Z116 Molecular phylogeny and HERV-W LTR elements in various cancer cells

Heui-Jung Park, Joo-Mi Yi, Young-In Park, Won-Ho Lee, and Heui-Soo Kim
Division of Biological Scienes, College of Natural Sciences, Pusan National University

Human endogenous retroviral long terminal repeats(LTRs) have been found to be coexpressed with sequences of genes closely located nearby. It has been suggested that the LTR element have contributed to the structural change or genetic variation of human genome connected to diseases and evolution. We examined the HERV-W LTR elements in various cancer cells(2F7, A431, A549, HepG-2, MIA-PaCa-2, PC-3, RT4, SiHa, U-937, and UO-31). Using genomic DNA from the cancer cells, we performed PCR amplification and identified twelve HERV-W LTR elements. Those LTR elements showed a high degree of sequence similarity (88.2-99.7%) with HERV-W LTR(AF072500). A phylogenetic tree obtained by the neighborjoining method revealed that HERV-W LTR elementscould be mainly divided into two groups through evolutionary divergence. Three HERV-W LTR elementscould belonged to group I from RT4, A431, and UO-31, whereas nine LTR elements belonged to the group II, suggesting that various copy numbers of the LTR elements are detectable in cells, but this phenomenon may directly not lead to human cancers.

Z117 Phylogenetic Analysis of HERV-K LTR in cDNA Library of Human Brain

Joo-Young Choi*, Young-In Park, Won-Ho Lee, and Heui-Soo Kim
Division of Biological Sciences, College of Natural Sciences, Pusan National University, Pusan 609-735, Korea

Solitary long terminal repeats (LTRs) of the human endogenous retroviruses, scattered in several thousand copies throughout the human genome, are potentially capable of affecting the expression of closely located genes. We have investigated the transcribed HERV-K LTR elements from the cDNA libraries of human fetal brain and brain. Twenty-four elements of HERV-K LTR were identified by PCR amplification. They showed a high degree of sequence similarity (98.0-99.7%) with human-specific LTR elements. A phylogenetic analysis of those elements using neighbor-joining method revealed that HERV-K LTR elements could be classified into two main groups through evolutionary divergence. Some HERV-K LTR elements (HKL-FB1, HKL-FB5, HKL-FB7, HKL-FB11 and HKL-B10) belonging to the group II from human fetal brain and brain cDNA were closely related to human-specific HERV-K LTR elements, suggesting that these HERV-K LTR elements, recently proliferated in human genome after divergence of the human and the chimpanzee, deserve further investigation in relation to neuropshychiatric diseases.