D-33 A *Pvu*II Polymorphism of Human Apo B mRNA Editing Protein Gene

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We have identified a genetic polymorphism of human apoB mRNA editing protein (HEPR) gene in Korean population. This polymorphism occurs according to absence (*P*1 allele) or presence (*P*2 allele) of the *Pvu*II restriction site. The allele frequency in 84 healthy subjects was 0.38 for *P*1 and 0.62 for *P*2 allele, respectively. Subjects with the *P*2*P*2 genotype was associated with the most elevated LDL cholesterol levels, and subjects with a heterozygous genotype had intermediate levels, indicating a gene dosage effect ($P<0.05$). Thus, current study might be provided for basic data in elucidating the interactions between this genetic variants and disorders related to lipid metabolism.

D-34 *Mae* III Restriction Fragment Length Polymorphism of the Alcohol Dehydrogenase 2 (*ADH2*) Gene in Korean

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Alcohol dehydrogenase (ADH:alcohol:NAD^+ oxidoreductase, EC 1.1.1.1) in huamn liver which is resposible for the oxidative metabolism of ethanol consists of eight genes (ADH 1-8) with corresponding subunits. The genes of *ADH* are polymorphic at *ADH2* and *ADH3* loci. *ADH2* gene located on 4q21-25 consists of nine exons. Three alleles of *ADH2* gene have been recognized in the exon 3 region such as : *ADH2*1* for β1 subunit (common in Caucasians), *ADH2*2* for β2 subunit (common in Orientals), and *ADH2*3* for β3 subunit (common in Blacks). The polymorphism of *ADH2* is due to an mutation of a single amino acid at position 47. *ADH2*1* has Arginine (CGC) while *ADH2*2* has Histidine (CAC). We determined *ADH2* genotype of exon 3 using the restriction fragment length polymorphism of leukocyte DNA in 287 unrelated Korean. *Mae* III RFLP analysis of *ADH2* gene showed fragments of 95bp and 60/35bp behaved as *ADH2*1* and *ADH2*2* allele. The allele frequencies for *ADH2*1* and *ADH2*2* were 0.294 and 0.706, respectively. The *ADH2*2* frequencies vary in different ethnic groups with the range of the lowest 0.0 in the American indians and the highest 0.65-0.80 in Mongoloids. The genetic variation of *ADH2* genotype may influence the risk of alcoholism through acetaldehyde formation. The frequency of *ADH2*2* of the alcoholics (0.373) is significantly ($p<0.01$) lower than that of the non-alcoholics (0.706).