

P61

Molecular Phylogeny and Evolution of the Human Endogenous Retrovirus HERV-W LTR Family in Hominoid Primates

Jae-Won Huh¹, Kyung-Won Hong¹, Joo-Mi Yi¹, Tae-Hyeong Kim¹,
Won-ho lee¹, Osamu Takenaka² and Heui-Soo Kim^{1*}

¹Division of Biological Sciences, College of Natural Sciences,
Pusan National University, Pusan, Korea

²Department of Cellular and Molecular Biology, Primate Research Institute,
Kyoto University, Inuyama, Japan

Long terminal repeats (LTRs) of human endogenous retrovirus (HERV) have contributed to the structural change or genetic variation of primate genome connected to various diseases and evolution. Using genomic DNAs derived from hominoid primates (chimpanzee, gorilla, orangutan, and gibbon), we performed PCR amplification and identified thirty HERV-W LTR elements. Those LTR elements showed 82-98% sequence similarity with HERV-W LTR (AF072500). Specifically additional sequences, GCCACCACCACTGTTT in gorilla and TGCTGCTGACTCCCATCC in gibbon, were noticed. Clone OR3 from orangutan and clone GI2 from gibbon showed 100% sequence similarity although they are different species, indicating that both LTR elements are proliferated recently from the original LTR element. A phylogenetic tree obtained by the neighbor-joining method revealed that HERV-W LTR family has evolved independently during hominoid evolution.