Секция «Биоинформатика»

Three-dimensional organization of chromatin in red blood cells

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Introduction: Three-dimensional organization is essential for genome folding and compactization. It has been shown that progression through mitosis is accompanied by spatial rearrangement of the chromatin. This process could be studied using Hi-C technique, which shows the genome-wide gain of spatial interaction between loci located ∼10 Mb away from each other during mitotic prophase [1]. Previously we found that the same feature of spatial organization is also present in Hi-C maps of chicken erythrocytes[2]. Mechanism of formation and conservativeness in the evolution of this phenomenon remains unknown. To resolve this issue, we investigated Hi-C data of blood cells in different classes of vertebrates.

Methods and Algorithms: We used publically available Hi-C data of blood samples from Takifugu flavidus and Pelteobagrus fulvidraco (bony fish), Leptobrachium leishanense and Leptobrachium ailaonicum (amphibians), Salvator merianae and Pelodiscus sinensis (reptilians), Casuarius casuarius and Gallus gallus (birds). For Homo sapiens and Mus musculus (mammals), nucleated terminal differentiation erythroid cells were used. Hi-C contacts were obtained using Juicer and processed with cooler software. We selected scaffolds longer than 9Mb and computed the contact frequency (P) as a function of genomic distance (s), the P(s) function using cooltools expected function.

Results: The mitotic-like long-range interactions are clearly visible on Hi-C maps of amphibians, reptilians, mouse and bird. In accord with this, we observed the local peak of P(s) curve for these data, as well as for mammalian samples. Position of the peak varies from 20 Mb in birds to 30 Mb in amphibians. We didn't find the presence of the peak in fish. Also, using chicken data we found that the local peak of P(s) curve is present only in the first five and the Z chromosomes, which are larger than 40 Mb. Position of the peak is constant in these six chromosomes.

Conclusion: Constant position of the peak in different long chromosomes data suggests a general mechanism explaining the formation of the long-range mitotic-like interactions. Whether short chromosomes are packed in a different manner, or the current method can not resolve the peak due to the smaller number of faraway loci remains to be answered. The mitotic-like feature presents in erythrocytes among each considered class, besides bony fish. This could be explained by the smaller size of bony fish chromosomes.

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Источники и литература

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