Секция «Клеточная биология и гистология»

Do lampbrush chromosome chromomeres correlate with large-scale A/B chromatin compartments in chicken somatic cells?

Научный руководитель – Куликова Татьяна Вадимовна

Rodriguez Juan Sebastian
Student (bachelor)
Санкт-Петербургский государственный университет, Биологический факультет, Санкт-Петербург, Россия
E-mail: tianshe998@gmail.com

3D genome architecture is an intensively developing area of research. HiC analysis allows to distinguish two types of large-scale chromatin compartments (A and B) according to the level of chromatin compactization and gene density. However, cytological manifestation of these compartments remains elusive. Lampbrush chromosomes (LBCs) are giant transcriptionally active meiotic chromosomes with distinctive chromomere-loop organization, that makes them a powerful tool for studying chromatin compartmentalization [2].

The aim of the study was to elucidate a possible correlation between distinct regions of LBCs and large-scale chromatin (A/B) compartments from interphase nuclei of chicken embryonic fibroblasts (CEFs). For this, cytological maps of chicken LBCs 1-6, 11-15 and Z were juxtaposed with the distribution of A/B compartments along corresponding chromosomes from interphase CEF. LBC maps based on DAPI staining patterns of chromomeres, relative length of lateral loops and mapped genomic markers were obtained from previous works [3]. A/B compartments were defined based on EIG vector values obtained by previous HiC analysis [1] and visualized in the Integrative Genomic Viewer.

Our analysis showed that in chicken LBCs clusters of DAPI-positive chromomeres with short lateral loops almost always correspond to B-compartment regions. This correspondence was found to be unidirectional, as DAPI-negative chromomeres do not show any particular correlation with A/B compartment status. Distribution of lateral loops lengths in LBCs did not significantly correlate to A/B compartment status. At the same time, FISH with BAC-clone probes reveal that some B-compartment regions are transcribed in lateral loops of LBCs. Our findings demonstrate that belonging of certain genomic regions to constitutive B compartments is conservative between transcriptionally hyperactive meiotic nuclei and interphase nuclei of somatic cells.

The research was supported by Russian Science Foundation (grant #19-74-20075). The work was performed with technical assistance by the Research Resource Center 'Molecular and cell technologies' (SPbU) and 'Genomics Core Facility' (Skoltech).

References

1) Fishman V, et al. 3D organization of chicken genome demonstrates evolutionary conservation of topologically associated domains and highlights unique architecture of erythrocytes' chromatin // Nucleic Acids Research, Vol. 47(2). 2019. P. 648–665
2) Gaginskaya E, et al. Avian lampbrush chromosomes: a powerful tool for exploration of genome expression // Cytogenetic and genome research, Vol. 124(3-4). 2009. P. 251-267
3) Galkina S, et al. FISH on avian lampbrush chromosomes produces higher resolution gene mapping // Genetica, Vol. 128(1-3). 2006. P. 241-251