

COMPARATIVE ANALYSIS OF THE GENOME CONSTITUTION FOR UNDERSTANDING THE CONFORMATION OF THE REPETITIVE SEQUENCE BLOCKS IN PRIMATE EVOLUTION.

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Comparative genome analysis in primates is a powerful tool to identify the species-specific structural changes and its relation to the species-specific phenotypes, which are acquired after the divergence from their common ancestor. We have been studying the chromosome-based comparative genome analyses and identified the number of the structural differences in primate lineage. By chromosomal FISH technique and genome sequencing analysis, we found that the most of the large-scale structural changes were identified as the repetitive sequence blocks, and the distribution pattern of these sequence blocks was identified in region-specific and species-specific manner. The different constitution of the repetitive sequence blocks may cause by the large-scale genome rearrangements such as duplication, deletion, recombination and inversion. Based on the results identified by our comparative analysis, we hypothesized that the formation and amplification of these sequence blocks are correlated to the gene territory and the spatial positioning of the sequence blocks in the three-dimensional cell nucleus. To elucidate the mechanisms of the region-specific and species-specific repeat expansion and the evolutionary aspects of the structural alteration of these repetitive sequences in primate evolution, we started to analyze the territory, position, and physical distance of the repetitive sequence blocks found in Japanese macaque by using 3D-FISH technique. We will demonstrate the structural characteristics of the repetitive sequence blocks in genomes and the spatial disposition in the three-dimensional nucleus.

Keywords: Repetitive sequence, Genome rearrangement, Comparative analysis, FISH