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Patterns of Allozyme Variation and Population Structure of *Alnus hirsuta* (Betulaceae) in Korea

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The genetic variation at 25 loci in trees from 15 distinct populations of *Alnus* in Korea was measured to estimate the amount and patterns of genetic diversity and population structure. The mean genetic diversity within populations was 0.166. Korean alder populations have slightly high levels of genetic diversity compared to those of two Canadian alder species. The genetic differentiation among populations accounted for 9% of the total variation. The rate of gene flow was estimated high ($Nm = 2.63$). Analysis of inbreeding coefficient, calculated for all polymorphic loci in each population, showed a substantial heterozygosity deficiency relative to Hardy-Weinberg expectations. The mean G_{st} value of *A. hirsuta* in Korea was 0.087. The low level of G_{st} in this species, reflecting little spatial genetic differentiation, may indicate extensive gene flow. A relationship between the mean heterozygosity and annual rainfall showed a positive relationship ($r^2 = 0.54$, $F = 4.67$).

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Isolation of Differentially Expressed Genes by cDNA-Amplified Fragment Length Polymorphism in cDNA Library from Different Stages of Fruit Development in Hot Pepper (*Capsicum annuum* L.)

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This study was conducted for the identification and characterization of differentially expressed genes in cDNA library from different stages of fruit development in hot pepper (*Capsicum annuum* L.). We cloned two cDNA fragments by cDNA-amplified fragment length polymorphism (cDNA-AFLP). One clone had 311 bp and it was detected in both young green and ripe-red stages of the fruit development in hot pepper. RNA gel blot analysis showed the same result. And amino acid sequence of this clone was similar to cytochrome p450 that was the characteristic of heme binding motif (FXXGXXXCXG) at C-terminal region. The other clone showed the specific expression pattern in ripe-red stage of the fruit development in hot pepper, and the length of this clone was 340 bp. The cDNA sequence is highly similar to capsanthin/capsorubin synthase of hot pepper.