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The analysis of mitochondrial DNA polymorphisms has proved to be efficient on highly degraded samples or samples having little or no genomic DNA such as hair shafts or blood remains. In order to identify polymorphic positions and to determine their frequency in the human mitochondrial control region, the mitochondrial DNA (mtDNA) hypervariable region I and II (HV I and II) of 300 unrelated individuals from Korea were amplified and directly sequenced. In our population data ,we have found the most prevalent substitutions are transitions (C-T) and occur at sites 16223 and 16362 in HV I region from korean population. Most insertions occur in the HV II region at sites 309.1 and 315.1, within a C-stretchs. This sequence data in this region indicates that the PCR-based mtDNA typing by direct automated sequencing is valid and a reliable means of standardization of Korean population mtDNA genotyping. Our study aims to establish a Korean population gene bank data base on the basis of sequence variability on control region of human mitochondrial DNA.

F816

Studies on Expressed Sequence Tags (ESTs) Derived from the Posterior Silk Gland (PSG) of *Bombyx mori*

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The silk of lepidopteran insects has been studied extensively on a protein of fibroin which is produced in the posterior section of silk glands, and sericin which is secreted in the middle section. To study the gene expression profile in the posterior silk gland (PSG) and to identify the tissue-specific gene, we randomly selected cDNA derived from the posterior silk gland (PSG) and sequenced the clones from one end or both ends. Analysis of this cDNA revealed that this library contained a variety of functional genes as well as the gene that were not detected in expressed sequence taqs (ESTs) data of the posterior silk gland ; it must be provided us as a useful resourc for molecular analysis of gene. In addition, we now revealed matters of weight and importance ; it found transcription factor, elongation factor, and translation factor etc of ESTs data. Therefore the fiborin protein is expected to be involved in the basal or regulating transcription factor.

F817

Studies on the Foreign Gene Expression Using Fibroin Gene Promoter in *Bombyx mori*

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The silkworm represents on a model for studies on transgenic animals because of its well-known genetics and the relatively large size of embryos and its potentia for biotechnical use. The fibroin genes consists of Fib-L and Fib-H, which have strong promoter in *Bombyx mori*. In this study, to investigate the gene expression using fibroin gene promoter, the fibroin promoter region was determined by DNA sequencing. To develop new expression vector system for foreign gene, we did to construct the

expression vector using fibroin gene promoter and P transposon vector containing luciferase as reporter genes(pFpLuc). The expression vector activities were analyzed with microinjection. In microinjection, we did microinject into eggs. 29 of 6815 microinjected eggs survived. After PCR analysis method, 3 silkworms were turned out transgenic silkworms and mated. Transgenic silkworms were assayed by PCR. We assayed F2 transgenic silkworms and got the positive PCR results and did PCR-sequencing. As for ClustalW results, PCR products were sequencing of of Luciferase. The studies on the gene expression using fibroin gene promoter may help to understand mechanisms in fibroin genes, i.e. transcriptional regulation, or many advantages to produce useful biological materials

F818

Production of New Translocated(1RS/1BL) and Added(1RL) Wheat lines in Backcross Derivatives of *Triticumaestivum* cv. Olmil x *Secalecereale* cv. Paldanghomil

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GISH analysis in BC_1F_6 generation of *T. aestivum* cv. Olmil x *S. secale* cv. Paldanghomil was carried out from seeds of the 467 plants (lines) selected in 77 BC_1F_5 families. Among total 293 seeds from the rye chromatin detected in 32 lines of BC_1F_6, 111 seeds were identified as one or two rye chromatin addition lines, 12 seeds as whole chromosome addition line, and 27 seeds as translocated line. From seeds of the 62-11 plant in BC_1F_6, one translocated and two translocated chromosomes were detected in 13 and 14 seeds, respectively. From sequential analysis of Giemsa C-banding patterns and GISH, translocated chromosome and added chromosome were identified as 1RS/1BL and 1RL, respectively. New wheat line (62-11-18) with two tranlocated 1RS/1BL showed normal meiotic configuration. GISH signal in the plant was visible as a single strand because of pairing between two translocated chromosomes at prophase I. Meiotic chromosome association at metaphase I showed 21 bivalents, and chromosome pairing between two translocated chromosomes was clearly identified by GISH analysis.

F819

Identification and Chromoson 1l Assignment of Rye Genome- and Chromosome-specific RAPD Markers

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Two rye genome specific- and four rye chromosome-specific RAPD markers were selected to identify the existence of rye chromatin in the wheat genome. Two genome-specific markers were identified by PCR amplification using OPC10 and OPH20 as a primer and cloned (named pSc10C and pSc20H, respectively) and sequenced. The size of pSc10C and pSc20H were 1,012 bp and 1,494 bp, respectively. In FISH anaiysis, pSc10C probe was predominantly hybridized to the centromeric regions of al rye chromosomes, while pSc20H probe was dispersed throughout rye genome except for telomeric and nucleolar organizing regions.