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.

Among 260 decamer primers used in this study, four primers, OPC01, OPF07, OPF11 and OPH09, were amplified from rye chromosome-specific DNA fragments. The OPC01 marker was amplified from the template DNA of rye chromosome 7, OPF07 from rye chromosome 1, and OPF11 and OPH09 from chromosome 6. These were cloned and designated as pSc01C, pSc07F, pSc11F and pSc09H, respectively. The sizes of pSc01C, pSc07F, pSc11F and pSc09H were 1,207 bp, 1,987 bp, 1,225 bp, and 1,354 bp, respectively.

F820

The Studies on Regulation of Arginine Biosynthesis by Disrupted *argR* in *Corynebacterium glutamicum*

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The *argR* gene encoding the arginine repressor (ArgR) is isolated from *Corynebacterium glutamicum*, sequenced and overexpressed. Sequence analyis shows that *argR* gene encodes the protein of 171 amino acids and SDS PAGE indicates ArgR protein has a molecular weight 18,428Da. According to amino acid alignment, the arginine repressor of *C. glutamicum* contains highly conserved domains with other several prokaryotes. One domin is the DNA binding site located in its N-terminal part and another is the arginine binding site and the sufficient region for its oligomerization in C-terminal part. The *argR* mutant with the C-terminal part containing the arginine binding site and the oligomerization region cut off, is constructed by integration. The disruption vector pSL18 carrying integral *argR* fragment is inserted into chromosomal *argR* by single cross-over recombination. The effect of disrupted *argR* on the regulation of arginine biosynthesis will be discussed.

F821

Mutations in the Head V1 and Rod 1A Domains of Keratin 1 gene in Korean Epidermolytic Palmar-Plantar Keratoderma Patients.

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Epidermolytic palmoplantar keratoderma (EPPK) is an autosomal dominant disorder. Patients with EPPK have palmoplantar skin blistering due to cytolysis in suprabasal layers and it was reported that EPPK is concerned with keratin 9 (K9) gene. In this study, to investigate a disorder of keratin genes of Korean patients with EPPK, the DNA sequences of K9 and keratin 1 (K1) genes were analyzed. Mutation in K9 gene was not found but in K1 gene found. PCR product (557 bp) including exon 1 of K1 gene was amplified by using primers in intron 1 and 2, then the DNA sequences were determined. Two mutations causing Gly (GTG) to Cys (GTT; G137C) substitution in the head V1 domain and Phe (TTC) to Ile (ATC; F194I) substitution in the rod 1A domain were found. To verify the polymorphism of these mutations, the allele specific-PCR (AS-PCR) by using mutation-specific primers in the ends of these mutations was carried out. In case of G137C, PCR products were obtained specifically from only these Korean patients at 65℃, F194I at 64℃. This result represented that two mutations in exon 1 of K1 gene were specific in this Korean pedigree with EPPK, and might be closely related with EPPK.

F822

Isolation and Phylogenetic Analysis of HERV-K LTR cDNA in Cancer Cells