

Z6 12     **The *Hinc* II RFLP of LDL receptor Gene in Korean Essential  
hypertensives**

Byung-Yong Kang, Ki-Tae Kim, Jung-Hee Shin<sup>1</sup>, and Chung-Choo Lee<sup>1</sup>  
Seoulin Bioscience Institute, Seoulin Bioscience, Co. Ltd., <sup>1</sup>School of  
Biological Science, Seoul National University

Essential hypertension is considered to be caused by a complicated combination of genetic and environmental factors. Alterations of lipid metabolism in plasma have been reported to be related to an increased risk of essential hypertension. The aim of present study was to examine the relationship between essential hypertension and *Hinc* II RFLP of LDL receptor gene that encode proteins having an influence on the cholesterol homeostasis in plasma. the genotype distribution of this RFLP was not significantly different between normotensives and essential hypertensives. However, this genetic marker was significantly associated with plasma Lp(a) levels in our study group ( $P < 0.05$ ). Therefore, our result suggest that *Hinc* II RFLP of LDL receptor gene may be genetic components of cardiovascular risk factors in Korean population.

Z6 13     **Identification and Phylogeny of HERV-F pol Elements in Old World  
Monkeys**

Seung-Heui Jeon\*, Joo-Young Choi, Won-Ho Lee, and Heui-Soo Kim  
Division of Biological Sciences, College of Natural Sciences, Pusan  
National University, Pusan 609-735, Korea

A new human endogenous retroviral family (HERV-F) has been identified from human chromosome 7q31.1-q31.3 that was identical to the XA34 cDNA clone isolated from a human glioma cDNA library with an ERV-9 probe. We identified new pol gene sequences of the HERV-F family from Japanese monkey and rhesus monkey, and analyzed them along with sequences detected on a human monochromosomal DNA panel (chromosomes 3, 6, 7, 10, 11, 14, 19, 20, X, and Y) and other Old World monkeys (crab-eating monkey, African green monkey, and baboon). A phylogenetic analysis by neighbor-joining method and maximum parsimony revealed the close relationships between and within the species with a high degree of sequence similarity. The data distinctively showed six groups, indicating that the HERV-F family could be amplified at least six times after the original integration into the monkeys genomes or could represent integration events that occurred separately during primate evolution.