By using a partial clone as a probe, we isolated and sequenced a corresponding full-length *ci* clone. Northern analysis of the CI7 transcript in response to low temperature, drought, exogenous abscisic acid (ABA) and high-salt treatments revealed that the transcript levels were induced by most treatments tested in tubers as well as in leaves. Whereas accumulation of CI7 transcripts during cold storage occurred within a day, CI7 transcripts in response to abiotic stresses and ABA were less expressed when compared to those of other stresses on transcript levels. The expressed pattern of CI7 was examined by reverse transcriptase-polymerase chain reaction (RT-PCR).

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배추로 도입된 RAG25 유전자의 ectopic expression에 따른 표현형의 변화

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배추의 자엽절편체에 개화시기 조절유전자인 RAG25 유전자를 도입하여 이러한 유전자의 발현을 확인하기 위해 reverse transcription(RT)-PCR을 수행하였다. NPTII 유전자와 RAG25 유전자의 primer를 이용한 PCR결과 각각 0.7kb와 0.6kb에서 band를 확인하였으며 floral bud를 이용하여 in situ hybridization을 실시한 결과 자방에서의 두드러진 발현을 관찰하였다. RAG25 유전자의 발현이 확인된 형질전환체 중에서 이른 개화를 보이는 개체의 표현형을 조사하였으며 크게 mild type과 severe type의 두 유형으로 분류할 수 있었다. Mild type의 경우 wild type과 거의 유사한 외관을 가지고 있었으나 정단우성과 암술크기의 감소가 나타났다. Severe type의 경우 wild type과 다른 외관을 보이며 잎의 크기가 감소하고 정단우성의 감소가 나타났으며 잎모양의 변화와 왜성형질이 관찰되었다. 이러한 severe type의 경우 floral bud가 형성되었으나 더 이상 발달되지 않았다.

D 205

The AGAMOUS-LIKE 20 MADS domain protein integrates floral inductive pathways in *Arabidopsis*

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The very late-flowering behavior of *Arabidopsis* winter-annual ecotypes is conferred mainly by two genes, *FRIGIDA* and *FLOWERING LOCUS C*. A MADS-domain gene, *AGAMOUS-LIKE 20* (*AGL20*), was identified as a dominant *FRI* suppressor in activation tagging mutagenesis. Overexpression of *AGL20* suppresses not only the late flowering of plants that have functional *FRI* and *FLC* alleles but also the delayed phase transitions during the vegetative stages of plant development. Interestingly, *AGL20* expression is positively regulated not only by the redundant vernalization and autonomous pathways of flowering but also by the photoperiod pathway. Our results indicate that *AGL20* is an important integrator of three pathways controlling flowering in *Arabidopsis*.

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Effects of Auxin on the Timing of Determination for Root Formation from Internodal Explants of Cassava

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The timing for the determination in root

primordia formation from nodal and internodal explants of cassava (cv. MCol 22) was justified. Nodal explants about 10 mm with an axillary bud developed adventitious roots in one step on MS basal medium containing 2% sucrose for 8 days of culture. But internodal segments without an axillary bud did not develop the adventitious roots on the same medium. However, most internodal segments excised from nodal explants after culture of 72-96 hours on MS basal medium developed adventitious roots. The segments rooted at 90% after culture on medium with 0.5 mg/L IBA for 132 hours, on medium with 1 mg/L IBA for 60 hours, and on medium with 2 mg/L IBA for 36 hours respectively. Thus the period of culture on IBA medium and IBA concentration affected the rooting rate. Anatomically root primordia were not formed in internodal segments cultured on medium with 2 mg/L IBA for 36 hours, but the primordia were formed when cultured on the medium longer than 72 hours. Therefore, it is suggested that the determination for root formation occurred before the differentiation of root primordia on medium with IBA, and root inducing factors from medium were absorbed and accumulated during the period of determination for root primordium differentiation in internodal segment of cassava.

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Cloning of Cytosolic Ascorbate Peroxidase Gene in Embryogenic Callus of Pimpinella brachycarpa

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Ascorbate peroxidase is an important enzyme that detoxify hydrogen peroxide within the cytosol and chloroplasts of the plant cells. A full length cDNA clone(993 bp) encoding cytosolic ascrobate peroxidase from Pimpinella brachycarpa was isolated and its nucleotide sequence determined. The nucleotide sequences of Pbapx were highly homologous to those of apx from Nicotiana tabacum, Cucumic sativus, and Pisum sativum. Pbapx and apx from Nicotiana tabacum, apx from Cucumis sativus and apx from Pisum sativum are 80%, 78% and 77% identical in highly conserved region. The Pbapx contained an open reading frame encoding mature protein of 250 amino acids with calculated molecular mass of 27.8 kDa. According to the k-NN of PSORT program, Pbapx seemed to be located in cytosol. The Pbapx gene was expressed in all tested organs of Pimpinella brachycarpa; mRNA levels were low in petioles and high in embryogenic calli and roots.

D 301

A LAMMER Kinase Homologue of *Schizosaccharomyces pombe* Regulates Expression of Genes for Catalase and Glutathione Peroxidase

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Previously we have identified the *Schizosaccharomyces pombe lkh1+* gene encodes a dual-specificity kinase of LAMMER family having both serine/threonine kinase and tyrosine kinase activity. And also showed that the *lkh1* null mutant is viable but shows increased susceptibility towards a reactive oxygen generating compound, hydrogen peroxide. To investigate possible involvement of *lkh1* in expression of genes for defence mechanism against oxidative stress, northern analyses was performed.