to 0.2 ng of template DNA when fluorescence labels were applied. The system was found satisfactory both in the sensitivity and in the reproducibility of typing results.

F832

Genetic Relationship among Abalone Species, Based on *MtCOI* and *16S rRNA* Gene Sequences

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6 *Haliotis* species were distributed in Korea (*H. discus hannai* INO, *H. discus discus* REEVE, *H. madaka* HABE, *H. gigantea* GMELIN, *H. diversicolor diversicolor* REEVE, *H. diversicolor supertexta* REEVE). The genetic relationships of these abalone were examined based on mitochondrial *COI* and *16S rRNA* gene sequences. We wished to determine whether detectable genetic differences exist among these. This information would be useful as a genetic marker for distinguishing between species and for the improvement of species through hybridization. Part of *COI* and *16S rRNA* genes was amplified with the polymerase chain reaction (PCR) and sequenced for five individuals respectively. Resultant sequence data analysis showed that these were grouped into two clusters; cluster I was constituted with *H. discus hannai, H. discus discus, H. madaka,* and *H. gigantea* and cluster II with *H. diversicolor diversicolor* and *H. diversicolor supertexta.* And cluster I was divided into two subclusters; subcluster I was constituted with *H. discus hannai, H. discus discus,* and *H. madaka* and subcluster II with *H. gigantea.*

F833

Variability in Ribosomal RNA Gene Loci in Korean *Lycoris*

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Physical maps of the 18S-5.8S-26S ribosomal RNA genes (rDNA) were generated by fluorescent in situ hybridization for seven *Lycoris* species, *L. chinensis, L. flavescens, L. flavescens* var. *uydoensis, L. sanguinea* var. *koreana, L. squamigera, L. chejuensis, L. radiata* in Korea. The number of rDNA loci of *L. chinensis* (2n=16) has eight and all of them are located on the telocentric chromosomes. *L. sanguinea* var. *koreana* (2n=22) and *L. radiata* (2n=33), which are all acrocentic chromosomes, have three and six rDNA sites carrying the nucleolus organizing regions (NOR) at the secondary consriction. *L. squamigera* (2n=27) has eleven rDNA sites. *L. flavescens* (2n=19), *L. flavescens* var. *uydoensis* (2n=19), and *L. chejuensis* (2n=30), which are natural hybrid species, were six, five, and seven rDNA sites respectively. The rDNA sites are always located on the telomeric region of chromosomes in all species. But the metacentric and submetacentric chromosmes do not have rDNA sites. The variability of rDNA loci suggests futher information about the relationships of Korean *Lycoris* species.

F834

Cloning and Characterization of Mutants Involved in the Cell Cycle Progression in Saccharomyces cerevisiae

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The cell cycle of eukaryotic cells is divided into four main phase; G1, S, G2 and M. Progression into each phase of the cell cycle is regulated in a tightly controlled manner. This order is maintained by mechanisms called checkpoint controls that monitor completion of earlier events and control cell cycle progression. To study the genes which related in cell cycle progression, we isolated the new mutants in S. cerevisiae. Cells were treated by MNNG mutagenesis , and then screened the sensitivity to ciclopirox olamine (CPO) which inhibits the cell cycle traverse at or very near the G1/S phase boundary in HeLa cell. In a screen for CPO sensitivity, we have 31 mutants and named as cos (cyclopirox olamine sensitivity cos27-57). To determine the phenotype of mutants, we examined the sensitivity to methylmethane sulfonate (MMS) and hydroxyurea (HU). In this study, we selected 8 mutants by their phenotype and started the gene cloning for these mutants. As a result, the DNA fragments which complement with the cos28, cos33, cos46 and cos47 mutants, were cloned and sequenced. And then cloned genes were surveyed though data base analysis. We will report the characterization of these mutants and their gene.