But, the pnumber of ositive lines were reduced to 65 through more stringent test. Prey vectors (pACTII) were rescued from the positive lines, and then the cDNAs were characterized using the sequencing analysis.

F830

Preparation of PCR-ready Genomic DNA from Saliva

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Blood is the traditional source of genomic DNA but is gradually giving way to more convenient sources such as hairs or buccal swabs as the analytical methods become more sensitive. Recently saliva emerged as an alternative to buccal swabs because saliva has an unexpectedly large amount of DNA and is relatively free of inhibiting activities. We developed a system for genomic DNA preparation from a small amount of saliva. The saliva was absorbed into the paper wetting around 1 cm^2 area. Saliva sample left on the bench for up to 3 month did not show any detectable degradation as judged by agarose gel electrophoresis or by PCR amplification. Small discs with a diameter of 1.2 mm were punched out from the paper containing saliva samples with the GS-punch. Although the disc was tiny, it contained enough genomic DNA, up to 5 ng, so that multiplex PCR including 9 primer pairs for individual identification could be performed without loss of the data quality. We concluded that the saliva sampling is the preferred method for routine genetic analysis such as diagnosis of the morbid genes, forensic identification and paternity tests.

F831

A Multiplex System of 8 Short Tandem Repeats and Amelogenin Gene for Forensic Identification and Paternity Tests.

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Short tandem repeats(STR) became the major tool for forensic identification and paternity tests during 1990s replacing the good old variable number of tandem repeats(VNTR). The alleles of STR are only a few hundred base-pairs long that they can be easily amplified by PCR. It is now a routine task for investigators to collect traces of biological evidences on a crime site for STR typing. Amelogenin is unique in that the copy on X chromosome is a little larger than that of Y chromosome so that the gender could be easily distinguished by PCR. Although it has only two alleles, it identifies the subject as either a man or a woman. Amelogenin is also powerful in detecting the presence of male DNA in mixed samples. We developed a multiplex PCR system in which 8 STRs and amelogenin gene were amplified simultaneously. The STR loci showing a large number of alleles either by our own survey of Koreans or by other studies were incorporated. This 8 STR plus amelogenin system had the cumulative power of discrimination of 1 in billionth that practically no two persons can have identical profiles. The amplified DNA could be visualized by silver-staining after the denaturing acrylamide gel electrophoresis. For enhanced sensitivity and for the automatic detection one of the 10 primer pairs could be labeled with fluorescent dyes. For example, four STRs including D6S1043, D9S925, D21S11, D4S2368 and amelogenin were labeled with FAM while the remaining primers of the five STR including D8S1477, D7S821, D3S2406, D13S317 were labeled with HEX. Discernable peaks could be read down

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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