

Chinese (6.0%), and Japanese (1.6%). It is known that most Caucasian and Negroid males examined so far completely lack the LY1 retroposon insertion, but present it at high frequency in the south of China. Two possible explanations would be migration from the south of China to Korea, or drift within Korean population. The dual patterns of the distribution of LY1 insertion is compatible with our earlier report that the Korean population may have evolved from two different waves of East Asians.

F825

Effect of Ultraviolet Radiation or 3-Aminobenzamide on Apoptosis in Chinese Hamster Ovary Cells

Kyu Seon Oh*, Dong Wook Lee, Jeong Hyun Chang and Kyung Il Um

Dept. of Biology, Dong-A University, Pusan 604-714

The present study has performed to elucidate the effect of ultraviolet radiation(UV) or 3-aminobenzamide(3AB) on apoptosis in Chinese hamster ovary(CHO) cells. Four assays were employed in this study : Gel electrophoresis of isolated DNA, quantitative assay of fragmented DNA, morphological assay of apoptotic cells and western blot analysis. Alteration of DNA level on apoptosis was determined by DNA ladder pattern. DNA ladder pattern in the cells irradiated with UV was observed from 12 hrs until 24 hrs after incubation. Whereas the DNA ladder pattern was not shown in the cells with 3AB. Expression of Hsp70 and poly(ADP-ribose)polymerase(PARP) pretreated with low-dose of UV and subsequently treated with high-dose of UV was higher than treated with high-dose of UV. Whereas Hsp70 and PARP expression treated with 50 J/m² UV and incubated with 5 mM 3AB was lower than without 5 mM 3AB.

F826

Characterization of a New Polycomb Group Mutation

Chun Taek Oh¹, Seung Hae Kwon¹,
Kyoung Dae Kang¹, Sang Hee Kim²,
Yun-Taik Kim³ and Sang-Hak Jeon¹

Department of Biological sciences¹ and Department of Chemistry², Konkuk University; Department of Life Science³, Sogang University

The *Polycomb* group (PcG) genes are responsible for the transmission through the rest of development of the early homeotic gene pattern determined by the transient expression of the maternal and segmentation genes. *pleiohomeotic* gene, which is a PcG gene, was found to encode a DNA binding protein. It is only a DNA binding protein among 13 PcG proteins so far discovered. So the *pho* was expected to play a main role among PcG group. But its mutant showed very weak phenotypes, which implied a requirement of another partner. A new PcG mutant was discovered as an enhancer of *pleiohomeotic (pho)* mutation. It is embryonic lethal, showing homeotic transformation at embryonic and adult stage. It synergistically interacts with other PcG mutation. Unlike other PcG mutation, C11 mutant showed an abnormal wing and leg pattern. These suggest that although C11 is a member of PcG gene, it has its own unique role.

F827

Isolation of Early-flowering Mutants by Activation Tagging Mutagenesis

Eunsook Park*, Euna Cho and Ilha Lee

Dept. of Biology, Seoul National University, Seoul 151-742

Floral induction is regulated by environmental factors. The major environmental factors are temperature and

photoperiod. Photoperiod induction pathway is relatively well studied at molecular level but vernalization pathway is not. To understand more about the flowering mechanism, we adopted activation tagging mutagenesis strategy using late flowering ecotype *Arabidopsis*(*FRI-Col*). The inserted 35S enhancer would cause the activation of nearby gene and give gain-of-function mutants phenotype. Using this strategy, we isolated two early flowering mutants and one morphological mutant which showed defect in leaf morphology. The genetic and physiological characteristics of these mutants are currently analyzed.

F828

Genetic Variation of Apolipoprotein CII Gene in Korean Population

Jung-Hee Shin¹, Byung-Yong Kang², Jeong-Mun Park², Yun-Ho Han², Ki-Tae Kim², Kyung-Ho Lee¹ and Chung-Choo Lee¹

School of Biological Science, Seoul National University, Seoul, 151-742¹; Seoulin Bioscience Institute, Seoulin Bioscience Co. Kr., Seoul, 134-030²

Apo CII(Apolipoprotein CII) plays an important role in lipoprotein metabolism as a cofactor for lipoprotein lipase(EC 3. 1. 1. 34), the enzyme which hydrolyzes the triglycerides on plasma chylomicrons and very low density lipoproteins. The aims of this study were to identify mutations in the apo CII gene and investigate the genotype/phenotype relationship using *Ava*II RFLP as a genetic marker. In order to identify the presence of mutation, SSCP analysis was used following exon amplification of the apo CII gene. However, any mutation was not detected in Korean samples. In the second result of our study, *Ava*II RFLP of apo CII gene was significantly associated with plasma TG level (one-way ANOVA test, $P < 0.05$). Also, A2A2

homozygote indicated significantly lower plasma TG level than that of other genotypes in this RFLP study. Therefore, our results suggest that *Ava*II RFLP of apo CII gene may be useful as a protective genetic marker for cardiovascular disease in Korean population.

F829

Functional Analysis of a Novel *Drosophila* Learning Gene *gomdanji* (*gom*) Using Yeast Two-Hybrid Assay

Young-Hwan Ryu¹, Sun-Ok Kim¹, Jin-Hee Han¹, Yun-Doo Chung², Won-Suk Son², Chung-Choo Lee² and Ki-Wha Chung¹

Dept. of Biology and RRC/NMR, Kongju National University, Kongju 314-701¹; School of Biological Sciences, Seoul National University, Seoul 151-742²

Mushroom bodies of *Drosophila barin* are believed to be the principle sites for learning/memory. From the previous study of P-element mediated enhancer detection screen, a novel learning mutant *gomdanji* (*gom*) was isolated. It was expressed preferentially in mushroom bodies, suggesting some roles of behaviors. The courtship conditioning behavioral assay showed that the mutant was significantly defective in learning. Sequence analysis of the 1.3 kb *gom* cDNA showed that it encodes a novel protein containing a proline-rich domain and a large KEKE motif. The KEKE motifs have been suggested as a domain responsible for Ca²⁺-binding activity as well as protein-protein interaction. In the present study, the protein-protein interaction partners of *gom* product were identified using the yeast two-hybrid assay. For the assay, two kinds of bait vector, pGBK7-Gom (containing full coding region) and pGBK7-KEKE (containing only KEKE motif region) were constructed. We have screened approximately 1×10^6 cfu of *Drosophila* adult pACT2 cDNA library. From the screen, about 400 positive yeast colonies were first isolated.