

Nebraska EPSCoR Seminar

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“The Genomic Code for Nucleosome Positioning”

Seminar abstract: Eukaryotic genomes encode an additional layer of genetic information that controls the organization of the genomic DNA into arrays of nucleosomes. This information is superimposed (multiplexed) on top of the regulatory and coding information that was previously understood. We have developed an ability to read this nucleosome positioning code and predict the in vivo locations of nucleosomes. Most recently, we showed that the distribution of nucleosomes reconstituted on genomic DNA in a purified in vitro system closely resembles the in vivo nucleosome distributions obtained in several different growth conditions. Thus, the genome's intrinsically encoded nucleosome positioning information accounts for the overwhelming majority of nucleosome-occupied versus nucleosome-depleted regions across the entire genome. Condition-specific actions of gene regulatory proteins and chromatin remodeling factors lead to specific localized changes in nucleosome occupancy and positioning, leaving much of the chromatin organization unaffected. A statistical model for nucleosome positioning trained on the yeast in vitro nucleosome map is highly predictive of in vivo nucleosome occupancy patterns in yeast, *C. elegans* and human. Our results suggest that genomes utilize the nucleosome positioning code to facilitate specific chromosome functions, including to delineate functional versus nonfunctional binding sites for key gene regulatory proteins, to regulate the expression noise characteristics of different promoters, and the replication firing characteristics of differing origins, and to define the next higher level of chromosome structure itself.

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12:00 p.m.

East Campus Nebraska Union
University of Nebraska-Lincoln

(Seminar is an interactive video broadcast from UNMC)

More information available at

<http://epscor.unl.edu>

