

Chromosome positioning of activity-based chromatin domain model

Soya Shinkai

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Abstract:

Chromosomes at interphase are not distributed randomly within nuclei. Recent experiments have suggested a relationship between the gene density of a chromosome territory and its radial distribution. And also, non-thermal ATP-dependent fluctuations contribute to the in vivo motion of chromosomal loci. These active and non-equilibrium fluctuations would drive and maintain the spatial segregation of chromosomes. However, the physical mechanisms are little known.

In this talk, I will review mainly the paper [1]. The authors simulated the spherical chromatin domain model [2], which is composed of spherical monomers representing 1 Mb domains and subdivided into active and inactive sites by use of data from the Gene Cards database. They showed the territorial organization of chromosomes, and discussed a mechanism of the spatial segregation.

References:

1. Ganai N., Sengupta S. and Menon G. I. (2014) Chromosome positioning from activity-based segregation. *Nucleic Acids Research*, 2014, 1-15.
2. Kreth G., Finsterle J., von Hase J., Cremer M. and Cremer C. (2004) Radial arrangement of chromosome territories in human cell nuclei: a computer model approach based on gene density indicates a probabilistic global positioning code. *Biophys. J.*, **86**, 2803-2812.