

Seminar

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Conformations of circular DNA bundles in viruses

Monday, May 11, 2015

at 13:15 h

ESI, Schrödinger Lecture Hall

Abstract: Some sort of DNA compression is required to pack the long DNA strand in a small space, such as the cell nucleus or bacteria. Viruses have, in particular, developed several strategies to physically compress the DNA genome molecule. In presence of basic proteins [1] or multi-valent counterions, DNA can be condensed, i.e. brought to a state where it self-attracts [2]. When condensed in confinement, e.g. in virus protein coatings (capsids), it is known that the, sufficiently short, DNA also assumes toroidal conformations, but the free energy balance is in that case additionally complicated by the adsorption energy (DNA-capsid interaction) and by the presence of the capsid [3]. It has been proposed in the literature that the, sufficiently long DNA, may condense in conformations which are non-toroidal, i.e. which do not have the cylindrical axis of symmetry [4]. I will present a model calculation that accounts for non-toroidal conformations of DNA condensed in confinement. The model reproduces conformations that were previously predicted [4], but also several intriguing conformations that were never predicted in the context of viruses.

[1] A. J. Perez-Berna, S. Marion, F. J. Chichon, J. J. Fernandez, D. C. Winkler, J. L. Carrascosa, A. C. Steven, A. Šiber, and C. San Martin, Nucl. Acids Res. 43, 4274 (2015). [2] J. Ubbink and T. Odijk, Europhys. Lett. 33, 353 (1996). [3] A. Leforestier, A. Šiber, F. Livolant, and R. Podgornik, Biophys. J. 100, 2209 (2011). [4] N. V. Hud, Biophys. J. 69, 1355 (1995).

P. Ziherl

May 8, 2015