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Genetic Variation and Population Structure of Endemic Crepidastrum lanceolatum (Compositae) in Korea

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Genetic diversity and population structure of six populations in Korea and four populations in Japan of isEnzyme were devermined using genetic variation at 23 allozyme loci. The percent of polymorphic loci within the enzymes was 43.5%. Genetic diversity at the species level and at the population level was Hes (0.178) Hep (0.168), respectively. The extent of the population divergence was relatively high (Gst = 0.101). F_{IS} was 0.433. An indirect estimate of the number of migrations per generation (Nm = 2.24) indicates that gene flow was moderate anomg ten populations of the species. Analysis of fixation indices received a substantial heterozygosity deficiency in populations level and allozymes level. C lanceolatum was consistent with the general concept that, for endemic species with narrow geopgaphic ranges, short-lived perennial herbaceous, and small population sizes are mainly assocoated with the low level of genetic variation.

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Spatial Autocorrelation among Korean Populations of Endemic Crepidastrum lanceolatum (Compositae)

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Crepidastrum lanceolatum is distributed in East Asia including Korea. The allelic frequencies of five different isozymes were applied to the spatial autocorrelation to microgeographic variation in this species. Spatial structuring of allele frequencies was found for five polymorphic loci within the two natural subpopulations C. lanceolatum, a perennial herb species in Korea. Allele selection has maintained spatial homogeneity for the loci studied, has been sufficient to prevent the random divergence of local demes. Moran's I was significant in 32 of 260 cases (12.3%). An indirect estimate of the number of migrations per generation (Nm = 2.24) indicates that gene flow was moderate among eight populations. C. lanceolatum is typically present in low frequency in rocky walls and has predominatly vegatative spread by formation of clona reproductive system (ramet).