hexamine [1], we studied short double-stranded DNA, RNA and a DNA/RNA hybrid in the presence of polyamines using UV spectroscopy and small and wide angle x-ray scattering. Polyamine-induced condensation of the nucleic acid constructs will be discussed.


1338-Pos Board B230
Aggregation of four-Stranded DNA Molecules
Bita Zamiri
University of Toronto, Toronto, ON, Canada.
Oligodeoxyribonucleotides (ODNs) that have four repeats of the human telomeric sequence d(TTAGGG) can assume several nonmolecular G-quadruplex topologies depending on the cation species present, the bases at the 5’ or 3’ end, and on the sample preparation. The study of G-quadruplexes is important and biologically relevant due to their potential in the development of anticancer drugs. We have previously reported that under certain experimental conditions some quadruplex ODNs aggregate to form multi-molecular structures. These structures may be biologically relevant because of the similarity of their experimental conditions to in-vivo environments. We are interested in exploring the characteristics of the associated species and the nature of their stabilizing interactions. To this end we are investigating the effect of several parameters such as the sequence of the ODN, the concentration of the ODN, and the nature and concentration of the stabilizing cations. The ODNs under investigation are all derivatives of the human telomeric sequence. The equilibrium, kinetics, and structural properties of these structures are studied using circular dichroism spectroscopy (CD), UV spectroscopy, Raman spectroscopy, Dynamic light scattering (DLS) and analytical ultracentrifugation as a function of temperature and pressure.

1339-Pos Board B231
Testing Theories of DNA Interaction and Condensation
Sceuk Yasar, V. Adrian Parsegian, Rudolf Podgornik
University of Massachusetts Amherst, Amherst, MA, USA.
By measuring and comparing DNA force curves under different temperature and ionic conditions, we investigate DNA condensation and interaction in dense aggregates. Oriented or unoriented bundles of parallel hexagonally arranged B-form DNA double helices are osmotically stressed in solutions of multivalent condensing counterions and simple monovalent salts. Helices are pushed together by known osmotic pressures. At each pressure, interaxial spacings are measured by x-ray diffraction. We observe osmotically induced phase transitions (DNA condensation) in force curves over a critical range of counterion concentrations that depend on the valence and type of the condensing counterion as well as the type and concentration of monovalent salt. We also determine critical osmotic pressures required to condense DNA. At certain concentrations of specific counterions, critical pressures can be temperature dependent. We investigate this dependence to distinguish entropic and enthalpic components of interaction. Furthermore, this allows determination of the binding properties of specific counterions to the DNA under osmotic pressures that induce phase transitions. In this way we can evaluate theories of DNA interaction in the presence of multivalent cations. A range of theories use diverse approximations to model and predict DNA interaction. Their different parameters are examined through controlled experimental variables. Mean-field electrostatic theories model DNA as a uniform monovalent salt to neglect counterion correlations. They always predict repulsion between like-charged homogeneous surfaces and therefore cannot explain attractive forces. In the opposite case, under the assumption that attractive counterion correlations are very strong, counterions might form a Wigner crystal in a bundle of DNA helices. Formulation of electrostatic interaction that includes helical structure and distribution patterns of adsorbed counterions also predicts attraction and rationalizes counterion specificity of DNA condensation. These models can be distinguished, critically tested, and compared with the hydration force interpretation of counterion-induced condensation.

1340-Pos Board B232
Mechanics of 3D DNA Crystals
Ehsan Ban, Catalin R. Piciu
Rensselaer Polytechnic Institute, Troy, NY, USA.
Single strands of DNA can self-assemble to form artificial 3D DNA crystals. The 3D crystals studied here are made of triangular units connected at their corners. Structures similar to Holliday junctions and their potential in the development of micromachines for structural characterization. They can also directly the assembly of nanoscale electronic circuits. In this work the mechanics of these structures is studied using classical molecular dynamics simulations. The prestress in the crystals is calculated for different configuration of bases. Then stability of the sticky end links is investigated. Links with different lengths and base sequences are compared in stretch. Further a cohesive complex is identified that can give unusual stability to the sticky end links. The results have implications in designing more mechanically stable DNA self-assemblies.

1341-Pos Board B233
Effect of Methylation on the Nanomechanical Properties of Double-Stranded DNA
Csaba I. Pongor1, Pasquale Bianco1,2, Miklos Kellermayer1.
1Semmelweis University, Department Of Biophysics and Radiation Biology, Budapest, Hungary, 2University of Florence, Laboratory of Physics, Budapest, Italy.
In mammalian cells 60-90% of cytosines in the genome are methylated. The methylation sites are unevenly distributed and are often found in clusters called “CpG islands”. Approximately 70% of promoters in the human genome contain or are preceeded by CpG-rich regions, suggesting that methylation may be important in gene regulation. Cyclization-kinetic and nucleosome-binding assays suggest that methylation may significantly affect DNA flexibility. However, a direct effect of methylation on the mechanics of DNA is yet unknown. To investigate the impact of methylation on DNA mechanics, here we manipulated single molecules of methylated dsDNA and compared their nanomechanical properties with those of unmethylated DNA. A 3500-base pair sequence of lambda-phage DNA composed almost entirely of CpG islands was cloned by PCR containing dm5 CTP to produce the fully methylated product. Individual DNA molecules were mechanically manipulated in stretch and relaxation cycles by using custom-built dual-beam counter-propagating optical tweezers. Force versus extension data were fitted with the extensible wormlike-chain model to obtain the contour length, the persistence length (entropic component of rigidity) and the stretch modulus (enthalpic component of rigidity) of dsDNA. Methylation reduced the contour length and stretch modulus of dsDNA from 1036 ± 22 nm to 966 ± 8 nm and from 1225 ± 115 pN to 373 ± 30 pN, respectively. Persistence length was 34 ± 2 nm for the non-methylated and 35 ± 2 nm in case of the hypermethylated DNA. The observed changes may be caused by a complex shift in tertiary structure, accounting for both the reduction of the contour length and the increase of the intrinsic compliance of the dsDNA chain. The methylation-induced effects on the nanomechanical properties of dsDNA may play an important role in the regulation of steric access to its sequence-specific sites.

1342-Pos Board B234
Dynamics of Plectonemic Supercouples along Stretched DNA by Brownian Dynamics
Todd D. Lillian1, David Bell2.
1Texas Tech University, Lubbock, TX, USA, 2University of Texas at Austin, Austin, TX, USA.
Intervern DNA structures (plectonemes) arise from processes such as replication, recombination and the formation of 100000-fold compacted dsDNA molecules into the cell nucleus. These supercoils can enhance or repress cellular processes such as replication, transcription, and recombination. In fact, an increased frequency of DNA-DNA juxtapositions within plectonemic supercoils facilitates DNA looping. Although plectonemes have been studied with recent single molecule techniques, little is known about their dynamic formation, dissolution, rearrangement, and dissolution. In fact, single molecule assays often are confounded by the extremely low slow and large magnitude magnetic force needed to manipulate the DNA. To characterize plectoneme dynamics, we employ Brownian dynamics simulations of stretched supercoiled DNA. Here we consider a range of system parameters describing length, extension, and superhelical density. Our model incorporates viscous drag, thermal fluctuations, bending, torsion, extension, and electrostatics. Additionally, we employ periodic boundary conditions to prevent plectonemes from diffusing off the ends of linear DNA. Our simulations reveal that both the number and size of plectonemes vary with time. Interestingly, this precludes the characterization of plectoneme motion with a diffusion constant. To quantify plectoneme dynamics, we define t as the median time for first juxtaposition of two sites on a DNA molecule separated by a prescribed distance. Here we show that t depends on system parameters as well as separation distance and ranges from milliseconds to seconds. Our simulations shift on processes requiring juxtaposition (e.g. DNA looping) as well as processes in which supercoils are transmitted along DNA (e.g. transcription).

1343-Pos Board B235
DNA supercoiling affects Stability of Genetic Switch
Yue Ding1, Carlo Mak2, David Dunlap3, Laura Finzi1.
1Emory University, Atlanta, GA, USA, 2ICFO - The Institute of Photonic Sciences, Castelldefels (Barcelona), Spain, 3Emory University School of Medicine, Atlanta, GA, USA.
DNA supercoiling has been known as a common transcriptional regulatory mechanism in cells facing environmental changes and coping with stress. Though it is acknowledged that the level of DNA supercoiling varies at

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