

Genetic Structure of *Viola nagasawai* in Yangmingshan, Taiwan

Jenn-Che Wang*, Shong Huang*, and Tsan-Piao Lin**

*Department of Biology

National Taiwan Normal University

**Taiwan Forestry Research Institute

ABSTRACT

Genetic structure within and among four subpopulations of *Viola nagasawai* was investigated using isozyme gel electrophoresis techniques. Eleven loci were surveyed from eight enzyme systems. The mean expected heterozygosity (H_E) was 0.142 and ranged from 0.07 to 0.186. The mean observed heterozygosity (H_O) was 0.160 and ranged from 0.097 to 0.252. The mean number of alleles per locus (A) was 1.7. The percentage of polymorphic loci (P) was 36.4. F-statistics revealed that the inbreeding coefficient within populations (F_{IS}) was -0.276. This negative value suggested that the species preferred outcrossing. The level of genetic differentiation among populations (F_{ST}) was 0.132, which suggested a medium-grade of infraspecific genetic differentiation. Gene flow rate among subpopulations was greater than one ($Nm=1.64$), and indicated that genetic differentiation among subpopulations was not likely contributed by restricted gene flow. However, natural selection probably played important role and caused genetic differentiation of *V. nagasawai* subpopulations in the Yang-ming-shan area.

Key words: gene flow, genetic differentiation, isozyme electrophoresis, population genetic structure, *Viola*, *V. nagasawai*