

Z609 **Genetic Variants of 7 Candidate Genes in Essential Hypertensives.**

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Essential hypertension is considered to be caused by a complicated combination of genetic and environmental factors. The aim of present study was to examine the relationship between essential hypertension and variants of genes that encode proteins having an influence on the cardiovascular system. Genotypes of 7 candidate genes (SA, antithrombinIII, factorVII, CETP, eNOS, paraoxonase and apoB) were determined by polymerase chain reaction/restriction fragment length polymorphism (PCR-RFLP) method. *Xba*I RFLP of apoB gene and *Alu*I RFLP of paraoxonase gene were significantly different between normotensivers and hypertensives (χ^2 -test; $P < 0.05$). Therefore, it suggests that both apoB *Xba*I and paraoxonase *Alu*I RFLPs may be useful as genetic marker for essential hypertension.

Z610 **Genetic Analysis of Fossil Animal Bones Excavated from Kwakji (Cheju) Archaeological Site**

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Genetic analysis of fossil animal bones (1,200-1,300 years B.P.) recovered from Kwakji (Cheju) archaeological sites was investigated by comparing the nucleotide sequences in the hypervariable D-loop region of mitochondrial DNA (mtDNA). The mtDNA sequences were amplified from the total DNA of the extracts of the fossil bones using polymerase chain reaction (PCR). The oligonucleotide primers used to amplify the mtDNA D-loop region by PCR were designed by referring to the sequences of tRNA^{Thr} and large conserved sequence block in the highly conserved regions of mtDNA common to animal species. The length of the DNA fragment amplified presented in 564 base pairs. Comparing the base sequences of the amplified DNA fragment with those of some mammals species, the nucleotide sequences were identical as 90% to those of Cheju native horse. These results suggest the new possibilities for researches on the origin and ancestry of Cheju native horse.