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Genetic and clonal structure in Korean populations of *Calystegia japonica* (Convolvulaceae)

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Abstract. The genetic and genotypic diversity of Korean *Calystegia japonica* Choisy populations were investigated using starch gel electrophoresis. *Calystegia japonica* is a clonal plant species that inhabits fields and roadsides and reproduces vegetatively by rhizomes. Although populations of the species are small, isolated, and distributed in patches, the species maintains a moderate level of genetic diversity—60% of the loci examined were polymorphic and the mean genetic diversity within populations (He_P) was 0.099. The mean number of multilocus genotypes per population was 11.6, and the genotypic diversity index (D_G) was 0.74. Slightly more than 38% of the total genetic variation was found among populations (G_{ST} = 0.383). In addition, significant differences in allele frequency were detected among populations at all loci examined ($P < 0.001$), suggesting low gene flow among Korean populations. Indirect estimates of the number of migrants per generation (*Nm*) were 0.40 (calculated from G_{ST}) and 0.20 (calculated from the mean frequency of five private alleles). Widespread geographical distribution, isolated populations in patchy distribution, clonal reproduction with relatively high genotypic diversity, low gene flow among populations, fragmentation of a once continuous range, and genetic drift may have played roles in shaping the population genetic structure of the species.

Keywords: *Calystegia japonica*; Clonal diversity; Gene flow; Genetic diversity; Genetic drift; Population genetic structure.

Introduction

Electrophoretic techniques have increasingly been applied to the study of clonal plants, because they provide genetic markers for the recognition of individual plant genotypes (e.g. Pleasants and Wendel, 1989; Bayer, 1990; Aspinwall and Christian, 1992; Chung, 1994; Kim and Chung, 1995). This has made it possible to better understand the spatial distributions of clones and the genotypic diversity maintained within populations. According to a recent review of the study of clonal plants (Ellstrand and Roose, 1987), species with predominantly vegetative reproduction generally have lower levels of genetic diversity than do species that successfully produce progeny by sexual reproduction. More recently, however, contrasting results were encountered in the study of *Vallisneria americana* (Lokker et al., 1994) and *Filipendula rubra* (Aspinwall and Christian, 1992). Although these two species are capable of clonal growth and sexual reproduction, *V. americana* has high levels of genetic diversity within populations, but the genotypic diversity of *F. rubra* is quite low. This may be partially because species, even congeners, often differ in many other aspects of their biology and ecology (Chung et al., 1991). The relationship between genetic diversity and modes of reproduction is still unclear. Further study of predominantly asexual plant species is necessary.

Calystegia japonica Choisy, a herbaceous perennial vine, is widely distributed in China, Korea, and Japan (Kitamura et al., 1986). In Korea, the species usually grows on small mounds in paddy fields and along roadsides, rarely colonizing sites or waste places which have been recently disturbed (S. Kang and M. Chung, pers. obs.). Typical populations of *C. japonica* are small and distributed in patches. Pink flowers (5–6 cm in diameter) are axillary and solitary from several axils. Mature capsules have not been encountered during field trips. It appears that the species is a nearly obligate clonal plant that propagates predominantly by rhizome. The species is diploid ($2n$ = 22) (M. Chung, unpubl. data). In this paper we report levels and partitioning of allozyme diversity within and among populations, and the extent of cloning within populations of *Calystegia japonica*. The purposes of this study were **1**) to estimate how much total genetic diversity is maintained in the species, **2**) to describe how genetic variation is distributed within and among populations, **3**) to compare the level of genetic diversity in populations of *C. japonica* with that of plant species having similar life history traits, and **4**) to characterize the population genetic structure to determine whether patches of the species comprise single clones or a mixture of genets.

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Materials and Methods

Population Samples

Leaves were collected from eight populations of *C. japonica* in Korea (Figure 1). Population samples of 25 or 50 were employed. Population codes and sample sizes are given in Table 1. Because the species exhibits extensive clonal growth, samples were collected randomly at intervals of greater than 2 m within each patch or population to avoid biasing samples toward certain clones. Leaf samples were wrapped with a wet paper towel, placed in plastic bags, and stored on ice for transport to the laboratory. Samples were then stored at 4°C until protein extraction.

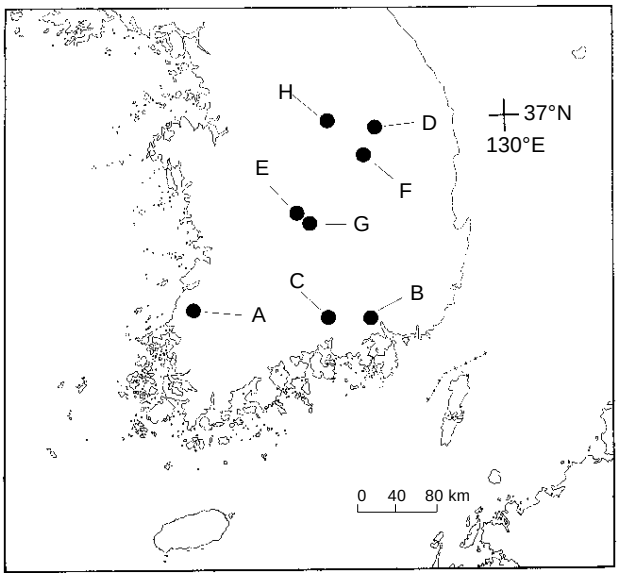

Figure 1. The locations of the eight Korean populations examined in this study (alphabetic codes as in Table 1).

Enzyme Extraction and Electrophoresis

Leaf samples were cut finely, and crushed with a mortar and pestle. A phosphate-polyvinylpyrrolidone extraction buffer (Mitton et al., 1979) was added to the leaf samples to facilitate crushing and to aid enzyme stabilization. The crushed extract was absorbed onto 4 × 6-mm wicks cut from Whatman 3MM chromatography paper, which were then stored at -70°C until needed for analysis. Electrophoresis was performed using 10.5% starch gel. Sixteen putative loci for *C. japonica* from seven enzyme systems were resolved using two systems of electrode and gel buffer. A Poulik buffer system, a modification (Haufler, 1985) of the Soltis et al. (1983) system 8, resolved phosphoglucomutase (PGM), leucine aminopeptidase (LAP), triosephosphate isomerase (TPI), and phosphoglucoisomerase (PGI). A morpholine citrate buffer system, a modification (Chung and Kang, 1994) of that of Clayton and Tretiak (1972), was used to resolve 6-phosphogluconate dehydrogenase (PGD), peroxidase (PER), and isocitrate dehydrogenase (IDH). All stain recipes were identical to those described by Soltis et al. (1983). Putative loci were designated sequentially, with the most anodally migrating isozyme designated 1', the next 2', etc. Likewise, alleles were designated sequentially with the most anodally migrating alleles designated a'. Although the genetic bases of the loci were not documented by controlled crosses, the isozymes expressed phenotypes that were consistent in subunit structure and genetic interpretation with most isozyme studies in plants, as documented by Weeden and Wendel (1989). *Lap-2* was expressed, but because of poor activity and/or resolution, it was not scored.

Data Analyses

A locus was considered polymorphic if two or more alleles were detected, regardless of their frequencies. Four standard genetic parameters were estimated using a com-

Table 1. Summary of allozyme variation and clonal diversity for 15 loci within eight populations of *Calystegia japonica*[a].

Pop[b]	N[c]	AL[d]	P	A	Ae	Ho (SE)	He (SE)	G	D_G	G/N	PG
A	25	80	26.7	1.33	1.16	0.104 (0.014)	0.089 (0.017)	9	0.78	0.36	0.36
B	50	50	40.0	1.47	1.28	0.206 (0.012)	0.158 (0.019)	26	0.95	0.52	0.18
C	50	70	33.3	1.33	1.15	0.148 (0.006)	0.085 (0.016)	5	0.40	0.10	0.76
D	50	850	40.0	1.47	1.24	0.160 (0.010)	0.122 (0.019)	15	0.84	0.30	0.30
E	50	750	26.7	1.33	1.15	0.096 (0.008)	0.078 (0.016)	12	0.80	0.24	0.34
F	50	920	20.0	1.27	1.17	0.120 (0.007)	0.079 (0.018)	7	0.73	0.14	0.46
G	25	650	26.7	1.27	1.15	0.139 (0.008)	0.081 (0.016)	4	0.47	0.16	0.72
H	25	820	40.0	1.40	1.14	0.088 (0.016)	0.097 (0.013)	15	0.93	0.60	0.24
Mean	40.6		31.7	1.36	1.18	0.133 (0.004)	0.099 (0.006)	11.6	0.74	0.30	0.42

[a]Abbreviations: **P**, percentage of polymorphic loci; **A**, mean number of alleles per locus; **Ae**, effective number of alleles per locus; **Ho**, observed heterozygosity; **He**, Hardy-Weinberg expected heterozygosity or genetic diversity; **G**, number of multilocus genotypes; $\mathbf{D_G}$, multilocus genotypic diversity indices; **G/N**, number of genotypes per population samples ("proportion of distinguishable genotypes" per population); **PG**, probability of the most common multilocus genotype.
[b]Alphabetic codes as in Figure 1.
[c]Sample size.
[d]Altitude (m).

puter program developed by M. D. Loveless and A. Schnabel—percent polymorphic loci (P), mean number of alleles per locus (A), effective number of alleles per locus (Ae), and gene diversity (He) (Chung and Chung, 1994; Hamrick et al., 1992). Subscripts refer to species (s) or population (p) level parameters.

Because *C. japonica* reproduces vegetatively, we assessed the amount of clonal diversity within and among populations. The first measure of clonal diversity we used was the probability that the next individual sample is a new multilocus genotype. This is simply G/N, where G is the number of distinct genotypes in a population and N is the number of individual samples ("proportion of distinguishable genotypes", Ellstrand and Roose, 1987). The second measure was the probability of getting the most common genotype by chance in each population (PG). The third measure of multilocus genotype diversity (D_G) was calculated as a modification (Pielou, 1969) of the Simpson index: $D_G = 1 - \{[ni(ni\text{-}1)]/[N(N\text{-}1)]\}$, where *ni* is the number of individuals of genotype *i* and N is the total number of individuals in the population. Finally, for comparisons of genotypic diversity among populations, numbers of "widespread genotypes" (genotype occurring in more than 75% of the populations) and "local genotypes" (genotypes occurring only one population) were counted (Ellstrand and Roose, 1987).

Observed heterozygosity was compared to Hardy-Weinberg expected values using Wright's (1922) fixation indices (*F*) or inbreeding coefficients. These indices were tested for deviation from zero by X^2-statistics following Li and Horvitz (1953).

Nei's (1973, 1977) gene diversity formulae (H_T, H_S, D_{ST}, and G_{ST}) were used to evaluate the distribution of genetic diversity within and among populations. In addition, an X^2-statistic was used to detect significant differences in allele frequency among populations for each locus (Workman and Niswander, 1970). Nei's (1972) genetic identity (I) was calculated for each pairwise combination of populations. A correlation between genetic distance and geographical distance was calculated using the PC-SAS program (SAS Institute Inc., 1989). In addition, we used NTSYS (Rohlf, 1988) to conduct a cluster analysis on genetic distances via the unweighted pairwise groups method using arithmetic average (UPGMA).

The genetic structure within and among populations was also evaluated using Wright's (1965) *F*-statistics: F_{IT}, F_{IS}, and F_{ST}. The F_{IT} and F_{IS} coefficients measure excesses of homozygotes or heterozygotes relative to the panmictic expectations within the entire sample and within populations, respectively. The F_{ST} coefficient estimates relative population differentiation. Deviation of F_{IT} and F_{IS} from zero were tested using X^2-statistics (Li and Horvitz, 1953). Two indirect estimates of gene flow were calculated. One estimate of *Nm* (the number of migrants per generation) was based on F_{ST} (Wright, 1951). The second estimate was based on the average frequency of private alleles (Slatkin, 1985; Barton and Slatkin, 1986).

Results

For *Calystegia japonica*, 9 of the 15 scoreable loci (P_S = 60%) were polymorphic in at least one population. *Tpi-1*, *Tpi-2*, *Pgi-1*, *Pgd-2*, *Idh-1*, and *Idh-2* were monomorphic in all eight populations. The mean number of alleles per locus was 2.13 for species (A_S), and the effective number of alleles for the species (Ae_S) was 1.82. At the population level, relatively low mean estimates of genetic variation were observed—P_P of 31.7%, A_P of 1.36, and Ae_P of 1.18. In addition, mean expected heterozygosity or genetic diversity within populations (He_P = 0.099) was lower than the overall values for the species (He_S = 0.178) (Table 1).

The number of multilocus genotypes in populations ranged from four to 26 (mean = 11.6). All populations comprised multiple genotypes. The proportion of resolved "distinguishable genotypes" (G/N) ranged from 0.10 to 0.60, with a mean of 0.30. The probability of getting the most common genotype by chance (PG) in each population ranged from 0.18 to 0.76, with a mean of 0.42. Genotype diversity indices (D_G) ranged from 0.40 to 0.95, with a mean of 0.74. The level of genotypic diversity among populations was considerably higher. Ninety-three multilocus genotypes were found among the 325 samples from the eight populations. All but three multilocus genotypes were "local genotypes" (90/93; slightly < 97%). Two genotypes in population D were shared with population E, and one genotype was shared between population G and H.

Analysis of fixation indices, calculated for all polymorphic loci in each population of *C. japonica*, showed an overall excess of heterozygotes, relative to Hardy-Weinberg expectations. Sixty-seven percent of fixation indices were negative (24/36), and 12 of those departed significantly from zero ($P < 0.05$). All but one of 12 positive fixation indices were also significantly different from zero ($P < 0.05$) (Table 2). In addition, Wright's *F*-coefficients showed that significant excesses of heterozygotes exist for five and three of the nine loci at the level of population and the sample as a whole, respectively (Table 3). The values of F_{IS} (Table 3) varied from -0.748 to 0.937, with a mean of -0.153. This range of values of the inbreeding coefficient was substantially greater than expected, suggesting that the unknown evolutionary forces have varied impact upon nine loci. It should be noted, however, that the species has an extensive rhizome and reproduces vegetatively, which violates basic assumptions of the Hardy-Weinberg Law. The Hardy-Weinberg model assumes that the reproduction is sexual. It is highly probable that the observed values of fixation indices are artifacts of clonal growth.

Significant differences in allele frequency among populations were found for all nine loci ($P < 0.001$ in each case). The G_{ST} values ranged from 0.058 for *Per-3* to 0.739 for *Pgd-1* (Table 3), and on average, about 62% of the total variation in the species is common to all populations. In addition, five private alleles were found in five popu-

Table 2. Fixation indices (*F*) for nine polymorphic loci in populations of *Calystegia japonica.*

Locus	Population							
	A	B	C	D	E	F	G	H
Pgm–1	–	0.3631**	0.0899ns	–	0.2369ns	–	–	–
Pgm–2	-0.6333***	-0.6780***	0.6598***	-0.8371***	-0.8165***	–	-0.9600***	-0.2895ns
Lap–1	–	–	–	–	–	-0.9800***	–	1.000***
Pgi–2	–	-0.2891*	-0.9800***	1.0000***	–	–	–	-0.0889ns
Pgd–1	–	1.0000***	–	1.0000***	–	–	1.0000***	–
Per–1	–	-0.9800***	-0.9800***	-0.0532ns	-0.0206ns	-0.0313ns	–	0.6525***
Per–2	-0.0331ns	-0.2222ns	–	-0.4863***	–	-0.1771ns	-0.8148***	-0.3429ns
Per–3	-0.0280ns	–	–	–	–	–	-0.0652ns	0.4674*
Idh–3	0.5116*	–	–	–	0.3631*	–	–	–

* = $P < 0.05$, ** = $P < 0.01$, *** = $P < 0.001$, and ns = not significant in chi-square tests of deviations of *F* from zero. Populations that were monomorphic for a particular locus are indicated with a dash.

Table 3. Nei's (1973, 1977) statistics of genetic diversity and the estimates of Wright's *F*-statistics for nine polymorphic loci in *Calystegia japonica.*

Locus	# Allele	H_T	H_S	G_{ST} [a]	F_{IS} [b]	F_{IT} [b]
Pgm-1	3	0.1434	0.1171	0.1836***	0.2643***	0.3994***
Pgm-2	3	0.4322	0.3429	0.1919***	-0.7305***	-0.3983***
Lap-1	3	0.1644	0.0976	0.4064***	-0.5763***	0.0644ns
Pgi-2	2	0.4924	0.1735	0.6477***	-0.5076***	0.4689***
Pgd-1	3	0.1881	0.0490	0.7393***	0.9371***	0.986***
Per-1	4	0.3011	0.2006	0.3336***	-0.7482***	-0.1650***
Per-2	4	0.4225	0.3328	0.2122**	-0.3498***	-0.0633ns
Per-3	2	0.0303	0.0286	0.0575***	0.1379*	0.1875***
Idh-3	2	0.4920	0.1616	0.6715***	0.2005***	0.7374***
Mean	2.89	0.2963	0.1678	0.3826	-0.1525	0.2460

[a]Am X^2 test for allele frequency heterogeneity between populations: ns = not significant; *** = $P < 0.001$.
[b]Asteriks indicate *F* values significantly different from zero: ns = not significant; * = $P < 0.01$; *** = $P < 0.001$.

lations: D (*Per-2*[c]), E (*Pgm-1*[b]), F (*Lap-1*[c]), G (*Pgd-1*[c]), and H (*Lap-1*[b]). The indirect estimate of gene flow, based on the mean G_{ST}, was low (*Nm* = 0.40), and was similar to the estimate based on private alleles (*Nm* = 0.20). Average genetic identity for all pairs of populations was 0.90 (SE = 0.007). The UPGMA dendrogram provided a few insights into the genetic structuring of the eight populations (Figure 2). In addition, the correlation between genetic distance and geographic distance was low ($r = 0.399$, df = 26, $P < 0.05$), and indicated that 84% of the variation in genetic distances was caused by unknown factors other than distance.

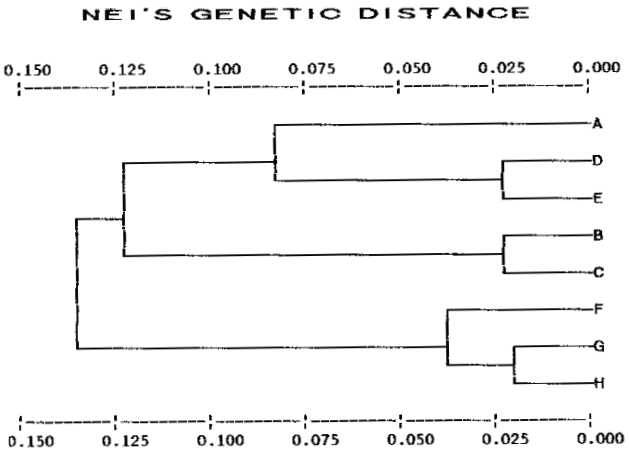

Figure 2. Phenogram from UPGMA cluster analysis, based on Nei's (1972) genetic distance between the eight populations of *Calystegia japonica*.

Discussion

The levels of genetic variation found within Korean populations of *C. japonica* were moderate in relation to the mean values of short-lived herbaceous perennials. According to a recent review of plant allozyme literature (Hamrick and Godt, 1989), short-lived herbaceous perennials at the species (*N*=152) and population (*N*=159) levels, have a mean polymorphic loci (P) of 41.3 and 28.0, mean number of alleles per locus (A) of 1.70 and 1.40, mean effective number of alleles per locus (Ae) of 1.15 and 1.12, and mean genetic diversity (He) of 0.116 and 0.096, respectively. For *C. japonica*, P_S is 60% and P_P is 31.7%, A_S is 2.13 and A_P is 1.36, Ae_S is 1.82 and Ae_P is 1.18, and He_S is 0.178 and He_P is 0.099. This level of genetic diversity is comparable with that of *Calystegia soldanella*, a herbaceous clonal

perennial that occurs widely on beach dunes in Europe and the Pacific region (Kim and Chung, 1995). Ellstrand and Roose (1987), in a review of studies of population genetic structure of primarily obligate clonal plant species, concluded that clonal plant species tend to have intermediate levels of genetic diversity. The results of the present study are consistent with the general conclusion of Ellstrand and Roose (1987) about the levels of genetic diversity.

The geographic range of a species is significantly correlated to the amount of genetic variation at the population and species levels (Hamrick and Godt, 1989). Usually, plant species with geographically widespread distributions tend to maintain higher levels of allozyme diversity than do plants with more restricted ranges (Karron et al., 1988). In addition, species with discrete populations in a patchy distribution have lower levels of variation within populations than do species with more continuously distributed populations (Chung and Kang, 1994). Although *C. japonica* has a wide geographic range in East Asia, populations in Korea have a patchy distribution. Vegetative reproduction and spread can also affect the genetic structure of populations (Murawski and Hamrick, 1990). Clonal reproduction can retard the loss of genetic diversity within populations because, in species with independent ramets, there is a reduced probability of genet death (Cook, 1983). The mechanism that maintains genetic variation in clonal plants, however, is still a matter of controversy (Eriksson, 1993). The combination of these factors may contribute to the maintenance of moderate levels of genetic variability in the species.

Population B had the highest values of D_G, G/N, and He_P (0.95, 0.52, and 0.158, respectively), but as expected, the lowest value of PG (0.18). Populations C and F had similar, and the lowest, "proportion of distinguishable genotypes" (G/N)—0.10 and 0.14, respectively, but population C had a considerably lower genotypic diversity index (D_G)—0.40, vs. 0.73 for population F. This is supported by the values of probability of the most common multilocus genotype (PG)—population C had a PG value of 0.76 while population F had a PG value of 0.46. This indicates that genotypes in population F are more evenly distributed than those in population C. The average genotypic diversity index for *C. japonica* is higher (D_G = 0.74) than the average (0.62) reported by Ellstrand and Roose (1987) in their review of primarily obligate clonal plant species. The mean "proportion of distinguishable genotypes" per population is also higher (0.30 vs. 0.17) for *C. japonica*. It has been known that the fruits of *C. japonica* are usually not fully matured (Kitamura et al., 1986). No fruit was encountered in the study areas during field trips, which suggests that the species propagates exclusively by a rhizome. If this is true, why was the genotypic diversity of *C. japonica* higher than mean values for primarily obligate clonal species? Genotypic diversity among populations was large. No "widespread genotypes" were observed. In addition, all but three multilocus genotypes were "local genotypes". These data suggest that the present populations might have been founded from sexually produced seed rather than asexually by the fragmentation and dispersal of preexisting clones. Because *C. japonica* has a relatively long, branched rhizome, and independent ramets can reduce the probability of genet death, Korean populations of the species consist of several genotypes brought about by sexual recombination, mutation, and other evolutionary forces acting for a long time. In addition, we can not rule out the possibility that sexual reproduction now occurs at a very low rate. Detailed breeding and demography studies of *C. japonica* are needed to confirm this speculation.

An overall excess of heterozygotes was observed in *C. japonica* (mean F_{IS} = -0.153, Table 3). The abundance of ramets of certain genets found in the populations may have been responsible for a potentially misleading "inbreeding-like effect" suggested by Lokker et al. (1994). If so, part of the fixation indices calculated here are probably artifacts of clonal growth. Similar results were observed in the populations of *Aechmea magdalenae*, a clone-forming tropical terrestrial bromeliad (Murawski and Hamrick, 1990).

The degree of population differentiation observed in *C. japonica* was higher than that in other plants with similar life-history characteristics (reviewed in Hamrick and Godt, 1989). Short-lived herbaceous perennials (G_{ST} = 0.233, N = 119), species with a widespread geographic range (G_{ST} = 0.213, N = 87), and species with sexual and asexual modes of reproduction (G_{ST} = 0.213, N = 54) have lower mean G_{ST} values than does *C. japonica* (G_{ST} = 0.383). This is supported by a low mean genetic identity for each pairwise combination of populations (mean I = 0.90). In addition, significant differences were found in allele frequencies among populations for all nine loci ($P < 0.001$). Because of their colonizing habit, populations of *C. japonica* may be founded by a few propagules, and generally have patchy distribution. Like *C. japonica*, species with discrete populations can be expected to show increased levels of genetic differentiation as gene flow decreases (Loveless and Hamrick, 1984). Overall, slightly less than 97% of the multilocus genotypes were unique to each population, and no "widespread genotypes" were observed. These factors may account for the rather-high observed G_{ST} value. The high G_{ST} value suggests that gene flow among populations is low. Indirect estimates of the number of migrants per generation (*Nm*) were 0.40 (calculated from G_{ST}) and 0.20 (calculated from the mean frequency of five private alleles). Similar results were observed in *Hosta clausa* (Liliaceae) (*Nm* = 0.48, recalculated from mean G_{ST}; Chung, 1994), a herbaceous perennial native to the central and northern Korean peninsula and northeastern China. This species reproduces vegetatively by rhizomes, and potentially by sexually produced seeds. In addition, populations of the species are small and isolated. For neutral genes, a *Nm* value of 1.0 is considered necessary to prevent divergence caused by genetic drift (Wright, 1931; Slatkin, 1987). The levels of gene flow calculated here are of insufficient magnitude to counterbalance genetic drift. It should be noted that there were differences in habitat altitude among populations exam-

ined (see Table 1). Since gene flow is low among populations, genetic differentiation may be the result of local selection. It appears that genetic drift and local selection are discriminating factors that affect the distribution of genetic variation among populations.

Although *C. japonica* maintains a moderate level of genetic diversity, the small, isolated populations that currently characterize the Korean populations of *C. japonica*, coupled with the recent increased destruction of natural habitats during the reconstruction of roads may result in further erosion of genetic diversity in the near future. The level of distribution of genetic variation among populations is of primary importance to the conservation of genetic diversity and the evolutionary potential of species (Hamrick and Godt, 1989). Based on the available data, such as relatively-high G_{ST} value, several populations of each group should be preserved, especially those with high variation, such as populations B, D, and H. These populations could be used as a source of genetic diversity for the restoration of genetically poor populations.

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韓國的打碗花(旋花科)族群遺傳結構研究

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本文報導以同功酵凝膠電泳方法研究生長在韓國的打碗花之族群遺傳及歧異度。打碗花是旋花科植物，靠根莖行無性繁殖，生長在路邊或田野間。雖然本種的各族群都不大，分布也很零散，但種以內仍保有中度的遺傳歧異；所檢視的基因座中，多型性的佔60%，族群內歧異度 (He_p) 爲 0.099。另外，族群中具有多型性基因座的個體平均爲每個族群 11.6個。基因型的歧異指標 (D_o) 爲 0.74。然而，從族群分化的情形來看，族群間的分化程度高達 38% (G_{ST}=0.383)，同時，全部檢測過的基因座上對偶基因頻率都有顯著分化 (P<0.001)，這應是長在韓國的這種植物族群間的基因流傳不順暢所致。事實上，間接計算基因遺傳的數量是 0.40 (G_{ST} 換算值) 或 0.20 (專有基因換算值)。總之，廣泛的分布，零星的隔離族群，無性繁殖的特性，高度遺傳分化，低度基因流傳，連續性棲地轉變成今日的零碎化棲地，以及基因漂變等因子均可能影響到本種的遺傳結構。

關鍵詞：*Calystegia japonica*；無性繁殖歧異度；基因流傳；基因漂變；遺傳歧異度；族群遺傳結構。