Chez Pierre

Presents ...

Monday, February 25, 2013
10:00am
MIT Room 4-331

SPECIAL CHEZ PIERRE SEMINAR

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"Positional Fluctuations of Interphase Chromatin"

Chromatin is the loosely packed functional form of DNA in cells in interphase, i.e. the time between two cell divisions. It fills the entire cell nucleus. Single chromosomes occupy distinct territories in the nucleus, and cross-linking reveals static genome folding with 1Mbp resolution. Tracking of single genes, foci and chromosome territories over time reveals diffusive and sub-diffusive dynamics, and in some cases micron-scale directed movements. How to reconcile these static and dynamic pictures to provide a physical picture of the interphase nucleus is unclear. We developed a novel approach, DCS (Displacement Correlation Spectroscopy) based on time-resolved image correlation analysis to map chromatin dynamics simultaneously across the whole nucleus in cultured human cells. This method revealed that chromatin movement was coherent across large regions (4-5μm) with correlation times in the second range. Regions of coherent motion extended beyond the boundaries of single chromosome territories suggesting elastic coupling of motion over length scales much larger than genes. These large-scale, coupled motions were ATP-dependent and unidirectional for several seconds, perhaps accounting for ATP-dependent directed movement of single genes. Perturbation of major nuclear ATPases such as DNA polymerase, RNA polymerase II and topoisomerase II eliminated micron-scale coherence, while causing rapid, local movement to increase, i.e. local motions accelerated but became uncoupled from their neighbors. We hypothesize that this may be due to DNA damage responses (e.g. damage sensing and repair) that physically relax chromatin and block long distance communication of forces.