

P58

Endogenous retroviral MuERV-L in Korea Wild Mice: Identification, Phylogeny and Evolution

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The sequences of long terminal repeats(LTRs) in wild mouse(*Mus. musculus*) from four regions(Anmyondo, Chuncheon, Gumi, Sokcho) in Korea were analyzed to determine the degree of genetic diversity. Using genomic DNA from regional wild mouse in Korea, we performed PCR amplification and identified nineteen LTR elements(MuLTR) of *Mus. musculus* endogenous retroviral sequence MuERV-L. They showed 67.7~96.6% sequence similarity with the sequence of the MuLTR that derived from MuERV-L. Sequence analysis indicated that the MuLTR elements had a deletion about 50bp at Anmyondo, Chuncheon, Gumi. A phylogenetic tree, obtained by the neighbor-joining method, revealed that GM4 LTR elements which was cloned from wild mouse of Gumi was primitive. The MuLTR elements from four regions in Korea have been proliferated independently during murine evolution.