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Fine Mapping of the Rsv4 Locus Associated with a Broad Spectrum of SMV Resistance in Soybean

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Soybean mosaic virus (SMV) is a prevalent viral pathogen that affects soybean [Glycine max (L.) Merr.] production in infested soybean fields worldwide. The Rsv4 gene of soybean confers extreme resistance to all the known strain groups of SMV, although it has been observed that the infected SMV moves locally in the old leaves. The Rsv4 gene was mapped to soybean molecular linkage group D1b between Satt542 and Satt558. The objectives of this study were to construct a fine genetic map near the Rsv4 locus in the soybean genome and to convert the closely mapped markers to high throughput markers for marker-assisted selection. An F2 population from a cross between V94-5152 (resistant) and Sowonkong (susceptible) was primarily used. Two recently reported microsatellite markers, Satt634 and Sat_254, were mapped between Satt542 and Satt558. Another two microsatellite markers from two EST have been reported to be near Satt634 but are not polymorphic in our mapping population. Thus, sequence information of the two ESTs was used to obtain their corresponding genomic DNA sequence and then develop PCR-based markers, AI1, AI2, and BF1. The closely linked PCR-based markers could facilitate marker-assisted selection to pyramid Rsv4 with other SMV resistance genes.

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The Effect of Overexpressed DNA Topoisomerase I on Protein Expression Patterns in *Saccharomyces cerevisiae*

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In most cells, DNA supercoiling is a precisely regulated procedure that influence many effects of DNA metabolism. Doutlessly, there are enzymes in most cell whose sole purpose is to underwind and/or relax DNA. The enzymes that increase or decrease the extent of DNA underwinding are called topoisomerase, and the property of DNA they affect is the linking number. These enzymes play an especially important role in processes such as replication and DNA packaging. In yeast, the topoisomerase I usually catalyzes relaxation of both negative and positive supercoils. It may participate in supercoiling only in the presence of additional proteins. The study of the topoisomerase I affecting cell growth was performed in yeast. To investigate the possibility that both induced proteins and repressed proteins could exist by overexpressed DNA topoisomerase I on protein expression patterns in *Saccharomyces cerevisiae* was analyzed by an immobilized wide range pH gradient in the first-dimensional separation of wholecell extracts using the 2D-PAGE technology, and analytical tool of high potential in global studies concerning changes in protein expressions.

G711

Identification of an Epileptic Gene in Sims (Sexual Immaturity, Megaencephaly, Seizure) Mutant Mouse and Genetic Study for the Diseases

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The new spontaneous mutant mouse sims has a smaller size at its weaning age and a mild tremor. The histological study also revealed severe developmental retardation of the secondary sexual organs in both sexes. Examination of brain did not show any histological difference but a 30% bigger weight. Another phenotype is seizure that occurs in both the homozygote and heterozygote though the severity is different between them. To identify a gene responsible for sims phenotype, we have constructed a genetic linkage map and a physical map of sims locus on chromosome 18. The result of linkage analysis shows that sims gene is located between D18Mit12 and D18Mit135. From in silico BAC contig constructed and analyzed, we chose 18 candidate genes and there is no known mutation matched for this phenotype at this region. Structure of the candidate genes was further studied by Southern blot analysis using genomic DNAs obtained from sims mutant mice and normal mice and no insertion or deletion was detected in the genome of 12 candidate genes. cDNA sequencing of candidate genes revealed that some base pairs do not match with that of the NCBI database. The mismatched sequences are being confirmed by cDNA sequencing of genomic cDNA prepared from congenic wild-type mouse. In addition, mice, transgenic to the candidate genes, were constructed using mouse BAC clones and the rescue of the sims phenotype by the wild-type candidate genes is being tested.

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The Role of *Corynebacterium glutamicum* ArgR in Arginie Metabolism

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Previously the *argR* mutant of *Corynebacterium glutamicum* were constructed by integration of gene disruption vector into chromosomal *argR* by single crossover recombination. We tried to find out the role of *C. glutamicum argR* in arginine metabolism used the in mutant cell. To confirm this, we tried to compare protein expression patterns of wild type cell and ArgRmutant. The different protein expression patterns between wild type and ArgR mutant of *C. glutamicum* were shown by two dimensional electrophoresis. The protein patterns of both wild type cell and ArgR mutant appear distinctively different when it was incubated in minimal medium. As a result to compare the protein expression patterns, it was found spots that putative arginine biosynthetic enzymes (ArgG and ArgJ) in gel. In other words, it was presumed that ArgR works as repressor in arginine metabolism. Furthermore there are the other spots in mutant cell. It was supposed that the ArgR protein of *C. glutamicum* is concerned in regulation of these proteins.