

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

Hye-Suck An<sup>1</sup>, Young-Ju Jee<sup>2</sup>,  
Seock-Jung Han<sup>3</sup>, Sung-Real Park<sup>4</sup>,  
Ho-Yong Ryu<sup>1</sup>, Bong-Seok Kim<sup>1</sup> and  
Bong-Lae Kim<sup>3</sup>

Biotechnology Division<sup>1</sup>, Aquaculture Division<sup>2</sup>,  
Cheju Marine Hatchery<sup>3</sup>, TongYeong Laboratory<sup>4</sup>,  
National Fisheries Research & Development  
Institute, Pusan 619-900

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

Myun-Soo Han<sup>1</sup>, Pil-Won Kang<sup>1</sup>,  
Sang-Kyu Choi<sup>1</sup>, Youl-Hey Cho<sup>2</sup>, Han-Jun  
Jin<sup>3</sup>, Kyoung-Don Kwak<sup>3</sup> and Wook Kim<sup>3\*</sup>

<sup>1</sup>DNA Analysis Section, National Institute of  
Scientific Investigation, Seoul 158-097, Korea

<sup>2</sup>Department of Genetics, Hanyang University  
School of Medicine, Seoul 133-791, Korea;

<sup>3</sup>Department of Biology, College of Advanced  
Sciences, Dankook University, Cheonan 330-714,  
Korea

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 for 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:  
0.9999999999999998). 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.

Young-Joon Kim, Jin Mo Park, Byeong  
Soo Gim

Yonsei University Department of Biochemistry  
National Creative Research Center for Genome  
Regulation

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

**Jae-Wook Bang<sup>\*</sup>, Soo-Young Kim, Joong-Yeon Cho, Woo-Ku Lee, Mi-Na Yu, June-Young Kim, Mi-Sung Jeon and Jee-Young Park**

Dept. of Biology, Chungnam National University, 220 Gung-Dong, Yousung-gu, Daejeon 305-764, Korea

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*.

**Soonjeung Kim<sup>\*</sup>, Seunghyun Sung, Ji-yeon Sung, Seungshic Yum and Dongsang Suh.**

Department of Genetic engineering, SungKyunKwan Univ. 440-746 Suwon, Korea.

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 laid 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.