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