

F820 Population Structure of the Clonal Herb, *Potentilla fragarioides* var. *sprengeliana* (Rosaceae) in Korea

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The genetic diversity and population structure of *Potentilla fragarioides* var. *sprengeliana* (Rosaceae) in Korea were determined using genetic variation at 22 allozyme loci. The percent of polymorphic loci within the enzymes was 59.1%. The two genetic diversity values at the species level ($H_{es} = 0.210$) and at population level ($H_{ep} = 0.199$) were higher than those of a similar life history herbaceous species. F_{IS} , a measure of the deviation from random mating the within the 19 populations, was 0.331. An indirect estimate of the number of migrations per generation ($Nm = 3.15$) indicates that gene flow is high among Korean populations of the species. Analysis of fixation indices, calculated for all polymorphic loci in each population, showed a substantial heterozygosity deficiency relative to Hardy-Weinberg expectations. It is highly probable that directional toward genetic uniformity in a relatively the homogeneous habitat is thought to be operated among Korean populations of *P. fragarioides* var. *sprengeliana*.

F821 Spatial Autocorrelation among Korean Populations of *Raphanus raphanstroides*

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We applied spatial autocorrelation to microgeographic variation in the wild radish, *Raphanus sativus* var. *hortensis* Baker *raphanstroides*. Counts of type of join (combination of genotypes at a single locus) for each allele separately, for each distance class of separation, were tested for significant deviation from random expectations by calculating a Standard Normal Deviate (SND) test statistics. There was genetic variability at each locus to be used for the autocorrelation analyses. Moran's I was significant in 48 of 96 cases (50%). Especially, the aggregation of an identical allele, called "patch", results in some loci including *Pgm-3*. Because fruits of wild radish disperse only short distance, hence gene flow occurs mainly through pollen movement. In addition, the results suggest that neighbor patches in which different alleles are predominant for 20 or 25 m apart on average.