F103 Genetic polymorphism of Apolipoprotein H in Korean

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The distribution of apolipoprotein H(ApoH) genetic polymorphism and their role in lipid metabolism has been studied extensively in various population groups but, little data is available in Korean population. In this study, Korean population (n=350) has been screened by isoelectric focusing and immunoblotting(polyclonal and monoclonal antibody 3D11) procedures to determine the distribution of genetic polymorphism in ApoH gene. In addition to the previously described three alleles, *ApoH*1, ApoH*2* and *ApoH*3*, a product of a putative new allele was observed in three samples. This unusual variant is provisionally designated as *ApoH*3Kongju*. All samples carrying the ApoH*3 allele reacted with monoclonal antibody 3D11. Interestingly, the product of the new allele, *ApoH*3Kongju*, also reacted with 3D11. The frequencies of the *ApoH*1, ApoH*2, ApoH*3* and *ApoH*3Kongju* alleles were 0.010, 0.913, 0.073 and 0.004, respectively.

F104 Identification of the UV-Responsive Element of *uvi15*$^+$ and Cellular Factor(s) Binding to It

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uvi15$^+$ gene, isolated on the bases of UV-responsiveness, was known to play some roles in various stress responses in *Schizosaccharomyces pombe*. Transcription of this gene is induced by DNA damaging agents including UV-light and MMS (Methyl Methanesulfonate), or environmental stress such as heat shock and starvation. Deletion and genome integration analysis identified a 154-bp fragment responsible for UV-induction in the 3'-regulatory region of *uvi15*$^+$. Gel retardation experiments have been used to demonstrate specific complex formation between this fragment and one or more *S. pombe* proteins. Formation of these complexes was competed by *S. pombe rhp51*$^+$ DRE (Damage-responsive element) with A(T)GGT(A) as a core consensus sequence but not by the fragments containing mutations in the core sequence. These results, together with the facts that sequence elements with A(T)GGT(A) as a core are found in the regulatory region of many of the DNA damage-inducible genes in *Saccharomyces cerevisiae*, suggest that *S. pombe uvi15*$^+$ gene is regulated through a very similar manner with those of the DNA damage-inducible genes in *S. cerevisiae*.