

Z 109     **Phylogenetic Analysis of Novel Human Endogenous Retroviral Sequences Belonging to the HERV-H Family on Human X and Y Chromosomes**

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Human endogenous retrovirus-H (HERV-H), a family of endogenous retroviral elements that has undergone successive expansions in the human genome, includes sequences that are expressed in placenta and T cells. With a PCR approach to the HERV-H using human monochromosomal somatic cell hybrid DNA, we identified 8 new HERV-H sequences on the X chromosome, and one novel HERV-H element, HY-1, the first reported such element on the Y chromosome, and compared these with sequences in the nucleotide sequence database. Phylogenetic analysis indicated that clone HX-1 and BAC clone 523A23 on the X chromosome were found to be in close relationship to the sequences of DJ088A21 on the human chromosome 7q31. This finding allows us to speculate that HERV-H elements may have evolved by intra-chromosomal spread. Our data may be relevant to an understanding of human genomic plasticity.

Z 110     **Genetic Variability In East Asian Dogs using Microsatellite Loci Analysis; The Origin of Korean Native Dogs**

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To investigate the genetic variability and relationship among East Asian native dogs, nine dog microsatellite loci were analyzed for 212 individuals from 11 dog populations. The overall difference between the observed and expected genotype frequencies across all the microsatellite loci was statistically significant in the Asian dogs, showing a significant deviation from the heterozygosity expected under Hardy-Weinberg equilibrium. Of the East Asian dogs, the Korean native dogs showed a relatively higher polymorphism, and vice versa in the case of the Japanese native dogs. The genetic relationships among Asian native dogs based on allele frequency were analyzed using Nei's formula and a principal component analysis (PCA). The analyses indicate that Asian native dogs are clustered principally on the basis of the geographical areas they are living in. Particularly, the PCA analysis showed that Korean native dogs formed a separated group from the dogs of other origins, and showed a close relationship with Eskimo dogs. Taken together, these data indicate that Korean native dogs were originated from the dogs of northern part of Far East Asia. The results also suggest that a PCA analysis may be a useful tool for studying of the phylogeny of domesticated animals in which crossbreeding seems to have occurred in the past.