

Genomic Features of HERV Elements in Primates

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Most of endogenous retroviral elements have been integrated in the primate genome after the split of New World monkeys in the Oligocene era, approximately 33 million years ago. They might be able to induce the genetic polymorphism and many kinds of diseases because they can change the structure of adjacent gene as moving on the chromosome. Comparative analysis of HERVs and their LTR elements in the primate genomes will help us to understanding the possible impact of HERV elements on evolution and phylogeny in the primates. We identified HERV-K LTR and SINE-R elements that have been subject to recent change in the course of primate evolution. They are specific elements to the human genome and could be related to biological function. The HERV-M element related to the super family of HERV-K has been integrated into the periphilin gene as the truncated form, 5'LTR-gag-pol-3'LTR. PCR and RT-PCR approaches were conducted to investigate its evolutionary traces. The insertion of various retroelements in a common ancestor genome may make different transcript variants in different species. We also examined HERV-W element, which env fragments were detected on human chromosomes 1, 3-7, 12, 14, 17, 20, and X, while the pol fragments were detected on human chromosomes 2-8, 10-15, 20, 21, X, and Y. Blast search showed that almost full-length of the HERV-W family was identified on human chromosomes 1-8, 11-15, 17, 18, 21, and X. Expression analysis of HERV-W genes (gag, pol, and env) by RT-PCR and sequencing was performed using 12 human tissues, indicating that gag and pol genes were expressed in specific tissues and env gene was actively expressed in all tissues examined. Phylogenetic analysis indicated that those genes have been evolved independently during primate evolution.