Nucleosome-nucleosome interactions play fundamental roles in chromatin assembly and chromosome conformation, and consequently regulate gene expression. The interaction between nucleosomes is in turn modulated by varied biological constituents such as ions, cationic ligands, and proteins. Despite its central role in biology, the sequence of DNA has not received substantial attention and “random” DNA sequences are typically used in biophysical studies. However, ~50% of human genome is composed of non-random-sequence DNAs, particularly repetitive sequences. Furthermore, the solvent properties of DNA such as methylation play key roles in gene functions. Such DNAs with specific sequences or modifications often take on structures other than the canonical B-form. Here we report series of quantitative measurements of the DNA-DNA forces with the osmotic stress method on different DNA sequences and modifications, from short repeats (e.g., poly(dA-dT) and poly(dG-dC)) to the most frequent sequences in genome, and to modifications such as bromination and methylation. We observe peculiar behaviors that appear to be strongly correlated with the incurred structural changes. We speculate the causality in terms of the differences in hydration shell and DNA surface structures (e.g., minor and major groove widths).

**Sequences and Structure Dependent DNA-DNA Interactions**

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Molecular forces between dsDNA strands are largely dominated by electrostatics and have been extensively studied both experimentally and theoretically. Quantitative knowledge has been accumulated on how DNA-DNA interactions are modulated by varied biological constituents such as ions, cationic ligands, and proteins. Despite its central role in biology, the sequence of DNA has not received substantial attention and “random” DNA sequences are typically used in biophysical studies. However, ~50% of human genome is composed of non-random-sequence DNAs, particularly repetitive sequences. Furthermore, the solvent properties of DNA such as methylation play key roles in gene functions. Such DNAs with specific sequences or modifications often take on structures other than the canonical B-form. Here we report series of quantitative measurements of the DNA-DNA forces with the osmotic stress method on different DNA sequences and modifications, from short repeats (e.g., poly(dA-dT) and poly(dG-dC)) to the most frequent sequences in genome, and to modifications such as bromination and methylation. We observe peculiar behaviors that appear to be strongly correlated with the incurred structural changes. We speculate the causality in terms of the differences in hydration shell and DNA surface structures (e.g., minor and major groove widths).

**Elucidating the Role of Ions in DNA Condensation: Measurements of the Ion Atmosphere Surrounding Condensed DNA Pellets using Inductively-Coupled Plasma Atomic Emission Spectroscopy**

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The importance of DNA as a biomolecule has prompted many investigations into the mechanisms that determine its behavior in polyvalent cation solutions remain unclear. In particular, research has yet to yield a definitive and experimentally verified model to explain the phenomenon of reentrant DNA condensation.

Using inductively-coupled plasma atomic emission spectroscopy on DNA condensed under controlled conditions, we have determined the complete cation atmosphere of condensed DNA pellets. These results will be compared directly to theoretical models of the ion atmosphere in condensed DNA and should be instrumental in creating a complete theoretical description of the electrostatics that drive DNA condensation.