

F804 Isolation and Molecular Characterization of the Osmotin Gene in *Petunia Hybrida*

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A petunia(*Petunia hybrida*) cDNA was isolated from the cDNA library produced from mRNA extracted from the cultured petal protoplasts of petunia. This clone contains 741bp open reading frame encoding for a 26kD polypeptide of 246 amino acid residues; the first 21 amino acids correspond to the sequence characteristic of a signal peptide. The predicted amino acid sequence shows homology with osmotin (82%) and osmotin-like protein(OLP; 89%) from tobacco. Thus, we designated this cDNA clone as PhOSM(*Petunia hybrida* osmotin). The accumulation of PhOSM mRNA was high in the root. The low levels of PhOSM mRNA was detected in the flower and leaf. Especially in the pistil, accumulation of PhOSM mRNA was increased after anthesis. Accumulation of PhOSM was also induced by abiotic stimuli, such as NaCl, abscisic acid(ABA), and low temperature in young seedlings. These results suggest that osmotin-like proteins may play important roles in normal development and plant defense against environmental stresses.

F805 Genetic Variation and Population Structure of *Pinus densiflora*

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Pinus densiflora is a perannual coniferous species to Asia. The level of genetic diversity of this species was surveyed using starch gel electrophoresis at putative six enzyme loci from 17 natural populations in Korea. Results from nineteen loci indicated that genetic diversity was higher and population divergence was found between genetic identity statistics and geographic distance between populations. Although the range in genetic diversity statistics among populations was low, genetic drift and gene flow did not appear to play major roles in structuring genetic variation. I concluded that the level of genetic diversity maintained within *P. densiflora* populations, and the level of population divergence was influenced by its status as forest and mode of gene flow.