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Allozyme Diversity and Population Genetic Structure of *Eurya emarginata* (Theaceae) from Korea

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Levels of genetic diversity, population genetic structure, and gene flow in six Korean populations of *Eurya emarginata* were investigated using starch gel electrophoresis. *Eurya emarginata* is a dioecious, evergreen shrub native to southern China, southwestern Japan and the southern coastal parts of the Korean Peninsula. Although most Korean populations are relatively small and isolated, with respect to their habitats, they maintain high levels of genetic variation. Seventy-eight percent of the loci examined were polymorphic in at least one population. Overall, mean genetic diversity ($H_e = 0.296$) was higher than those for most species with very similar life history traits. Analysis of fixation indices showed an overall slight deficiency of heterozygotes relatively to Hardy-Weinberg expectations (54% were positive). Although significant differences in allele frequencies among populations were found for all loci ($P < 0.05$), slightly more than 92% of the total variation in the species is common to all populations ($G_{ST} = 0.079$). The correlation between genetic and geographic distance was substantially high ($r = 0.727$, $P < 0.01$), yet indirect estimates of the number of migrants per generation (N_m) (2.92, calculated from mean G_{ST} : 1.10, calculated from the mean frequency of six private alleles) indicate that gene movement among populations of *E. emarginata* is comparable with those for plants with similar life history traits. It is likely that factors such as dioecy, high fecundity, long generation time, occurrence in late-successional forests, and occasionally secondary seed dispersal by humans and pollen transfer by honey bees may contribute to maintain high levels of genetic diversity within populations and low levels of genetic divergence between adjacent populations of the species.

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Isolation and Characterization of Mutants and Genes Associated with *Arabidopsis* Leaf Senescence

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The plant leaf senescence is now believed to be genetically controlled events that constitute the final phase of leaf development. In order to understand the molecular genetic mechanism of leaf senescence, we have isolated mutants and genes associated with leaf senescence from *Arabidopsis thaliana*. By examining the changes of chlorophyll loss of leaves *in planta* or of detached leaves incubated in darkness, we were able to isolate 11 delayed-yellowing mutants and 3 early-yellowing mutants from chemically (EMS, DEB) or T-DNA mutagenized seed pools. In addition, we have isolated 6 senescence-associated genes by differential screening of cDNA libraries of naturally senescing and dark-induced senescing leaves. We are characterizing these mutants and genes biochemically, physiologically, and genetically.