dissociation constant of 150 ± 10 mM. Hence, high concentrations of Na^+ ions appear to stabilize DNAs with asymmetric internal loops, most likely because of electrostatic screening of the closely spaced phosphate groups near the kink site. Surprisingly, none of the oligomers bind K^+ ions over the concentration range tested.

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413-Pos Board B213

Unfolding and Targeting Thermodynamics of DNA Hairpins Containing Internal Loops

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In this work, we use a set of DNA hairpins as a model to mimic a common motif present in the secondary structures of mRNA, i.e., a stem-loop motif with an internal loop in the stem. Specifically, we used a combination of UV and differential scanning calorimetry (DSC) melting techniques to determine thermodynamic profiles for the unfolding of a set of hairpins with sequence: d (GCGC$\mathbf{T_n}$GTAACT_5GTTAC$\mathbf{T_n}$GCGC, where n = 1, 3 or 5,"T_5" is an end loop of five thymines. UV melting curves of each hairpin show monophasic transitions with T_Ms that are independent of strand concentration, confirming their intramolecular formation. Analysis of the DSC profiles indicates that the unfolding of each hairpin results from the typical compensation of a unfavorable enthalpy (breaking of base-pair stacks) and favorable entropy contributions (release of ions and water molecules). The increase in the size of the internal loop from 2 to 10 thymines yielded: a) lower T_Ms and lower enthalpy contributions, corresponding to free energy contributions of ~0.7 kcal/mol of thymine; b) lower heat capacity effects that correlated with the lower releases of structural water molecules; and c) higher releases of ions. Furthermore, we used isothermal titration calorimetry to investigate the thermodynamics for the reaction of each hairpin with their partially complementary strands. The overall results showed that all three targeting reactions yielded favorable free energy contributions and were enthalpy driven. This approach works because of the favorable heat contributions resulting from the formation of base-pair stacks involving the unpaired bases of the loops. Supported by Grant MCB-0315746 from the National Science Foundation.

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Characterization of DNA and RNA Ion Atmospheres Using Multiple-Energy Asaxs

Suzette A. Pabit, Steve P. Meisburger, Li Li, Joshua M. Blose, Christopher D. Jones, Lois Pollack.

The number and spatial distribution of small positively-charged ions around highly negatively charged DNA or RNA contribute to the free energy of binding in vitro and in vivo. However, the majority of charge compensating ions around nucleic acids forms a diffuse counterion "cloud" that is not amenable to investigation by traditional methods that rely on rigid structural interactions. With 2 x-ray energies, one near and the other 100 eV away from the ion absorption edge, we have successfully used Anomalous Small-Angle X-ray Scattering (ASAXS) to compare and differentiate the ion spatial distribution around comparably sequenced short DNA and RNA helices. Here, we present further information gained when using multiple x-ray energies (up to 5) in an ASAXS experiment. We describe proper treatment of multiple-energy SAXS data including absolute SAXS intensity calibration and measurement of scattering factors from x-ray fluorescence. We discuss the strengths and limitations of this approach and derive useful parameters in depicting the nucleic acid ion atmosphere.

415-Pos Board B215

Improving Electrostatic Descriptions of Ions Around Double-Stranded DNA

Zhipeng Wang, Yong Huang, Li Li, Dennis G. Thomas, Lois Pollack, Alexey Onufriev, **Nathan A. Baker**.

Ions play an essential role in governing the structure and function of nucleic acids, due to the large negative charge associated with the nucleic acid backbone. The addition of even small numbers of multivalent, positively charged ions induces intra-strand attraction in DNA and thus efficiently packages the extended polymer into compact toroids. Anomalous small angle X-ray scattering (ASAXS) has emerged as a powerful technique to report the spatial distribution of ions associated to nucleic acids with unprecedented levels of detail and resolution. To determine more detailed information about these highly mobile ions relative to the underlying nucleic acid surface requires tight coordination with theoretical or computational tools. Presently, very few robust theoretical or computational tools exist for understanding ion-nucleic interactions. Current atomically-detailed computational approaches that represent the solvent environment explicitly, as discrete water molecules and ions, are prohibitively expensive for systematic studies of biologically relevant structures on time scales needed to fully understand these interactions. The alternative approach of "implicit solvent" models, that represent solvent implicitly as a continuum, could potentially overcome this difficulty. However, most "implicit solvent" models reduce computational effort at the expense of simplifying assumptions that preclude their application to highly charged systems in the presence of concentrated salt solutions or multivalent ions. We have been examining the ability of traditional and "size-modified" Poisson-Boltzmann models to predict the distribution of multivalent ions at low concentration around B-form DNA. These predictions are tested through direct comparison with ASAXS data on similar systems. The goal of this work is to examine the role of size-exclusion in the well-known failure of traditional Poisson-Boltzmann approaches for describing multivalent ions in highly charged systems. This work lays the foundation for a systematic approach to improve implicit solvent models for nucleic acid systems.

416-Pos Board B216

The Influence of Osmolytes on Electrostatic Interactions Among DNA Duplexes

Joshua M. Blose, Suzette A. Pabit, Steve P. Meisburger, Li Li, Christopher D. Jones, Lois Pollack.

Osmolytes, which function as a vital component of the cellular stress response, are small, chemically diverse, intracellular organic solutes. Protecting osmolytes enhance protein stability via preferential exclusion, where denaturation of the protein in the presence of the osmolyte is less favorable than in an aqueous environment. Thus, the correct ratios of protecting to non-protecting osmolytes and protecting osmolytes to ions are critical to maintain protein structure and protein-nucleic acid interactions. In contrast to the effects of osmolytes on protein stability, structure, and function, there is much less understood concerning the effects of osmolytes on nucleic acids. Although non-protecting osmolytes can destabilize both protein and nucleic acid structures, protecting osmolytes have different effects depending on the complexity of the nucleic acid structure. Furthermore, the influence of osmolytes on the ion atmosphere surrounding nucleic acids is not well understood. As a first step in quantifying the effects of osmolytes on nucleic acid electrostatics we used small angle x-ray scattering (SAXS) techniques to monitor 25-bp DNA duplexes and their interactions in the presence and absence of sucrose, a protecting osmolyte and important contrast matching agent in SAXS studies of protein-nucleic acid complexes. Results will be discussed.

417-Pos Board B217

Determination of the Composition of the Ion Atmosphere of Condensed DNA Utilizing Inductively-Couple Plasma Atomic Emission Spectroscopy

John Giannini, Xiangyun Qiu, Kurt Andresen.

The problem of reentrant DNA condensation has been studied for decades. Yet despite the immense amount of theoretical and experimental work on this problem, a definitive, experimentally verified model of condensation remains elusive. Using inductively-coupled plasma atomic emission spectroscopy, we have measured the ion composition of condensed DNA under a variety of solution conditions. We have studied not only the ion atmosphere in the condensed DNA, but also how the osmotic pressure and the presence of competing, non-condensing ions affect the final condensed ion atmosphere. These data provide a strong basis against which to measure the various theories of condensation.

418-Pos Board B218

Comparing Double-Strand DNA and RNA Condensation

Li Li, Suzette Pabit, Steve Meisburger, Lois Pollack.

DNA condensation is of great interest due to its fundamental biological importance. With the discovery of the important roles of RNAi, recent attention has been focused on efficient packaging of dsRNA for therapeutics. In this study, we applied UV spectroscopic and small angle x-ray scattering to investigate the mechanism of RNA condensation. Our results show that double-strand DNA and RNA behave very differently under certain ionic conditions. The forces that lead to side-by-side attraction and subsequent condensation of DNA molecules may be highly correlated with the differing geometric property of RNA and DNA.

419-Pos Board B219

Nucleic Acid Helical Conformation and Sequence Effects on Cationic Binding

Latsavongsakda Sethaphong, Yaroslava Yingling.

Conformation dependent molecular recognition has often been more associated with proteins which must be able to sense thousands of different molecules within a cell. Despite lacking as extensive a repertoire, nucleic acids also depend on nuances of structure with their environment to gain specificity for regulating genetic duplication, editing, expression, and suppression. In order to explore this topic further, molecular dynamics simulations of nucleic acid duplexes of DNA and RNA were performed to examine subtleties with their inherent cation binding behavior. We discovered that despite small differences