F826 Extraction, amplification, and DNA Typing of Nuclear DNA from a Korea Human Remain in Damp Environmental Area

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Although polymerase chain reaction(PCR) methods for the recovery of DNA conserved in bones and hairs from archaeological remains have been developed, damp conditions in particular can cause a rapid degradation of DNA, even in bone and teeth, and thus reduce the chances of successful typing. We performed nuclear DNA typing based on PCR from a Korea human remain in damp environmental area for periods ranging from 150 to 200 years. Samples of a femur bone, a phalanx, and beard hairs were collected and successfully subjected to DNA extraction, quantitation, amplification, and subsequently typed for several shot tandem repeat(STR) loci. This studies are primarily concerned with the amplification of degraded DNA samples for ancient Korea human remains in damp environmental area.

F827 Genetic Variations at Five Short Tandem Repeat Loci in Population of Korea

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The analysis of short tandem repeat (STR) loci makes it useful tools for population genetics and forensic investigations. We examined the allele and genotype frequencies of five STR loci (D10S2325, D13S325, D20S470, D18S51 and D19S253) having 4-bp repeating unit in a population of Korea (n=130) using the methods of multiplex PCR and denatured polyacrylamide gel electrophoresis. As the results, 11 alleles for D10S2325, 11 alleles for D13S325, 14 alleles for D20S470, 11 alleles for D18S51 and 9 alleles for D19S253 were observed. No deviations of genotype distribution from the Hardy-Weinberg equilibrium were found at the five loci (D10S2325 P=0.4796; D13S325 P=0.6593; D20S470 P=0.5384; D18S51 P=0.1328; D19S253 P=0.8696). The matching probability of the combined system is $7.5X10^{-5}$. Our results indicate that these STR systems are very useful for application in forensic casework analysis.

F828 Screening of early flowering *mutants by fast-neutron mutagenesis* in Arabidopsis

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Floral transition of plants is affected by several endogenous and environmental signals. Flowering of winter-annual ecotype in Arabidopsis is promoted by exposure to cold (vernalization). *FRIGIDA (FRI)* and *FLOWERING LOCUS C (FLC)* are known to confer winter-annual trait to Arabidopsis. The interaction of these two genes delays flowering time severely in the absence of vernalization. To understand molecular basis of floral transition, we performed genetic dissection of Arabidopsis containing *FRI* and *FLC*. From the screening of *FRI* suppressor mutants, 29 early flowering mutants were isolated. The complementation tests among these early flowering mutants were performed by genetic crosses. More then 4 genetic loci that affect floral transition more newly identified. The physiological and molecular characterization of these mutants will be presented.

F829 Characterization of phytochrome negative regulatory factor in Arabidopsis

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We have isolated an *am118* mutant showing *phyB* mutant phenotype by activation tagging mutagenesis of winter annual strain of Arabidopsis (*FRI-Col*). T1 generation of *am118* (*FRI-Col*) showed interesting phenotype, such as elongated hypocotyl and petiole, serrated rosette leaves, pale green leaves and early flowering time. T2 progenies showed 2.6:1 segregation ratio indicating that *am118* (*FRI-Col*) is dominant. T2 progenies of *am118* (*FRI-Col*) showed cosegregation of basta resistance and mutant phenotype. For genetic and molecular analyses of mutants regarding phytochrome signaling, we introduced the *am118* (*FRI-Col*) to wild type *Columbia* (*Col*). The mutant *am118* in *Col* showed same phenotypes with *am118* (*FRI-Col*). The *am118* (*Col*) mutant was named as *dhy1* (*dominant long hypocotyl 1*). Because *dhy1* mutant showed similar morphology to *phyB* mutant, we checked if *dhy1* has a defect in *PHYB* gene by DNA gel blot analysis and protein expression. We verified that *dhy1* mutant was not caused by the mutation of *PHYB* gene. DNA gel blot analysis confirmed that there was several copies of T-DNA insert in *dhy1* mutant. The plant DNA flanking the left border of the T-DNA insertion site was isolated by plasmid rescue and used DNA gel blot analysis and RT-PCR. The result of DNA gel blot analysis showed polymorphism between *dhy1* and wild type (*Col*) but the inserted 35S enhancer did not cause overexpression of nearby genes. Genetic and molecular analyses are in progress to gain insights into the function of *DHY1* gene.

F830 Characterization of Activation T-DNA tagging root mutants in Arabidopsis thaliana

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Root is very important in plant survival and productivity. While it is known the importance of studies on root morphology and development, little is known about the principle and mechanism of root development. In this study, we have applied the activation T-DNA tagging strategies. Activation-Tagging vectors that confer resistance to the antibiotic hygromycin have generated several transformed plants exhibiting abnormal root morphology. Some lines were identified on the basis of the short roots and aberrant lateral root formation. These lines represented the inhibition of root growth under hygromycin or cefotaxime sodium, even though they had no effect on the growth without antibiotics. As this response may provide a mechanism for roots to toxic, further studies are aimed at isolation of genes of these mutants.

F831 The First Intron of Petunia Actin-Depolymerizing Factor Gene Enhances GUS Expression in Transgenic Arabidopsis

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Two genomic clones of petunia actin-depolymerizing factor, *PhADF1* and *PhADF2*, which regulate cellular actin dynamics, were isolated and analyzed. It was revealed that the first intron of *PhADF1*(1i1) increases GUS activity, and can induce GUS expression in roots as shown in *PhADF2::GUS* with the intron. To elucidate how the intron enhances GUS expression, transgenic *Arabidopsis* lines harboring constructs with various modifications were generated. It seems that splicing event may play an important role more than sequence element based on results of GUS staining pattern in