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Long terminal repeat (LTR) elements of human endogenous retrovirus (HERV-K) may have contributed to the structural change or genetic variation connected to diseases in human genome. The LTR elements have been found to be coexpressed with sequences of closely located genes. We identified seven HERV-K LTR elements from mRNA of human cancer cells (HepG2, MCF7, and SiHa) using RT-PCR approach. Four of them are closely related to the human specific HERV-K LTR elements with high degree of sequence homology in neighbor-joining phylogenetic tree. The data suggests that recently proliferated HERV-K LTR elements are expressed actively in various cancer cells. These HERV-K LTR elements deserve further investigation as potential leads to the human cancer.

F823

Long Terminal Repeat (LTR) Elements of the Endogenous Retrovirus (ERV-9) on Human Chromosomes

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Endogenous retrovirus (ERV-9) exists in the human genome as 30-50 members. The ERV-9 LTR elements have been proliferated into the human chromosomes during hominoid evolution. The LTR elements contain an unusual U3 enhancer region composed of various tandem repeats, which contain several transcriptional regulatory sequences with recurrent GATA, CACCC and CCAAT motifs. We identified such LTR elements from the GenBank database using BLAST searching and found 137 different elements on human chromosomes 1, 3, 4, 5, 6, 7, 12, 14, 16, 17, 19, 20, 21, 22, X and Y. These elements were grouped into 18 subfamilies base on several characteristic nucleotide differences. Our finding suggests the possibility that the ERV-9 LTRs may serve a relevant host function in regulation the transcription of nearby genes.

F824

LY1 Retroposon Insertion Polymorphism on the Centromere of the Y-Chromosome in Northeast Asian Populations

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The human Y-chromosome of the non-recombining portions has special features of a haploid and a father-to-son transmission pattern. The DNA sequence of these portions, therefore, contains a genetic record of the mutational events occurred in their past. As a consequence, Y-chromosome can be used for studies of paternal lineages and population history in humans. We have examined a polymorphic LY1 retroposon insertion in the centromeric alphoid array of the Y-chromosome in samples from a t 'al of 662 unrelated males in four ethnic groups of Northeast Asia. The LY1 insertion was detected by PCR amplification using flanking primers, and electrophoresis on denaturing polyacylamide gels followed by silver staining. The Koreans were revealed to have the highest frequency of the LY1 insertion (10.1%), followed by Mongolians (8.8%),

Chinese (6.0%), and Japanese (1.6%). It is known that most Caucasian and Negroid males examined so far completely lack the LY1 retroposon insertion, but present it at high frequency in the south of China. Two possible explanations would be migration from the south of China to Korea, or drift within Korean population. The dual patterns of the distribution of LY1 insertion is compatible with our earlier report that the Korean population may have evolved from two different waves of East Asians.

F825

Effect of Ultraviolet Radiation or 3-Aminobenzamide on Apoptosis in Chinese Hamster Ovary Cells

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The present study has performed to elucidate the effect of ultraviolet radiation(UV) or 3-aminbenzamide(3AB) on apoptosis in Chinese hamster ovary(CHO) cells. Four assays were employed in this study : Gel electrophoresis of isolated DNA, quantitative assay of fragmented DNA, morphological assay of apoptotic cells and western blot analysis. Alteration of DNA level on apoptosis was determined by DNA ladder pattern. DNA ladder pattern in the cells irradiated with UV was observed from 12 hrs until 24 hrs after incubation. Whereas the DNA ladder pattern was not shown in the cells with 3AB. Expression of Hsp70 and poly(ADP-ribose)polymerase(PARP) pretreated with low-dose of UV and subsequently treated with high-dose of UV was higher than treated with high-dose of UV. Whereas Hsp70 and PARP expression treated with 50 J/m^2 UV and incubated with 5 mM 3AB was lower than without 5 mM 3AB.

F826

Characterization of a New Polycomb Group Mutation

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The *Polycomb* group (PcG) genes are responsible for the transmission through the rest of development of the early homeotic gene pattern determined by the transient expression of the maternal and segmentation genes. *pleiohomeotic* gene, which is a PcG gene, was found to encode a DNA binding protien. It is only a DNA binding protein among 13 PcG proteins so far discovered. So the *pho* was expected to play a main role among PcG group. But its mutant showed very weak phenotypes, which implied an requirement of another partner. A new PcG mutant was discovered as an enhancer of *pleiohomeotic (pho)* mutation. It is embryonic lethal, showing homeotic transformat n at embryonic and adult stage. It synergistically interacts with other PcG mutation. Unlike other PcG mutation, C11 mutant showed an abnormal wing and leg pattern. These suggest that although C11 is a member of PcG gene, it has its own unique role.

F827

Isolation of Early-flowering Mutants by Activation Tagging Mutagenesis

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Floral induction is regulated by environmental factors. The major environmental factors are temperature and