Expressed sequence tags (ESTs) are short, single pass cDNA sequences generated from randomly selected library clones. The ESTs are widely used to clone genes and/or elucidate their structures and/or functions. Chinese cabbage (*Brassica* spp.) is economically important crop in orient. Its genome size is relatively small ($7.7X10^8$), so that it has been served as a favorite model system in studying plant genome. In this study, 30 ESTs were generated from the chinese cabbage (*Brassica rapa* L ssp. *pekinensis*) as follows. Poly A+ RNAs were isolated from 10-day-old seedlings germinated in dark. Randomly selected cDNA clones were sequenced by the Sanger and/or by using ALFexpress™ DNA Sequencer (Phamacia Biotech, Sweden). A number of ESTs showed similarity to the protein coding sequences in Genbank and EMBL databases. Four clones had high levels of similarities in the reported amino acid compositions. DII#215 clone showed very high level of homology to a gene for homeodomain-leucine zipper protein in *Arabidopsis thaliana*. It has been repoted that homeodomain-leucine zipper protein has a role of responsibility to stress condition such as dehydration and higher salt. Sequence of a homeodomain-leucine zipper in Chinese cabbage has been determined and full clone of the gene has been isolated by screening cDNA library from Chinese cabbage.

F808

Genetic Analysis of *Prunus yedoensis*, Native and Cultivar, Based on Nucleotide Sequences of *rbcL* and *psbA* in Chloroplast DNA

Yong-Hwan Jung*, Sang-Hyun Han, Mi-Hee Ko, You-Sung Oh and Moon-You Oh

Department of Biology, Cheju National University, Cheju 690-756

Expressed sequence tags (ESTs) are short, single pass cDNA sequences generated from randomly selected library clones. The ESTs are widely used to clone genes and/or elucidate their structures and/or functions. Chinese cabbage (*Brassica* spp.) is economically important crop in orient. Its genome size is relatively small ($7.7X10^8$), so that it has been served as a favorite model system in studying plant genome. In this study, 30 ESTs were generated from the chinese cabbage (*Brassica rapa* L ssp. *pekinensis*) as follows. Poly A+ RNAs were isolated from 10-day-old seedlings It has long been disputed whether *Prunus yedoensis* was originated from Mt. Halla in Cheju or Cheju originatied taxon is the same as the cultivated one from Japan. By comparing the base sequences of *rbcL* and *psbA* in chloroplast DNA (cpDNA), genetic analysis was assesed between *P. yedoensis*-Native and Cultivar. The cpDNA sequences were amplified from the total DNA using polymerase chain reaction (PCR). The oligonucleotide primers used to amplify the *rbcL* and *psbA* coding regions by PCR were designed by referring to the sequences of tobacco cpDNA. In the comparing of the nucleotide sequences, base substitutions in twenty sites (8 transition and 12 transversion) were found from 1398 base pairs (bp) of *rbcL* and twenty sites of base substitution (6 transition and 14 transversion) were observed from 1062 bp of *psbA*. The value of amino acid sequences divergence between two taxa was 3.66% (17/465) in *rbc* and 3.97% (14/353) in *psbA* coding region, respectively. These results being same as those of the previous studies on the basis of random amplified polymorphic DNA and internal transcribed spacer region, we can suggest that *P. yedoensis*-Native should be distinguished from *P. yedoensis*-Cultivar, and at the same time, the scientific name of *P. yedoensis*-Native should be changed.

F809

Genetic Variation of *Goodyera velutina* (Orchidaceae) Based on Chloroplast DNA Sequences from *trn*L-*trn*F Region

Yong-Hwan Jung*, Yong-Uk Chung, Sang-Hyun Han, Ji-Hoon Song, Che-Hoan Kim and Moon-You Oh
Department of Biology, Cheju National University, Cheju 690-756

To investigate the genetic variation of the *G. velutina*, we carried out the single stranded comformation polymorphism (SSCP), restriction enzyme digestion and comparing the nucleotide sequences of *trn*L (Leu) and *trn*F (Phe) intergenic spacer. The *trn*L (Leu) and *trn*F (Phe) intergenic spacer in chloroplast DNA (cpDNA) were cloned from 10 individuals of the *G. velutina* by polymerase chain reaction (PCR). The total number of bases in the *trn*L (Leu) and *trn*F (Phe) intergenic spacer were 489. SSCP analysis of denatured and amplified products was carried out by polyacrylamide (10%) gel electrophoresis followed by silver staining. PCR products from 10 individuals were digested with 4 restriction enzymes, *Bam*H I, *Eco*R I, *Hinf* I, and *Fok* I. The results of the SSCP and restriction enzyme digestion clearly showed two different types, contained same results as those detected in the SSCP analysis. Comparing of the nucleotide sequences between two different taxa, base substitutions in twelve sites were found. These results show that SSCP, restriction enzyme digestion and DNA sequencing were useful in elucidating the interspecific variation in the *G. velutina* population.

F810

PCR-RLFP Analysis of Mitochondrial Cytochrome *B* Gene in Cheju Native Horses

Sang-Hyun Han*, Yong-Hwan Jung, Mi-Hee Ko, You-Sung Oh and Moon-You Oh
Department of Biology, Cheju National University, Cheju 690-756

We analyzed mitochondrial DNA (mtDNA) cytochrome *B* (Cyt*B*) gene in Cheju native horses using polymerase chain reaction (PCR) - restriction fragment length polymorphism (RFLP). *CytB* in mammals flanks in tRNA-Glu and tRNA-Thr in mitochondrial genome and 1140 bases long. To acquire the complete fragment of mtDNA *CytB*, we designed PCR primers in tRNA-Glu (H14158) and in tRNA-Thr (L15368) among *Equus*, *Sus* and *Bos*. The amplified PCR products were digested with 6 restriction endonucleases (*Bam*H I, *Eco*R I, *Rsa* I, *Msp* I, *Hae* III and *Hinf* I). Throughout the electrophoretic patterns, we found two types of fragments digested with *Rsa* I, *Msp* I and *Hae* III in Cyt*B* gene, respectively. Two kinds of *CytB* in Cheju native horses were found, though the frequency of variant was low. In addition, it is necessary to analyze the nucleotide sequences of *CytB* to develop a useful marker for identifying the maternal lineage and investigating the origin of Cheju native horses and relationships among other populations of east Asian native horses.

F811

Molecular Genetic Studies on the Structural and the Evolutionary Relationship of the Late Chorion Locus(Hc) from Wild Silkmoth, *Bombyx mandarina*.

Jun-Ok Moon*, Jong-Gil Kim[2], Ki-Sei Kim[3], Ki-Hwan Kim[3] and Dong-Sang Suh[3]
Dept. of Biology, jeonju University, jeonju 560-759; Dept. of National Institute of Agricultural Science and Technology, Suwon 441-707[2]; Dept. of Genetic engineering, SungKyunKwan University, Suwon 440-746[3]