Among 260 decamer primers used in this study, four primers, OPC01, OPF07, OPF11 and OPH09, were amplified from rye chromosome-specific DNA fragments. The OPC01 marker was amplified from the template DNA of rye chromosome 7, OPF07 from rye chromosome 1, and OPF11 and OPH09 from chromosome 6. These were cloned and designated as pSc01C, pSc07F, pSc11F and pSc09H, respectively. The sizes of pSc01C, pSc07F, pSc11F and pSc09H were 1,207 bp, 1,987 bp, 1,225 bp, and 1,354 bp, respectively.

F820

The Studies on Regulation of Arginine Biosynthesis by Disrupted *argR* in *Corynebacterium glutamicum*

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The *argR* gene encoding the arginine repressor (ArgR) is isolated from *Corynebacterium glutamicum*, sequenced and overexpressed. Sequence analyis shows that *argR* gene encodes the protein of 171 amino acids and SDS PAGE indicates ArgR protein has a molecular weight 18,428Da. According to amino acid alignment, the arginine repressor of *C. glutamicum* contains highly conserved domains with other several prokaryotes. One domin is the DNA binding site located in its N-terminal part and another is the arginine binding site and the sufficient region for its oligomerization in C-terminal part. The *argR* mutant with the C-terminal part containing the arginine binding site and the oligomerization region cut off, is constructed by integration. The disruption vector pSL18 carrying integral *argR* fragment is inserted into chromosomal *argR* by single cross-over recombination. The effect of disrupted *argR* on the regulation of arginine biosynthesis will be discussed.

F821

Mutations in the Head V1 and Rod 1A Domains of Keratin 1 gene in Korean Epidermolytic Palmar-Plantar Keratoderma Patients.

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Epidermolytic palmoplantar keratoderma (EPPK) is an autosomal dominant disorder. Patients with EPPK have palmoplantar skin blistering due to cytolysis in suprabasal layers and it was reported that EPPK is concerned with keratin 9 (K9) gene. In this study, to investigate a disorder of keratin genes of Korean patients with EPPK, the DNA sequences of K9 and keratin 1 (K1) genes were analyzed. Mutation in K9 gene was not found but in K1 gene found. PCR product (557 bp) including exon 1 of K1 gene was amplified by using primers in intron 1 and 2, then the DNA sequences were determined. Two mutations causing Gly (GTG) to Cys (GTT; G137C) substitution in the head V1 domain and Phe (TTC) to Ile (ATC; F194I) substitution in the rod 1A domain were found. To verify the polymorphism of these mutations, the allele specific-PCR (AS-PCR) by using mutation-specific primers in the ends of these mutations was carried out. In case of G137C, PCR products were obtained specifically from only these Korean patients at 65℃, F194I at 64℃. This result represented that two mutations in exon 1 of K1 gene were specific in this Korean pedigree with EPPK, and might be closely related with EPPK.

F822

Isolation and Phylogenetic Analysis of HERV-K LTR cDNA in Cancer Cells

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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%),