Conclusions: Here we show that the loss or over-expression of CHD1 severely and very specifically affect the global chromatin organization of Drosophila polytene chromosomes. Our finding suggests a new link between the organization of hyperactive chromatin of the male X – chromosome and of transcriptionally silent heterochromatin.

This work was partially supported by RFBR grant 15-04-99583.

doi: http://dx.doi.org/10.7124/bc.0009AF

High-resolution mapping of A/B compartments and topologically associated domains on giant lampbrush chromosomes

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Progress in studies aimed at "deciphering" the spatial architecture of the genome is determined by the development of several key technologies: the chromatin conformation capture, ultrahigh resolution optical microscopy and genomic locus imaging. At the same time, it remains unclear how the domains, determined by chromatin conformation capture technology, including topologically associated domains (TADs) and A/B compartments, are correlated with the chromatin domains detected at the cytological level. In the framework of this problem, a comprehensive study of the chromatin domains of giant lampbrush chromosomes characteristic of the growing oocytes in birds, amphibians and reptiles, seems appropriate. Methods: Here we aimed at comparing the chromomeres – the main structural unit of lampbrush chromosome axes – and topologically associated domains and A/B compartments in domestic chicken (Gallus gallus domesticus), whose genome was the first among the deciphered avian genomes. In addition, earlier, using the full-genome Hi-C method a number of hierarchical structural domains, such as A and B compartments and TADs, were identified in chicken embryonic fibroblasts. Results: The results obtained allowed us to verify the hypothesis of the correspondence between the globular-loop chromatin domains of the interphase nucleus and the chromomere-loop complexes of lampbrush chromosomes, as well as to shed light on the nature of the lampbrush chromosome chromomeres.

The research was supported by Russian Science Foundation (grant # 19-74-20075). The work was partially performed using equipment of the Research Resource Center 'Molecular and cell technologies' of SPbU.

doi: http://dx.doi.org/10.7124/bc.0009B0

Roles of actin family proteins in chromatin and nuclear functions

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Genome functions are regulated by local chromatin structure and also by the association of individual genes with nuclear structures. As

candidates for involvement in functional chromatin and nuclear organization, we investigated the actin family, which consists of conventional actin and actin-related proteins (Arps). Interestingly, a portion of actin and some Arp subfamilies are localized in the cell nucleus. Monomeric G-actin and the nuclear Arps are known to contribute to genome functions (including transcription and DNA damage repair) as components of chromatin remodeling complexes and histone modification complexes. In addition to nuclear G-actin, nuclear actin filament (F-actin) is also involved in genome functions and nuclear organization. Although a sufficient amount of actin is found in the nucleus, information regarding factors involved in regulating the formation of nuclear F-actin is still limited. We showed that Arp4 (one of the nuclear Arps) is a suppressor of nuclear F-actin formation, which suggests that crosstalk between actin family proteins in the nucleus performs important roles in chromatin functions and nuclear organization. For further analysis and operation of nuclear actin family proteins, we screened and evaluated bicyclic peptides binding to these molecules. Bicyclic peptides contain two macrocyclic rings, and this structure contributes to high affinity binding to target molecules. We performed screening of bicyclic peptide libraries by the phage display technique, and obtained bicyclic peptides for nuclear Arps and G-actin. We introduced these bicyclic peptides into living cells by electroporation, and evaluated the peptides. Bicyclic peptides for Arp5 and Arp8 (components of the INO80 chromatin remodeling complex) inhibited functions of INO80 complex in the living cells. We also successfully delivered bicyclic peptides for G-actin into the nucleus by tagging a nuclear localization signal (NLS). We observed that the NLS-bicyclic peptides for G-actin suppressed nuclear F-actin formation and impaired the function of nuclear F-actin in DNA damage repair. These bicyclic peptides provide novel information on the roles of actin family proteins in the nucleus.

doi: http://dx.doi.org/10.7124/bc.0009B3

Nuclear lipid Islets as integrators of Polymerase II transcription and pre-mRNA processing

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The eukaryotic nuclear environment possess a dynamic highly organized architecture. Processes such as gene expression, DNA repair or RNA processing occur often in membraneless compartments. These structures constitute of e.g. nucleic acids, proteins, lipid multimolecular condensates. Our laboratory recently discovered nanoscale globular (~100 nm) Nuclear Lipid Islets (NLIs) structures containing PI(4,5)P2 (PIP2), which are involved in efficient RNAPII transcription [1]. We aim to describe the possible function of PIP2-containing NLIs in integrating RNAPII tran-