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Allozyme Variation and Population Structure of Korean Alder, *Alnus japonica* (Betulaceae)

Choi Joo Su*, Huh Hong Wook¹, and Huh Man Kyu¹ Biology of Department, Dongeui University and ¹Biology Education, Pusan University

The allozyme variation and population structure of *Alnus japonica* (Thunb.) Steudel in Korea were studied and compared with those of alder from Canada. Nineteen of the 25 loci studied (76.0%) showed detectable polymorphism. The mean genetic variation with populations was 0.207, which was higher than that for two Canadian alder species (*Alnus rugosa* (Du Roi) Spreng. and *A. crispa* (Ail.) Pursh). Analysis of fixation indices, calculated for all polymorphic loci in each population, showed a a substantial heterozygosity deficiency relative to Hardy-Weinberg expectations. The mean population differentiation value of *A. japonica* in Korea (Gst = 0.095) is similar to those of *A. rogosa* in Canada (Gst = 0.052). Those low values in two countries, reflecting little spatial genetic differentiation, may indicate extensive gene flow (via pollen and (or) and (or) recent colonization.

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Allozyme Variation and Population Structure of *Liriope muscari* in Korea

Huh Hong Wook, Huh Man Kyu*, and Moon Sung Gi¹ Biology Education, Pusan National University and ¹Biology of Department, Kyungsung University

Enzyme electrophoresis was used to estimate genetic diversity and population structure of *Liriope muscari* Bailey in Korea. The percent of polymorphic loci within the enzymes was 55.9%. Genetic diversity at the species level and at the population level was high (Hes = 0.178; Hep = 0.168, respectively), whereas the extent of the population divergence was relatively low (Gst = 0.064). F_{IS} , a measure of the deviation from random mating the within the 11 populations, was 0.311. An indirect estimate of the number of migrations per generation (Nm = 3.66) indicates that gene flow is high among Korean populations of the species. In addition, analysis of fixation indices received a substantial heterozygosity deficiency in some populations and at some loci. Mean genetic identity between populations was 0.988. It is highly probable that directional toward genetic uniformity in a relatively the homeogenous habitat is thoght to be operated among Korean populations of L. muscari.