mice are to be assisted. In this study it was suggested that the skin is a possible target organ for ectopic expression of the insulin gene as a potential treatment modality for type 1 diabetes mellitus and also this system is one of the candidates for gene therapy as gene carrier.

F813

The First Intron of Petunia Actin-Depolymerizing Factor Gene, *PADF-1*, Is Essential for Gene Expression

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ADF is one of the small actin-binding proteins that regulate actin dynamics in cells. We have previously isolated two cDNA clones,*PhADF1* and *PhADF2*, encoding ADF from *Petunia hybrida*. Northern and western blot analyses indicated that the gene expressions of PhADFs are regulated at transcriptional level. In addition, immunolocalization exprement confirmed that *PhADFs* are abundant proteins within the vascular tissues of petunia. To characterize the structure and regulation of ADF gene, we have isolated a genomic clone *PADF-1*, corresponding to *PhADF1* from a petunia genomic library. Comparison to cDNA sequence revealed that the coding region of *PADF-1* gene is consisted of three exons and two introns. The 1.6 kb of first intron was located immediately 3′ of the translation start codon. Promoter/GUS expression study in transgenic *Arabidopsis* demonstrated that the first intron is the essential element for *PADF-1* gene expression.

F814

Expression of Pathogenesis-related Gene by Chemical Inducers and Wounding in *Lithospermum erythrorhizon*

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cDNA clones encoding pathogenesis-related protein were previously isolated from a cDNA libraries prepared from shikonin-producing cells of *Lithospermum erythrorhizon* (Yu *et al* ., 1999). *LePR1* transcripts is predominantly accumulated in the root. However, *LePR1* transcripts is not detected in young leaves. To characterize the gene expression of *LePR1* , we investigate the accumulations of *LePR1* transcripts by several signal molecules for systemic acquired resistance(SAR) and by wounding in young leaves. *LePR1* gene expression is strongly induced by treatment of salicylic acid. Furthermore, accumulation patterns of *LePR1* transcripts by salicylic acid analogues, such as acetyl salicylate and benzo(1,2,3)thiadiazole-7-carbothioic acids S-methylester, are similar to those of salicylic acid treatment. After wounding treatment, accumulation of the *LePR1* transcripts is increased until 30 h. *LePR1* transcripts is induced by H_2O_2, after 100 mM H_2O_2 treatment, reached a peak at 12 h and thereafter gradually decreased. *LePR1* gene is induced in treatment with jasmonic acid, linolenic acid, and linoleic acid as well as abscisic acid. *LePR1* is accumulated after pathogen infection and is more susceptible to *Pseudomonas syringae* and *Erwinia stewartii* .

F815

Mitochondrial DNA Control Region Polymorphism in a Population from Korea

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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