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

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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 AvaII 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, AvaII 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 AvaII 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

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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 Ca^{2+}-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 X 10^6 cfu of *Drosophila* adult pACT2 cDNA library. From the screen, about 400 positive yeast colonies were first isolated.

But, the pnumber of ositive lines were reduced to 65 through more stringent test. Prey vectors (pACTII) were rescued from the positive lines, and then the cDNAs were characterized using the sequencing analysis.

F830

Preparation of PCR-ready Genomic DNA from Saliva

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Blood is the traditional source of genomic DNA but is gradually giving way to more convenient sources such as hairs or buccal swabs as the analytical methods become more sensitive. Recently saliva emerged as an alternative to buccal swabs because saliva has an unexpectedly large amount of DNA and is relatively free of inhibiting activities. We developed a system for genomic DNA preparation from a small amount of saliva. The saliva was absorbed into the paper wetting around 1 cm^2 area. Saliva sample left on the bench for up to 3 month did not show any detectable degradation as judged by agarose gel electrophoresis or by PCR amplification. Small discs with a diameter of 1.2 mm were punched out from the paper containing saliva samples with the GS-punch. Although the disc was tiny, it contained enough genomic DNA, up to 5 ng, so that multiplex PCR including 9 primer pairs for individual identification could be performed without loss of the data quality. We concluded that the saliva sampling is the preferred method for routine genetic analysis such as diagnosis of the morbid genes, forensic identification and paternity tests.

F831

A Multiplex System of 8 Short Tandem Repeats and Amelogenin Gene for Forensic Identification and Paternity Tests.

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Short tandem repeats(STR) became the major tool for forensic identification and paternity tests during 1990s replacing the good old variable number of tandem repeats(VNTR). The alleles of STR are only a few hundred base-pairs long that they can be easily amplified by PCR. It is now a routine task for investigators to collect traces of biological evidences on a crime site for STR typing. Amelogenin is unique in that the copy on X chromosome is a little larger than that of Y chromosome so that the gender could be easily distinguished by PCR. Although it has only two alleles, it identifies the subject as either a man or a woman. Amelogenin is also powerful in detecting the presence of male DNA in mixed samples. We developed a multiplex PCR system in which 8 STRs and amelogenin gene were amplified simultaneously. The STR loci showing a large number of alleles either by our own survey of Koreans or by other studies were incorporated. This 8 STR plus amelogenin system had the cumulative power of discrimination of 1 in billionth that practically no two persons can have identical profiles. The amplified DNA could be visualized by silver-staining after the denaturing acrylamide gel electrophoresis. For enhanced sensitivity and for the automatic detection one of the 10 primer pairs could be labeled with fluorescent dyes. For example, four STRs including D6S1043, D9S925, D21S11, D4S2368 and amelogenin were labeled with FAM while the remaining primers of the five STR including D8S1477, D7S821, D3S2406, D13S317 were labeled with HEX. Discernable peaks could be read down