

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 conversion, genetic transformation and mutation breeding. Therefore we discuss what is the most efficient way of plant regeneration on the clonal propagation and genetic transformation in *P. ginseng*.

(W-II-3) :

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

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*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  $\mu$ M 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  $\mu$ M 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**

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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,