Histone acetylation level regulates formation of topologically associating domains in *Drosophila*

Ekaterina Khrameeva

Skolkovo Institute of Science and Technology, Nobelya st. 3, Moscow, 143026 Russia, e.khrameeva@skoltech.ru

Aleksandra Galitsyna, Sergey Ulyanov, Sergey Razin

Institute of Gene Biology, Vavilova St. 34/5, Moscow, 119334 Russia

Yuri Shevelyov

Institute of Molecular Genetics, Akademika Kurchatova sq. 2, Moscow, 123182 Russia

Mikhail Gelfand

A.A.Kharkevich Institute for Information Transmission Problems, Bolshoy Karetny per. 19/1, Moscow, 127051 Russia

Recent progress of next-generation sequencing methods for 3D chromatin organization analysis [2] has unraveled many details of its fine structure. In particular, chromosomes of higher eukaryotes have been shown to be organized into spatially compact Topologically Associating Domains (TADs) [1]. *Drosophila melanogaster* is a popular model organism for chromatin studies, however, the mechanism of TAD formation in unknown there. Here, we test the hypothesis that the mechanism of TAD self-assembly is based on the ability of nucleosomes from inactive chromatin to aggregate, and lack of this ability in acetylated nucleosomal arrays [3]. We analyzed data of Hi-C and Chip-Seq (with antibodies against pan acetylated H3 histone) experiments in control *D. melanogaster* late embryonic (Schneider-2) cells, as well in HDAC1-depleted cells and in cells treated with histone acetyltransferase inhibitor curcumin and histone deacetylase inhibitor trichostatin A. Acetylation level changes were studies, in association with TAD position and density differences. Inhibition of HDAC1 was found to lead to a relative increase of acetylation level in interTAD regions, and coordinated changes in TAD structure. Thus, histone acetylation plays a key role in the mechanism of TAD formation.

This study was supported by the Russian Science Foundation (project 14-24-00022).

1. J.R. Dixon et al. (2012) Topological domains in mammalian genomes identified by

analysis of chromatin interactions, Nature, 485:376-380.

2. E. Lieberman-Aiden et al. (2009) Comprehensive mapping of long range interactions reveals folding principles of the human genome, Science, 326:289-293.

3. S.V. Ulianov et al. Active chromatin and transcription play a key role in chromosome partitioning into topologically associating domains, Genome Research, 26(1):70-84.