garlic DNA was extracted from leaf nuclei. A total of about 10,000 clones were obtained. This BAC library has more than 92% recombinants and 50-150 kb of genomic DNA inserts. Using several candidates from first BAC library as a probe, PFGE Southern blot analysis and FISH analysis were performed to assign the locations of each DNA inserts on Not I -restricted chromosomal DNA and on the chromosomes, respectively. Its experimental result will be discussed.

F202

Isolation and Characterization of Annexin cDNAs in *Capsicum annuum* L.

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Annexins are a family of structurally related proteins that exhibit Ca^{2+}-dependent phospholipid-binding. Also they are involved in variety of plant cellular processes. Most annexins are abundant intracellular proteins, composing often more than 2% of total cellular proteins. They have been implicated in multiple aspects of cell biology including regulation of membrane trafficking, trans-membrane channel activity, inhibition of phospholipase A2, inhibition of coagulation, transduction of mitogenic signal, and settlement of cell-matrix interaction. But the exact biological functions of the annexins are not known yet. By polymerase chain reaction (PCR) using degenerated primers, we isolated partial cDNA encoding hot pepper (*Capsicum annuum* L.) annexin P38. And by cDNA library screening, we isolated two full-length cDNAs related to annexin and annexin P38 of bell pepper. As the results of sequencing analyses, annexin is about 1.2 kb nucleotide encoding 317 amino acid-long peptide that shows 98% sequence identity and annexin P38 is about 97% sequence identity with bell pepper. Using Southern blot analyses, these cDNA clones were represented small copy number, and in northern and western blot analyses, the potential roles of these cDNA clones in variety of stresses and hormone-induced cellular functions are discussed.

F301

Organization and Regulation of the *arg* Operons in *Corynebacterium glutamicum*: ArgR Acts as the Arginine Repressor Protein

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We have studied the organization and regulation of the arginine biosynthetic genes in *Corynebacterium glutamicum*. A genomic library for *Corynebacterium glutamicum* was screened for clones carrying arginine biosynthesis genes by complementation of *Escherichia coli* mutants. As based on the complementing and sequencing analysis of the plasmids that carries a cluster of *argCJBDFGH*. It was found that *C. glutamicum* has an arginine repressor ArgR, located in the upstream region of *argG*, homologous to the other bacteria. The gel filtration indicated that molecular mass of the native protein is 110-kDa meaning that ArgR is a hexamer of equal subunits. Gel mobility shift assays revealed that in the presence of arginine, ArgR binds to a site upstream from the *arg* promoters.

F302

Expression Vectors Containing *ars* (aryl sulfatase) Promoter of *Neurosporacrassa*

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Neurosporacrassa, the orange bread mold has become a model system for the study of fungal genetics including sexual and asexual cycles. To facilitate the molecular studies in N. crassa, two expression vectors, pBL-ARS1 and pBL-ARS2, were constructed. The common features of the plasmids are: 1) the multiple cloning sites (MCS), 2) the inorganic sulfur-inducible ars promoter sequence and the qa-4 terminator sequence, 3) a partial his-3 gene sequence for homologous integration into the his-3 locus by recombination and 4) pUC19 base. The multiple cloning sites contain unique restriction endonuclease digestion sequences for *MscI*, *EagI*, *NsiI*, *SpeI*, *NotI*, and *SmaI*. While pBL-ARS1 has a Kozak sequence and an initiation codon in front of MCS, pBL-ARS1 does not have them.

F303

Molecular Analysis of *vanA* Gene Cluster in Vancomycin Resistant Enterococci (VRE) by Using PCR Amplification

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Recently infections of vancomycin resistant enterococci containing *vanA* gene have been increasing worldwide. The genes encoding the VanA type are located on mobile DNA elements, and conjugative transfer from VRE to the other enterococci may exist. We wanted to know about the distribution of the resistance genes and *vanA* gene cluster types in Korea. The internal and structural regions of *vanA* cluster were analyzed by using PCR fragment length polymorphism with 50 *E. faecium*, 12 *E. feacalis*, 3 *E. casseliflavus*, and 1 *E. gallinarum* isolated from clinical specimens. For *vanR* (645 bp), *vanS* (1,094 bp), *vanH* (943 bp), *vanA* (1,029 bp), *vanX* (424 bp), *vanY* (866 bp), and *vanYZ* (336 bp) intergenic regions, PCR products of expected size were obtained from *vanA* cluster (Tn1546). But for the *vanXY* and *vanSH*, amplicons of variable size were observed. For examples, the *vanXY* amplicons of 554 bp were obtained from 16 isolates and those of approximately 1,500 bp from 50 isolates. While 65 isolates produced amplicons of expected size (311 bp) for the *vanSH*, one produced about 1,900 bp amplicon. Therefore, dissemination of the resistance genes carried on transposable elements may be of greater importance than clonal spread.

F304

RFLP Pattern's of the IGS Region in *Fusarium* Species.

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The intergenic spacer (IGS) region, which is located between the 3′ end of 28S ribosomal DNA (rDNA) and the 5′ end of 18S rDNA, of *Fusarium* species was investigated using polymerase chain reaction-restriction fragment lenghth polymorphisms (PCR-RFLPs). The intergenic spacer of the rDNA is highly polymorphic, so provide useful tools for fungal taxonomic and phylogenetic studies. To investigate the genetic relatedness among 21 strains belonging to *F. graminearum*, *F. oxysporum*, *F. sambucinum*, and *F. solani*, after the IGS