F834 Genetic Relationship among Six Species of the Genus Haliotis by Random Amplified Polymorphic DNA (RAPD) Analysis

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The RAPD technique was used to identify genetic relationships among six species of the genus *Haliotis* distributed in Korea. A dendrogram was constructed using UPGMA from the polymorphic patterns generated by RAPD profiles. The molecular data clustered into two groups. Cluster I included *Haliotis discus hannai*, *H. discus*, *H. madaka* and *H. gigantea*, which was subsequently divided into two subclusters. Subcluster I included *Haliotis discus hannai*, *H. discus* and *H. madaka*, subcluster II with *H. gigantea*. Cluster II contained *H. diversicolor supertexta* and H. *diversicolor diversicolor*. The RAPD markers were found to be a useful tool for detecting genetic relationship within the six species of the genus *Haliotis*.

F835 Population Genetic Data on the Thirteen CODIS Short Tandem Repeat Loci in Koreans

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We analyzed variations at thirteen Combined DNA Index System (CODIS) short tandem repeat (STR) loci (CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, and D21S11) in a sample from 130 unrelated individuals in the Korean population. Allele and genotype frequencies were determined with commercial PCR-based DNA profiling kits. The Exact Test demonstrated that all loci were found to be no deviations from Hardy-Weinberg expectations (P>0.05). For forensic testing, the discriminating powers (PD) were 0.866 for CSF1PO, 0.961 for FGA, 0.826 for TH01, 0.760 for TPOX, 0.931 for vWA, 0.863 D3S1358, 0.909 for D5S818, 0.904 for D7S820, 0.948 for D8S1179, 0.930 for D13S317, 0.915 for D16S539, 0.958 for D18S51, and 0.917 for D21S11, respectively (combined PD: 0.99999999999998). Therefore, the Korean 13 CODIS STR data could be useful for the regional specific and prerequisite references to the forensic community.

F836 Requirement of Mediator complex for gene-specific transcriptional activation during Drosophila development.

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Mediator of transcriptional regulation is the evolutionary conserved coactivator complex that plays the central role in the integration and recruitment of diverse regulatory signals and transcription machinery to certain promoters. In yeast, each Mediator subunit is required for transcriptional regulation of a distinct group of genes. In order to decipher the mechanistic roles of Mediator proteins in regulating developmental specific gene expression, we isolated, and analyzed a multiprotein complex containing Drosophila Mediator homologs (dMediator). dMediator interacts with several sequence-specific transcription factors and basal transcription machinery,

and is critical for activated transcription in response to diverse transcriptional activators. In order to elucidate the function of Mediator in metazoan development, we isolated mutants of a conserved Mediator subunit, Drosophila Med6 (dMed6). dMed6 null homozygotes failed to pupate and died in the third larval instar. Larval mitotic cells and most imaginal discs showed severe defects in proliferation, but no apparent morphological defect was observed in other larval tissues. Clonal analysis of dMed6 mutant cells revealed that dMed6 is essential for cell viability and proliferation of most adult cell types. Drosophila cDNA microarray, quantitative RT-PCR, and in situ expression analyses of developmentally regulated genes in dMed6 mutants showed that transcriptional activation of a subset of genes involved in neuroblast proliferation in the larval brain were most affected. Our results suggest that dMed6 is required in most cells for transcriptional regulation of a subset of genes important for cell proliferation and metabolism.

F837 The chromosomal study of native plants in Korea

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There are about 90 families and 3600 species of native plants in Korea. In this study, chromosomes of 18 families and 46 species were observed by Feulgen staining. The numbers in the family Compositae chromosome were observed diversely. The somatic chromosome number of Carduus crispus was 2n=16, Lactuca sativa was 2n=18, Atractylodes japonica and A. ovata were 2n=24, Matricaria chamomilla was 2n=28, Taraxacum coreanum was 2n=32, Arctium lappa and Achillea sibirica were 2n=36 and Aster ageratoides was 2n=72. The chromosome numbers of 4 species in the family Umbelliferae were 2n=22. The other families and species also have different chromosome numbers.

F838 Construction of transgenic silkworm using P element based expression vector in Bombyx mori.

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Transgenesis is a powerful method of studying the role and expression mechanism of genes and organism. It is also a way to confer genetically useful characteristics to animals and plants that can be used in biotechnological applications. Introducing new genes into silkworms has proved difficult, but we have developed an efficient method of transgenesis for the silkworm Bombyx mori. The method makes use of the microinjection technique and P-derived vector to transfer the foreign genes into the chromosomes. We constructed the expression vector using fibroin gene promoter and P transposon vector containing luciferase as reporter genes (pFpLuc). We microinjected into eggs layed at the preblastoderm stage. 29 of 6815 microinjected eggs were survived. After PCR analysis, 3 of them were tured out transgenic silkworms. Also, F1 were assayed by PCR. We assayed F2 and F5 transgenic silkworms and got the positive PCR results and did PCR-sequencing. As for ClustalW result, PCR products had the sequence of luciferase. The studies on the gene expression using fibroin gene promoter may help to understand mechanism in fibroin genes, i.e. transcriptional regulation, or many advantages to produce useful biological materials. Transgenic silkworm technique will be very useful for basic research of silkworm and may be used for the massive production of proteins for diagnostic and therapeutic purposes.