embryogenesis, 2) callus-derived somatic embryogenesis, 3) direct adventitious shoot formation, 4) epicotyl-like shoot formation. Each pattern of plant regeneration has advantages and disadvantages on the yield of plant production, the rate of plant coversion, genetic transformation and mutation breeding. Therefore we discuss what is the most efficient way of plant regeneration on the clonal propagation and genetic trasformation in *P. ginseng*.

(W-II-3) :

In vitro PROPAGATION OF *Pinus densiflora* AND *Larix leptolepis* THROUGH SOMATIC EMBRYOGENESIS

Yong-Wook KIM
Forest Genetic Research Institute

In vitro propagation methods have numerous advantages for tree breeding and reforestation programs. Among the methods, somatic embryogenesis seems to be the most promising tool to achieve the purposes, particularly with conifer trees. Somatic embryogenesis was induced from the female gametophytes with immature zygotic embryos of *P. densiflora* (Japanese red pine) and the immature zygotic embryos of *L. leptolepis* (Japanese larch). The induction of embryogenic tissues in both species was strongly affected by the collection dates and the developmental stages of zygotic embryos. In *P. densiflora*, somatic embryos were produced when the embryogenic tissues were treated with 100 μM abscisic acid (ABA) and 1.0% gellan gum for 12 weeks. The germinating plantlets were also recovered from the somatic embryos. We have also succeeded in obtaining plantlets through somatic embryogenesis in *L. leptolepis*. The somatic embryos were obtained by culturing embryogenic tissues on the medium containing 4.1 μM ABA and 0.4% gellan gum for 3 weeks. We recovered germinating plantlets from the somatic embryos, and subsequently produced the potted plants.

(W-III-1) :

ANALYSIS OF THE TRANSCRIPTION OF *Arabidopsis* LEAF BY SAGE METHOD

Dong-Hee LEE
Department of Biological Science, Ewha Womans University, Seoul, 120-750, Korea

The characteristics of an organism or cell are determined by the genes expressed within it. A method called serial analysis of gene expression (SAGE) allows the quantitative and simultaneous analysis of a large number of transcripts. Short diagnostic sequence tags can be isolated, concatenated,

and cloned. Sequencing of many tags can reveal a gene expression pattern characteristic of function of the cell. New transcripts corresponding to novel tags can be identified. SAGE should provide a broadly applicable means for the quantitative cataloging and comparison of expressed genes in a variety of normal, developmental, and altered states.

We have utilized SAGE technology to analyze the set of genes expressed from the Arabidopsis genome, herein called the transcriptome. Messenger RNAs of OGA-treated leaf were prepared and converted into cDNA. After cDNA cut and linker ligation, ditags production, PCR amplification, and construction of ditag concatemers, cDNA tag library was constructed. Many tag sequences were analyzeded using FASTA program. Some known genes and ESTs including hsp90A and ACC oxidase homolog, which are known to be related to responses against various stresses, were obtained, and also unknown new ESTs were obtained.

(W-III-2) :

CLONING OF GENES INVOLVED IN TUBERIZATION IN POTATO BY DIFFERENTIAL DISPLAY REVERSE TRANSCRIPTION (DDRT)

Jun-Gyo IN

Dept. of Agrobiology, College of Agriculture, Chungnam National University, Yuseong, 305-764, Taejon, Korea

The differential display was employed for cloning of novel tuber specific expression genes or tuberization related genes in potato plant (*Solanum tuberosum* L.). The differential screening of mRNA expression via differential display has been described for detection and isolation of differentially expressed genes based on polymerase chain reaction (PCR) amplification of cDNA, in absence of the construction of cDNA libraries. The essence of differential display method is to use an anchored oligo-dT primer for reverse transcription which anneals to the beginning of a subpopulation of the poly(A) tails of mRNAs. The advantages of differential display as compared to alternative methods for differential screening include the ability to compare simultaneously numerous samples for both induction and repression of specific gene expression. In addition, differential display is likely to permit identification of rare transcripts via the PCR component of this technique.

In vitro cultured potato (*Solanum tuberosum* L. cv. Irish Cobbler) was used for experiments. Many genes expressed during tuberization in potato plant were isolated by using differential display. Lots of them were storage proteins such as patatins (30-40% in soluble proteins) or proteinase inhibitors (10-15% in soluble proteins). One of these genes was showed organ specific expression. These novel genes are expressed only storage organs; fruit including ovary after anthesis, tuber from stolon. In differential display analysis, it may be no wonder that many storage protein genes were specifically amplified at tuber, because theirs are accumulated in tuber during tuberization of potato. For cloning of the key gene responsible for tuberization in potato plant, it may be needed to establish more critical conditions than performed in this study.