

LTR elements have potential relevance to structural change and genetic variation of the hominoid genome. In our previous study, we found that the SINE-R retroposons were hominoid specific. Here we identified seventeen new SINE-R retroposons (14 from orangutan and 3 from gibbon) from Asian apes and phylogenetically analysed them in comparison with those of the humans and African great apes. None of the retroposons from Asian apes were closely related to SINE-R.C2 that is human specific, originally identified in the gene for the C2 component of complement, whereas some retroposons (Ch-M10, Ch-M16, Gor-M, Gor-F1, Gor-M6, Gor-F9) from African great apes showed very close relationship with that of the SINE-R.C2 retroposon. The phylogenetic tree based on the SINE-R retroposons revealed wide overlap of the retroposons across species, suggesting that the SINE-R retroposons have been evolved parallel pattern in the course of hominoid evolution.

A114 Molecular Cloning and Phylogeny of the Human Endogenous Retrovirus HERV-W in cDNA Library of the Human Fetal Brain

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A new human endogenous retroviral family (HERV-W) has recently been described that is related to multiple sclerosis-associated retrovirus (MSRV) sequences that have been identified in particles recovered from monocyte cultures from patients with multiple sclerosis. Using the PCR approach with cDNA library of human fetal brain, two pol fragments (HWP-FB10 and HWP-FB12) of HERV-W family were identified and analyzed. They showed 89 percent sequence similarity with that of the

HERV-W. Translation of the pol fragments from human fetal brain showed frameshift and termination codon by deletion/insertion or point mutation. Phylogenetic analysis of the HERV-W family from GenBank database indicates that the HWP-FB10 is very closely related to the AC000064 derived from human chromosome 7q21-q22. Further studies on the genetic relationship with neighbouring genes and functional role of this sequence are indicated.

A115 A Theoretical Model-building for Intraspecific Taxa Base on Morphometric Analyses the *Ixeris chinensis* plex (Asteraceae, Lactuceae)

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Morphological discrete plays a prime role in the superficial recognition of microspecies within the species. However, most morphological characters scoring in the species complex usually show considerable overlap in each, And the separation of microspecies and their hierarchical arrangements are then usually intractable. In order to have a biosystematic study for the *Ixeris chinensis* complex as well as to establish a theoretical model-building for microspecies, morphometric procedures were used with 40 morphological characters from each of 110 individuals. Of them, 20 individuals of *I. tamagawaensis*, known to a nearest relative to the complex were included as an outgroup. After the huge amount of original data measured was firstly reduced by a factor analyzed, implied data values newly produced by factor score were continuously analyzed by a series of statistic methods. We will not only discuss taxonomic categories at the levels of both species with the result of these analyses but test taxonomic schemes proposed for the complex.