analysis at 0.1 μM GA3 was significantly higher than that at control, indicating GA3 had a effect on both subunits. The stimulation effects of the activation of rubisco by GA3 seem to be caused by the expression of rubisco genes at the transcriptional level. Under the assumption that effects of GA3 on rubisco may be related to rubisco activase, in addition to, its activity and content were determined. The rubisco activase activity at 0.1 μM GA3 was more increased than the control. A similar change pattern was also observed in content of rubisco activase. The intensity of two 46 and 42 kD polypeptide bands at GA3 was higher than that of corresponding bands at control. These results suggest that the change in the levels of rubisco activase leads to a subsequent alteration of rubisco levels.

E215

Structure and Expression of a CTP: Phosphocholine Cytidylyltransferase Gene from *Arabidopsis thaliana*

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A genomic clone which includes the CTP:phosphocholine cytidylyltransferase (CCT) open reading frame and its 5'- and 3'-flanking non-coding regions has been isolated from Arabidopsis thaliana and sequenced. The CCT gene is approximately 3.0 kb in length and contains 8 exons interrupted by 7 introns, which range from 74 to 626 nucleotides. All nucleotide sequences for the intron 3' splice sites are consistent with the consensus AG sequence of plant pre-mRNA processing, while the major GT consensus sequence for the 5' splice site is conserved in 5 of 7 introns. Introns 5 and 6 have the minor GC consensus sequence instead. In 5'-flanking region there are two sequences related to a cold-responsive element found in the cold-inducible promoter of the *A. thaliana* cor15a gene, plus one gibberellin-response element. The results from reverse transcriptase-PCR indicate that expression of *A. thaliana* CCT was regulated by temperature. The expression level of CCT increased after a 30-min treatment at 5℃. When the plants were returned to 22℃, the expression of CCT also decreased to the original level.

E216

Cloning and Expression of a cDNA Encoding Aminoalcoholphosphotransferase from *Pimpinella brachycarpa*

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Aminoalcoholphosphotransferase catalyzes the synthesis of phosphatidylcholine and phosphatidylethanolamine from diacylglycerol plus CDP-choline or CDP-ethanolamine as the phosphobase donor. A cDNA library was screened to isolate a clone for use in study of the structure and expression pattern, of this enzyme from *Pimpinella brachycarpa*. The *P. brachycarpa* aminoalcoholphosphotransferase cDNA contains an open reading frame of 1,170 bp coding for a protein of 389 amino acids. The deduced amino acid sequence shares over 90% similarity with other aminoalcoholphosphotransferase sequences. Hydropathy profile analysis suggestes that the secondary structure of *P. brachycarpa* aminoalcoholphosphotransferase is very similar to that of the soybean and Chinese cabbage enzymes, having an overall hydrophobicity and the same number of predicted transmembrane helices. The catalytic domain contains the CDP-alcohol

phosphotransferase motif with two aspartate residues. Reverse transcriptase-PCR analysis indicated that the expression of *P. brachycarpa* AAPT was regulated by temperature.

E217

*Synechocystis*sp. PCC 6803 Mutants Culture Collection (SMCC)

박연일[1], 조미선[1,2], 유용철[2], 이진숙[2], 문윤정[2], 정영호[2], 허윤강[1], 임용표[1], 박영목[2]
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광합성박테리아 남세균돌연변이주은행(SMCC)은 최근 한국과학재단의 지원아래 설립되었다. 본 은행에서는 남세균이 가지고 있는 모든 유전자의 돌연변이를 유도하여 다양한 돌연변이주를 생산하고, 동정 및 장기 보존을 수행하며, 특히 이를 연구, 교육, 산업의 목적으로 이용하려는 국내의 여러 기관에 분양함을 목적으로 한다. 식물생명공학 분야에서 기능성 유전체 연구의 가장 좋은 재료의 하나로 이용되고 있는 광합성 박테리아, *Synechocystis* sp. PCC 6803 (Syn6803)은 고등식물과 유사한 광합성, 광독립타가영양, 높은 형질전환 능력을 가지며, 다양한 돌연변이 유도가 가능하고 이미 모든 유전자 염기서열이 공개되어 있는 장점을 가지고 있다. 기능성 유전자 탐색을 가장 효율적으로 할 수 있는 random transposon mutagenesis 기법을 통해 약 4,500종의 Tn mutant를 확보하여 분석하고 있고, Syn6803의 모든 유전자의 돌연변이를 유도하기 위해 약 12,000 (3,570 kbp/genome x 3/kbp)종의 돌연변이를 생산할 계획이다. 본 은행에서는 이렇게 생산한 돌연변이주들을 식물 생명공학분야 뿐만이 아니라 식물 기초과학 연구자들에게도 좋은 재료를 제공하여 식물자원의 확보, 청정환경의 유지 및 신의약 개발등과 같은 많은 분야의 연구에 자료를 제공하고자 한다.

E218

Molecular Cloning and Characterization of Nonsymbiotic Hemoglobin cDNA from Small Radish (*Raphanus sativus* L. var. *sativus*)

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Plants not only make oxygen during photosynthesis, but also use it for respiration through the electron transfer chain in mitochondria. In higher plants two families of hemoglobins are distinguished; the symbiotic and nonsymbiotic hemoglobin. Symbiotic hemoglobins such as leghemoglobins are found in the nodules where they transport oxygen to the nitrogen-fixing endosymbiotic bacteria. But the function of nonsymbiotic hemoglobins in non-host plants tissues has not been established. To study the function of nonsymbiotic hemoglobins, we have isolated nonsymbiotic hemoglobin cDNA clone (*RsHb*) from the cDNA library of Small Radish (*Raphanus sativus* L. var. *sativus*). Analysis of nucleotide and amino acid sequences and result of genimic hybridization will be presented. Also expression levels of this gene in seedlings treated with 1% sucrose, chilling (4℃), nitrate, flooding, dehydration, heat shock and wounding will be presented.

E219

The Role of Cytosolic Ascorbate Peroxidase During Germination and under Oxidative Stress in Hot Pepper.

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Ascorbate peroxidase (APX) is the enzyme that catalyze the removal of potentially harmful hydrogen peroxide in higher plants, algae and some cyanobacteria. It is localized in chloroplasts, microbodies, mitochondria and cytosol. The increases of