

F209

Genetic Structure in Korean Populations of *Camellia japonica* (Theaceae)

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The genetic structure of the Korean populations of *Camellia japonica*, a broad-leaved evergreen tree native to Taiwan, the main Japanese islands of Kyushu, Shikoku, Honshu, and the southern and southwestern coast of the Korean peninsula, were examined. Starch-gel electrophoresis was conducted on leaves collected from 600 plants in 12 populations. Fifteen of 18 loci examined were polymorphic in at least one population, and the mean number of allele per locus was 2.54. In addition, expected heterozygosity (H_{ep} = 0.327) and total genetic diversity (H_T = 0.389) were similar with those for species with other eastern Asian endemic broad-leaved evergreen woody angiosperms such as the Korean populations of *Eurya japonica* (0.462 vs. 0.496), *E. emarginata* (0.296 vs. 0.412), and the Japanese populations of *C. japonica* (0.265 vs. 0.355). A relatively higher level of heterozygote deficiencies was observed in *C. japonica* (mean F_{ST} = 0.213) than those of *E. japonica* (0.101) and *E. emarginata* (0.075), indicating that the populations of *C. japonica* are more structured than those of euryas. The two euryas are dioecious, whereas flowers of *C. japonica* are perfect. Significant interpopulational differences in allele frequency were detected by low mean genetic identities for each pairwise combination of population (I = 0.884). In addition, the mean F_{ST} value of 0.141 indicates that gene flow among populations is moderate.

F210

Genetic Variation and Population Structure in Korean Endemic Species: III. *Hosta minor* (Liliaceae)

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Hosta minor, an insect-pollinated and rhizomatous herbaceous perennial, occurs in eastern and southern Korean Peninsula. Although *H. minor* is a Korean endemic species and most populations of the species are scattered, the species maintains considerably high levels of genetic variation within the species, with a moderate level of variation (14%) found among populations. Nineteen of the 29 putative loci resolved (66%) were polymorphic within the species, the mean number of alleles per locus was 2.10 across all populations and averaged 1.68 within populations. In addition, genetic diversity was a considerably higher (for species and population level, mean estimates of genetic diversity were 0.275 and 0.230, respectively) than the average for other long-lived herbaceous perennials. Indirect estimate of the number of migrants per generation (N_m = 1.03, calculated from mean G_{ST}) was moderate. Factors contributing to the high levels of genetic diversity found within populations of *H. minor* include population maintenance via sexual modes of reproduction, primarily outcrossing breeding system, long generation time, probable ancient polyploid origin of the species, and moderate levels of seed dispersal by wind. Human disturbance in South Korea such as road and apartment constructions appears to be the major threat to this genetically diverse species.