

transgenic plants responded equally well to dehydration by 10% PEG-treatment. After dehydration by PEG-treatment, transgenic plants stayed in much less withered state than nontransformants. Subsequent rehydration fully restored the turgor and revived the transgenic plants, but not the nontransformants. Water potential of leaves in all lines of transgenic plants was same or higher compared with nontransformants indicating no accumulation of solutes acting as an osmoprotectant. Quantification of trehalose in transgenic plants revealed no significant accumulation of trehalose to be effective as osmoprotectant (less than mg trehalose per g fresh wt). Decrease in water potential by dehydration through PEG-treatment was in parallel phase in both nontransformants and transgenic plants implying that trehalose confers resistance to dehydration, not through the maintenance of osmotic potential in the leaves. These results suggest that enhanced resistance to water stress in transgenic plants through trehalose production is not through its action as an osmoprotectant, but elsewhere. Furthermore, our preliminary results indicated that trehalose-producing plants exhibited enhanced tolerance against high salt or chilling. Trehalose production may activate a common signalling pathway to cope better against various abiotic stresses involving dehydration.

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Isolation and Purification of Pneumococcal Surface Protein A (PspA) of *Streptococcus pneumoniae*A43 Isolated in Korea

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As a basic study for the rapid detection and identification of pneumococcal disease

and preventive vaccine development, this study researched on the isolation, purification and characteristics of PspA protein. *Streptococcus pneumoniae* A43 was chosen as selected strains through the former study of serotype, genotype, and antimicrobial resistance pattern. PspA protein was isolated and purified by using the binding characteristics to human lactoferrin in *Streptococcus pneumoniae* A43. Also, when PspA protein was isolated after *Streptococcus pneumoniae* A43 strain had been cultivated in the general media, there were a lot of problems in the isolation process and in the acquired rate. So in this study, PspA was isolated and purified after *Streptococcus pneumoniae* A43 strain had been cultivated in the CDM-ET media, and purified through affinity column. This experiment, it was identified that pure isolation and purification of PspA protein could be acquired simply with high rate. In order to confirm the immunity of PspA protein purely isolated and purified from *Streptococcus pneumoniae* A43 strain, clinical test was done with mice. According to this test, it was observed that the isolated and purified PspA protein had immunity and protective force.

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Cloning and the Nucleotide Sequence of PspA Gene from *Streptococcus pneumoniae*A43 in Korea

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In order to analyze the characteristics of PspA (pneumococcal surface protein A) protein in the domestic pathogenic *Streptococcus pneumoniae*, *S. pneumoniae* A43 showing immunity and protective force among the pathogenic strains collected was chosen in former study. So, the nucleotide sequences of PspA gene in *S. pneumoniae* A43

was analyzed. As a result ORF (open reading frame) was 1,824 nucleotides, it encodes a 608 amino acid that was confirmed the formation of protein, molecular weight of 66 kDa. Compared with the nucleotide sequences of PspA gene of *S. pneumoniae* Rx1 (type 2) and *S. pneumoniae* A43 (type 19F) was confirmed highly variable region except the conserved region. These results demonstrate that PspA of *Streptococcus pneumoniae* A43 (type 19F) has antigenic variability from that of streptococcus pneumoniae Rx1 strain (type 2).

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**Isolation, Purification and
Identification of New Antibiotics
Produced by *Streptomyces* 192**

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This study has been tried to develop new antibiotics from microbial sources. S192 strains, isolated from a soil collected in USA, was found to produce antibiotics active against bacteria, algae and fungi in the process of antibiotics screening. The active ingredients were subjected to the measurement of molecular weights, ^1H , ^{13}C , ^1H - ^1H COSY, HMBC NMR spectra, and it was confirmed that the new antibiotics is actinomycin family according to the NMR data, but the structure is difference between molecular weight by Mass analysis. The results of reference on the basis of the obtained molecular weight by mass analysis was different the known actinomycin and so, the new antibiotics have given a name to actinomycin C₃.

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**Genetic and Phenotypic Diversity
of *Streptococcus pyogenes* Isolated**

from Korea

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A total of 152 strains of *Streptococcus pyogenes* were isolated from patients with pharyngitis, scarlet fever, skin infection, and invasive streptococcal infections in Seoul, Korea from January 1988 to December 1999. All the isolates were epidemiologically characterized to decide phenotypes by T protein serotype and serum opacity factor (OF) detection. To analyze the genetic diversity, prevalence of T serotype strains were attempted to the *emm* gene type (M protein type; PCR-ELISA) and the pulsed-field gel electrophoresis (PFGE). T protein serotype showed 17 kinds in distribution including T12 and T4. Among the total isolates, T type 12 was the most common (40.1% of study strains), followed by T types 4 (19.1%) and 1 (7.9%). When T serotype of *S. pyogenes* isolates were analyzed by *emm* gene type distribution, of the 61 strains of T12 type, 47 strains (77.0%) belonged to the *emm* type 12 (M12) and all of these isolates were OF negative. Of 24 strains of T4 type, 25 strains (86.2%) belonged to the *emm* gene type 4 (M4) and all of these isolates revealed that OF detection were negative. PFGE patterns of genomic DNA for *emm* gene type (*emm12*, *emm4* and *emm1*) showed distinctive differences. These results suggest that genotypic analysis showed more diversity than those of the phenotypes. The used phenotype and genotype analysis were discriminative and appropriate for epidemiological marker of *S. pyogenes*.

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**The Changes of Phosphate
Metabolism and Biosynthesis of
Organic Compounds and
Accumulation Capacity of Metal**