1 kb DNA molecular weight marker; Lane 2, Structure 3; Lane 3, Structure 4; Lane 4, reaction products (Structure 5) of DNA ligase with Structure 3; Lane 5, reaction products (Structure 7) of DNA ligase with Structure 4; Lane 6, reaction products (Structure 6) of proteinase K with Structure 5; Lane 7, reaction products (Structure 8) of proteinase K with Structure 7 (detailed descriptions about the sample preparations are given in Supporting Information).

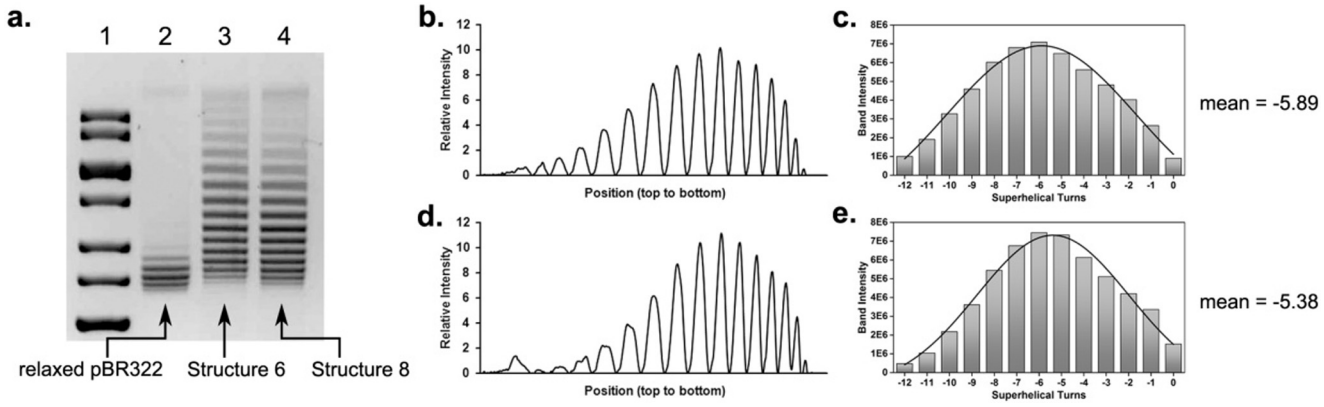


Fig. 4. (a) Chloroquine-based agarose gel electrophoretic analysis on Structure 6 and Structure 8. Lane 1, 1 kb DNA molecular weight markers; Lane 2, relaxed forms of pBR322; Lane 3, Structure 6; Lane 4, Structure 8 (detailed descriptions about the sample preparation are given in Supporting Information. (b) Densitometry tracing of gel electrophoretic results in Lane 3 (Structure 6). (c) Plot of Gauss fit on the data shown in Fig. 4b, which gave rise to −5.89 as its mean value of ΔLk. (d) Densitometry tracing of gel electrophoretic results in Lane 4 (Structure 8). (e) Plot of Gauss fit on the data shown in Fig. 4d, which gave rise to −5.38 as its mean value of ΔLk.

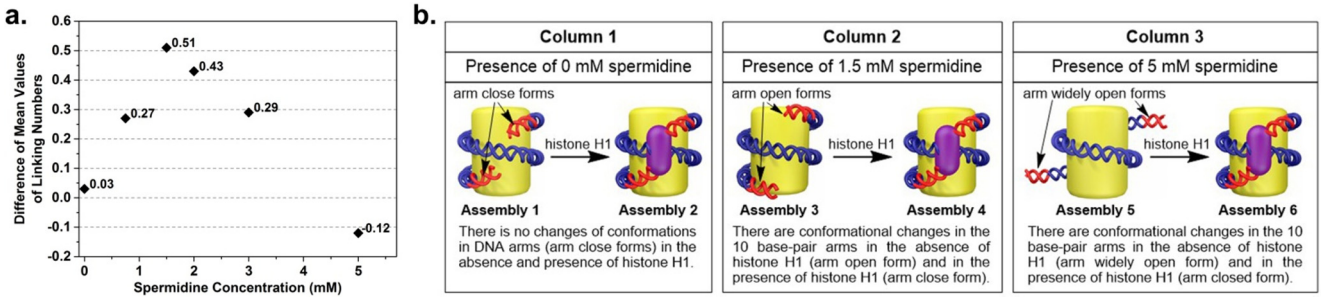


Fig. 5. (a) Plot of concentrations of spermidine *vs.* differences of mean linking numbers between histone H1-free circular polynucleosomes and histone H1-bound circular polynucleosomes (this plot was created based on the data derived from Fig. 4 in this article and Figs. 1–5 in Ref. 19). (b) Illustration of DNA arm conformations of nucleosomes in the presence of 0 mM, 1.5 mM and 5 mM spermidine.

H1-bound polynucleosomes, on the other hand, additional studies were carried out during our investigations as well. As shown in Figs. 3–5 in Ref. 19, in the presence of 2 mM, 3 mM and 5 mM spermidine, linking number differences of DNA topological isomers between histone H1-free polynucleosomes and histone H1-bound polynucleosomes decreased from +0.43 to +0.29 to −0.12 (Fig. 5a). One of the likely causes of this decrease is that at its higher concentrations, spermidine molecules would enforce the DNA segments in nucleosome core particles to widely open up, which will relax left-handed negative supercoils in the DNA segments that enter and exit nucleosome core particles. Once histone H1 binds to nucleosomes, negative supercoils at the ends of nucleosomal DNA and positive supercoils in the two 10 base-pair DNA arms will form at the same time (Column 3 in Fig. 5b). Because the

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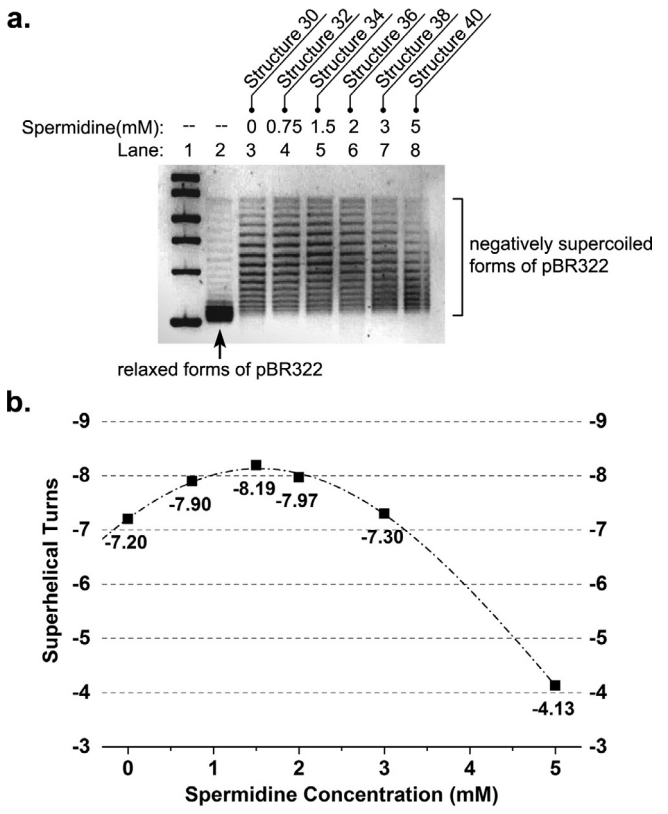


Fig. 6. (a) Electrophoretic analysis of circular polynucleosomes prepared in the presence of different concentrations of spermidine. Lane 1, 1 kb DNA molecular weight markers; Lane 2, relaxed forms of pBR322; Lane 3 to Lane 8, circular polynucleosomes prepared in the presence of 0 mM (Lane 3), 0.75 mM (Lane 4), 1.5 mM (Lane 5), 2 mM (Lane 6), 3 mM (Lane 7) and 5 mM (Lane 8) spermidine respectively. (b) Plot of spermidine concentrations *vs.* mean ΔLk values of circular polynucleosomes (data of mean ΔLk values of circular polynucleosomes for Fig. 6b are shown in Fig. 6 in Ref. 19).

simultaneously formed negative supercoils and positive supercoils cancel out each other upon proteinase K's digestion, difference of linking numbers of DNA topological isomers between histone H1-free polynucleosomes and histone H1-bound polynucleosomes at high spermidine concentrations diminished (Fig. 5a).

If spermidine alone could indeed affect DNA arms of nucleosomes in the manner as portrayed in Fig. 5b,[7] their effects on linking numbers of circular polynucleosomes should in theory exist in the absence of histone H1 as well. Correlations of spermidine concentrations with linking numbers of circular polynucleosomes were accordingly examined in our studies without involvement of histone H1 (Fig. 6). As shown in Fig. 6a, Structure 3 was first allowed to form close circular polynucleosomes by the action of DNA ligase in the presence of 0 mM, 0.75 mM, 1.5 mM, 2 mM, 3 mM and 5 mM spermidine respectively, followed by proteinase K hydrolysis. The mean ΔLk values of topological isomers of Structure 30, Structure 32, Structure 34, Structure 36, Structure 38 and Structure 40 were subsequently determined (Fig. 6a in this article and Fig. 6 in Ref. 19) in the same manners as those described in Fig. 4. As illustrated in Fig. 6b, mean ΔLk values of pBR322 increased when spermidine concentrations increased from 0 mM to 1.5 mM. When spermidine concentrations increased from 2 mM to 5 mM, however, the mean ΔLk values of polynucleosomes decreased (Fig. 6b). These observations are consistent with the suggestion that the arm-open and arm-closed forms of DNA exist in the ways as presented in Fig. 5b.

In conclusion, quantitative determination of linking number differences between histone H1-free circular polynucleosomes and histone H1-bound circular polynucleosomes were newly carried out through using chloroquine-based agarose gel electrophoresis. It was demonstrated in our studies that binding of ~11.5 histone H1 proteins to nucleosomes produces a change of one linking number in circular polynucleosomes in the presence of 1.5 mM spermidine. Our studies also showed that in the absence of spermidine or in presence of 5 mM spermidine, difference of linking numbers between histone H1-free and histone H1-bound polynucleosomes falls drastically. These observations indicate that the spatial arrangements of histone H1 in its binding to DNA in circular polynucleosomes can be probed by varying concentrations of spermidine. In addition, since linker DNA and histone H1 are present in entire chromosomes, the handedness of 30 nm fibers, loops, rosettes, coils, chromatids and chromosomes could be determined by DNA arm closure-affiliated negative supercoils that were observed in our studies.

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A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.bmcl.2017.10.072.

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