을 초래하는 환경조건에 처하게 되는 경우가 많다. 폴리아민은 모든 식물체에 존재하는 다가양이온으로서 세포분열과 세포 생장을 촉진하는 물질로 알려져 있다. 폴리아민 생합성의 rate limiting step에 관여하는 *S*-adenosylmethionine decarboxylase (SAMDC) 유전자를 sense 방향으로 도입한 식물체를 제조하였다. 또한 SAM과 경쟁적으로 작용하면서 에틸렌 생합성에 관여하는 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase) 및 ACC oxidase의 유전자를 antisense 방향으로 담배에 형질전환시킨 식물체를 제조하였다. 이들 T_1 세대의 식물체 잎에 fungal pathogen인 *Phytophthora parasitica* var.*nicotianae*를 감염시켰을 때 야생형 식물체와 positive control 식물체는 줄기가 검은색으로 변하면서 7 일후 부터 서서히 죽어가면서 10 일째에는 거의 죽었지만 폴리아민 생합성량이 비교적 크게 증가한 SAMDC 과다발현 식물체, ACC synthase 발현저해 식물체와 ACC oxidase 발현저해 식물체들은 10 일이 지나더라도 아주 건강한 상태를 유지하였다. 또한 bacterial pathogen인 *Pseudonomas syringae* pv.*tabaci* 를 감염시킨 후 5 일째 결과를 보면 야생형 식물체는 박테리아 생장이 1.2 배 증가함에 비해 SAMDC 과다발현 식물체에서는 박테리아 생장이 크게 저해되어 박테리아의 colony forming unit (CFU)가 1/16로 줄어들었다. 따라서 생물적 스트레스에 상당한 저항성을 갖고 있는 형질전환 식물체들의 스트레스에 의한 손상이 폴리아민 특히 spermidine에 의해 크게 완화된 것으로 생각된다.

E213

Differential Gene Expressions during Early Development Stages of Pear (*Pyrus pyrifolia* Nitaka) Leaf Necrosis Disease

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Plants react to environmental changes by altering their gene expression to meet the imposed conditions. Most genes involved in plant defense mechanism against invading pathogens are expressed in response to necrosis. To elucidate plausible causes of Pear leaf necrotic disease, total soluble proteins from wild and diseased plants were isolated. The protein patterns were resolved by one and two dimensional gel electrophoresis. SDS-PAGE of crude extracts of wild and diseased leaves of pear revealed differences in several protein patterns. Synthesis of new proteins was observed, while other proteins were not found on the gel in response to necrosis. Analysis by two-dimensional electrophoresis detected 6 distinct spots (pH 5.5-6.0, pH 6.7-7.0) in infected leaves. These suggest that distinct proteins could be originated from the virus. The proteins are being characterized to figure out their amino acid compositions. Based upon the amino acid sequences, DNA sequences of the gene will be deduced and DNA probes will be synthesized to clone the gene responsible for the disease.

E214

Activation of Rubisco by GA3 in Soybean

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Our experiments were studied the effect of application of exogenous GA3 upon rubisco activation in soybean leaves. Rubisco activity at 0.1 μM GA3 was significantly greater than that at no treatment. Rubisco content showed patterns of change similar to rubisco activity. These data suggest that rubisco activity was associated with an amount of rubisco protein, and that the activation of rubisco is promoted by GA3. The degree of intensity of 50 and 14.5 kD polypeptides identified as the large and small subunit of rubisco by SDS-PAGE

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