The "self-stirred" genome: Bulk and surface dynamics of the chromatin globule

Alexandra Zidovska

Center for Soft Matter Research, Department of Physics, New York University

Abstract:

Chromatin structure and dynamics control all aspects of DNA biology yet are poorly understood. In interphase, time between two cell divisions, chromatin fills the cell nucleus in its minimally condensed polymeric state. Chromatin serves as substrate to a number of biological processes, e.g. gene expression and DNA replication, which require it to become locally restructured. These are energy-consuming processes giving rise to non-equilibrium dynamics. Chromatin dynamics has been traditionally studied by imaging of fluorescently labeled nuclear proteins and single DNA-sites, thus focusing only on a small number of tracer particles. Recently, we developed an approach, displacement correlation spectroscopy (DCS) based on time-resolved image correlation analysis, to map chromatin dynamics simultaneously across the whole nucleus in cultured human cells [1]. DCS revealed that chromatin movement was coherent across large regions (4–5μm) for several seconds. Regions of coherent motion extended beyond the boundaries of single-chromosome territories, suggesting elastic coupling of motion over length scales much larger than those of genes [1]. These large-scale, coupled motions were ATP-dependent and unidirectional for several seconds. Following these observations, we developed a hydrodynamic theory of active chromatin dynamics, using the two-fluid model and describing the content of cell nucleus as a chromatin solution, which is subject to both passive thermal fluctuations and active (ATP-consuming) scalar and vector events [2]. In this work we continue in our efforts to elucidate the mechanism and function of the chromatin dynamics in interphase. We investigate the chromatin interactions with the nuclear envelope and compare the surface dynamics of the chromatin globule with its bulk dynamics [3]. Furthermore, we explore the rheology of the chromatin inside the cell nucleus using the native subnuclear structures [4].

[1] Zidovska A, Weitz DA, Mitchison TJ, *PNAS,* 110 (39), 15555-15560, 2013
[2] Bruinsma R, Grosberg AY, Rabin Y, Zidovska A, *Biophys. J.,* 106 (9), 1871-1881, 2014
[3] Chu F, Haley SC, Zidovska A, *PNAS,* 114 (39), 10338-10343, 2017
[4] Caragine CM, Haley SC, Zidovska A, *PRL, Under Review*

Friday, October 27th, 2017, 13:00

Room PH 127

Contact: Andreas Bausch, abausch@ph.tum.de, phone: 089-289-12408