GENETIC DIVERSITY AND POPULATION STRUCTURE OF SILK TREE (*ALBIZIA JULIBRISSIN* DURAZZ) IN KOREA

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ABSTRACT

The temporal genetic diversity and population structure of two groups of natural populations (ca. 30–45 yr.) and artificial populations (10–15 yr.) of *Albizia julibrissin* Durazz in Korea were determined using enzyme electrophoresis. Significant differences in four genetic parameters except genetic diversity were little between artificial populations and natural populations. Eighteen of the 25 loci (72.0%) showed detectable polymorphism. Genetic diversity (0.224) was higher than average values for species with similar life history traits. Wide geographic ranges, perennial woody nature and the outcrossing reproduction are associated with the high level of genetic variation. Analysis of fixation indices, calculated for all polymorphic loci in each population, showed a substantial deficiency of heterozygotes relative to Hardy-Weinberg expectations. Its deficiency is expected that all of the inbreeding detected is due to consanguineous and selfing mating. The average G_{ST} for polymorphic loci was 0.065, indicating that most (93.5%) of the genetic diversity occurred within populations. The indirect estimate of gene flow based on mean G_{ST} was moderate (Nm = 3.60). Given limited population differentiation are expected to diverge genetically due to transplants, the random lose of alleles due to small population size by genetic drift.

Key words: genetic diversity, population structure, artificial populations, natural populations, *Albizia julibrissin*.

INTRODUCTION

Recently, collection has found on allozyme studies of woody angiosperms that are comparable to conifers with respect to their ecological and/or life history trait (SCHNABEL & HAMRICK 1990, SHERMAN-BROYLES *et al.* 1992). These studies have that such angiosperms have high levels of genetic variation and low proportion of their genetic diversity among populations. Generalizations derived from the allozyme literature provide a basis on how to build sound programs for the conservation of genetic diversity of rare and endangered species (HAMRICK *et al.* 1991). In addition, allozyme diversity can be used as a yardstick to measure the effectiveness of *in situ* and *ex situ* conservation programs (HAMRICK *et al.* 1991). Despite the importance of knowledge on genetic variation data for providing information for conservation purposes, detailed studies of the levels and distribution of genetic variation have not been performed on most native taxa in China and Korea, particularly woody plants (HUH *et al.* 1998, 1999). In addition, almost no information is available from the flora-rich countries Africa and China (BENNETT & LEICH 1995).

The forest populations in Korea have undergone a wide variety of human-induced changes in distribution and abundance, including isolation due to deforestation. Plantation from natural forest to artificial conditions may reduce natural population (source) sizes or altogether eliminate some local natural populations. Moreover, irresponsible and exceeding plantation may lead to genetic isolation of once continuous natural populations, which, following isolation, may lose genetic diversity as a result of inbreeding and genetic drift. Plantation may lower population density and, to the extent inbreeding is a function of strand density, lead to an increased level of inbreeding.

The genus Albizia include about 50 species of medium to large sized trees distributed throughout tropical and subtropical Asia, Africa, and Australia (WOODLAND 1991). *Albizia julibrissin* Durazz was introduced into the southern United States in 1745, and has been planted widely for ornamental purposes (WOODLAND 1991). In the early 1990s, gardeners in more northern climates attempted to cultivate this most appealing tree. Several effects had been made to

establish it at the Arnold Arboretum without success until WILSON in 1918 collected seeds of a single *A. julibrissin* growing the garden of the Chosen Hotel in Seoul, Korea (HEINS *et al.* 1987). *A. julibrissin* is a perennial woody plant that distributes in natural habitats of mountains. The species of Albizia are small trees (3–5 m in height) with nitrogen-fixing bacteria associated in rootlet nodules. *A. julibrissin* is bisexual, insect-pollinated, and diploid ($2n$ = 26) that blooms from late spring to early fall. Seeds usually dispersed by birds and wind. The purpose of this paper are; (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, and (3) to compare our estimates those for species having very similar life history traits.

MATERIALS AND METHODS

Sampling procedure and enzyme electrophoresis

Seeds of *Albizia julibrissin* were collected from ten natural populations and nine plantation populations in Korea during the period from 1996 to 1997 (figure 1). Thirty-one to 47 pods were collected from each population and one seed per each legume was used in this study. Seeds are dormant because of an impermeable seed coat. Dormancy can be broken by treatment in a mechanical scarifies until break begin to appear in the seed coat and by soaking seed in sulfuric acid for 3 to 5 minutes and rinse in water for 30 minutes. Germinating seeds were collected and homogenized with phosphate buffer described in SOLTIS *et al.* (1983). Electrophoresis was performed using 10% starch gels. Buffer systems and enzyme staining procedures from SOLTIS *et al.* (1983) were used to assay fifteen enzyme systems; acid phosphatase (ACP), alcohol dehydrogenase (ADH), fluorescent esterase (FE), glutamate oxaloacetate transaminase (GOT), isocitrate dehydrogenase (IDH), leucine aminopeptidase (LAP), malate dehydrogenase (MDH), malic enzyme (ME), octanol dehydrogenase (ODH), peroxidase (PER), 6-phosphogluconate dehydrogenase (PGD), phosphoglucose isomerase (PGI), phosphoglucomutase (PGM), shikimate dehydrogenase (SKD), and superoxide dismutase (SOD). For enzymes resolving in more than one zone of activity, the most anodal isozyme was arbitrarily designated '1' and subsequent isozymes sequentially assigned higher numbers. Likewise, alleles were designated sequentially with the most anodally migrating allozyme designated 'a' and progressively slower forms 'b', 'c', and so on.

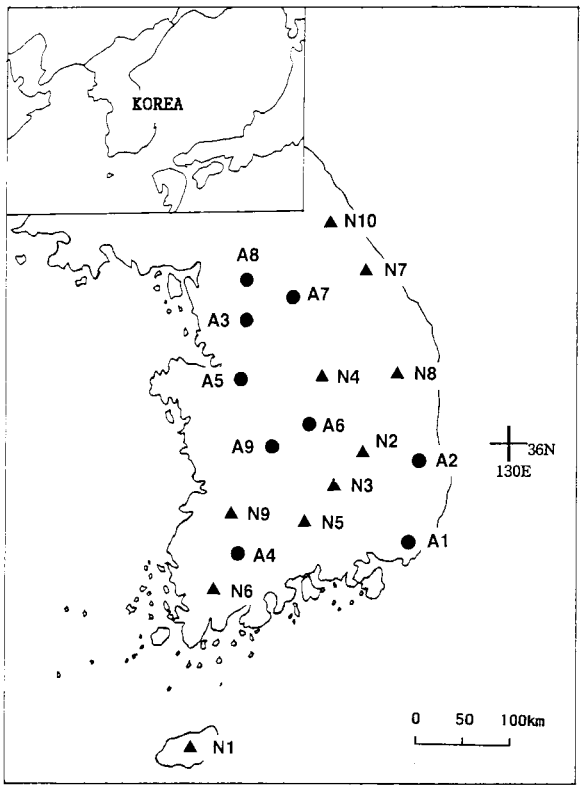

Figure 1. Location of ten natural populations (triangles) and nine artificial populations (circles) of *A. julibrissin* use din this study from Korea.

Data analysis

A locus was considered polymorphic if two or more alleles were detected, regardless of their frequencies. Allozyme diversity was calculated for the species as a whole and on a population basis using five standard genetic parameters; percent polymorphic loci (P), mean number of alleles per locus (A), mean number of alleles per polymorphic locus (A_P), effective number of alleles per locus (A_E), and gene diversity (H_E) (HAMRICK *et al.* 1992). A_E is calculated as the reciprocal of the sum of squares of allele frequencies. Subscripts refer to species (s) or population (p) level parameters. Observed heterozygotes (H_o) was compared to Hardy-Weinberg expected values using WRIGHT's fixation index (F) or inbreeding coefficients (WRIGHT 1922). These indices were tested for deviation from zero by χ^2-statistics (LI & HORVITZ 1953). NEI's 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 (NEI 1973, 1977). In addition, χ^2-statistics were used to detect significant differences in allele frequencies among populations for each locus (WORKMAN & NISWANDER 1970). NEI's genetic identity (I) was calculated for each pairwise combination of populations

Table 1. Percentage of polymorphic loci (P), mean number of alleles per locus (A) and mean number of alleles per polymorphic locus (A_p), effective number of alleles per locus (A_E), observed heterozygosity (H_o), Hardy-Weinberg expected heterozygosity or genetic diversity (H_E) for nineteen populations of *A. julibrissin*.

Population	S	N	P	A_p	A	A_E	H_o (s.d.)	H_e (s.d.)
Natural populations								
N1	2.5×10^4	46	64.00	2.69	2.08	1.56	0.192 (0.014)	0.259 (0.049)
N2	2.0×10^3	46	60.00	2.80	2.08	1.52	0.177 (0.014)	0.253 (0.047)
N3	1.1×10^3	46	52.00	2.85	1.96	1.49	0.169 (0.014)	0.228 (0.048)
N4	1.6×10^3	47	60.00	2.73	2.04	1.48	0.171 (0.014)	0.236 (0.046)
N5	2.0×10^3	37	60.00	2.60	1.96	1.44	0.154 (0.013)	0.211 (0.045)
N6	1.8×10^3	45	52.00	2.77	1.92	1.51	0.171 (0.014)	0.231 (0.049)
N7	2.1×10^3	33	60.00	2.73	2.04	1.43	0.175 (0.014)	0.224 (0.045)
N8	0.5×10^3	35	60.00	2.53	1.92	1.40	0.156 (0.014)	0.207 (0.043)
N9	0.7×10^3	36	56.00	2.86	2.04	1.57	0.169 (0.014)	0.240 (0.052)
N10	1.5×10^4	44	60.00	2.73	2.04	1.48	0.167 (0.014)	0.227 (0.048)
Mean			58.40	2.73	2.01	1.49	0.170 (0.014)	0.232 (0.047)
Artificial populations								
A1	4.1×10^2	40	52.00	2.77	1.92	1.43	0.145 (0.013)	0.205 (0.046)
A2	2.5×10^2	42	60.00	2.73	2.04	1.46	0.170 (0.014)	0.217 (0.047)
A3	0.7×10^2	38	56.00	2.71	1.96	1.42	0.163 (0.014)	0.212 (0.045)
A4	3.2×10^2	38	52.00	2.69	1.88	1.44	0.159 (0.014)	0.201 (0.047)
A5	4.0×10^2	34	60.00	2.40	1.84	1.30	0.131 (0.013)	0.177 (0.038)
A6	2.2×10^2	37	56.00	2.50	1.84	1.38	0.149 (0.013)	0.198 (0.042)
A7	1.3×10^3	38	52.00	2.54	1.80	1.38	0.148 (0.013)	0.196 (0.043)
A8	2.0×10^2	30	40.00	2.70	1.68	1.35	0.126 (0.012)	0.179 (0.046)
A9	3.0×10^2	36	60.00	2.60	1.96	1.37	0.137 (0.013)	0.192 (0.042)
Mean			54.20	2.63	1.88	1.39	0.148 (0.013)	0.197 (0.044)
Total			56.42	2.68	1.95	1.44	0.159 (0.003)	0.215 (0.011)

Note: S and N are population sizes and sample sizes, respectively.

(NEI 1972). A correlation between genetic distance and geographical distance was tested using Mantel's test as advocated by SMOUSE *et al.* (1986). PC-SAS program (SAS Institute Inc. 1989) was used to conduct a cluster analysis on genetic identities via the unweighted pair-wise 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 G_{ST}. The F_{IT} and F_{IS} coefficients measure excesses of homozygotes or heterozygotes relative to the panmictic expectations within the entire samples and within populations, respectively. The G_{ST} coefficient estimates relative population differentiation. Deviations of F_{IT} and F_{IS} from zero were tested using χ^2-statistics (LI & HORVITZ 1953). Two indirect estimates of gene flow were calculated. One estimate of Nm (the number of migrants per generation) was based on G_{ST} (WRIGHT 1951) and the other was based on the average frequency of "rare" alleles found in only one population (SLATKIN 1985, BARTON & SLATKIN 1986). The absolute population differentiation (D_m) was calculated using the formulae: $D_m = \Sigma D_{ST}/(s-1)$ where s is the number of subpopulation in the analysis and D_{ST} is the genetic diversity among populations (NEI 1973).

RESULTS

Genetic diversity

Eighteen of the 25 loci (72.0%) showed detectable polymorphism in at least one population. The remaining seven loci (*Acp-2, Adh-1, Idh-1, Mdh-1, Odh, Per-3*, and *Pgm-1*) were monomorphic in all populations. The percentage of polymorphic locus was 58.4% for natural populations and 56.4% for artificial populations (Table 1). The natural population and artificial populations had A (the average number of alleles per

Table 2. Total genetic diversity (H_T), genetic diversity within population (H_S), deviations of genotype frequencies from Hardy-Weinberg expectations over all populations (F_{IT}) and within individual populations (F_{IS}), the absolute population differentiation (D_m), and proportion of total genetic diversity partitioned among populations (G_{ST}) of *A. juribrissin*.

Locus	H_T	H_S	D_m	F_{IS}	F_{IT}	G_{ST}
Adh-2	0.186	0.172	0.016	0.566	0.600	0.079
Mdh-2	0.684	0.636	0.051	0.300	0.349	0.070
Mdh-3	0.037	0.033	0.004	0.189	0.272	0.103
Pgd-1	0.585	0.569	0.018	0.241	0.262	0.028
Pgd-2	0.192	0.179	0.014	0.080	0.144	0.070
Pgm-2	0.075	0.070	0.005	0.039	0.104	0.069
Idh-2	0.321	0.281	0.042	0.432	0.503	0.124
Fe-1	0.597	0.574	0.024	0.195	0.226	0.039
Fe-2	0.245	0.225	0.020	0.278	0.335	0.078
Me	0.269	0.253	0.016	0.248	0.291	0.057
Acp-1	0.445	0.413	0.034	0.249	0.288	0.072
Skd-1	0.365	0.355	0.011	0.233	0.279	0.027
Skd-2	0.226	0.221	0.005	0.257	0.354	0.022
Got	0.432	0.420	0.013	0.339	0.291	0.028
Lap	0.265	0.245	0.021	0.271	0.365	0.074
Sod	0.219	0.201	0.020	0.314	0.397	0.084
Per-1	0.444	0.395	0.052	0.342	0.179	0.110
Per-2	0.004	0.004	0.000	0.078	-0.002	0.035
Mean	0.311	0.291	0.020	0.242	0.291	0.065
Mean of nat. pop.	0.325	0.310	0.016	0.216	0.276	0.051
Mean of art. pop.	0.290	0.270	0.028	0.243	0.348	0.095

locus) of 2.01 and 1.95, respectively. The average of A_E for natural populations was slightly higher than the value (2.68) for the artificial populations. The mean genetic diversity within populations was 0.215. The population N1 (natural population) had the highest expected diversity (0.259), while population A5 (artificial population) had the lowest (0.177). The plantation populations, particularly urban populations were shown low levels of genetic diversity than natural populations. Significant differences in four genetic parameters except genetic diversity were little between artificial populations and natural populations. The mean genetic diversity of the natural populations (0.172) was higher than that of the artificial populations (0.159). The overall level of total genetic diversity for ten natural populations (H_T = 0.325) was also much higher than the average of for nine artificial populations (H_T = 0.290) (Table 2).

Genetic structure

Wright's F coefficients showed that significant deficiencies of heterozygotes exist for all loci at the population level (F_{IS} = 0.242) and the sample as a whole (F_{IT} = 0.291) (weight). Mean F_{IT} in natural populations equaled 0.276, while the mean F_{IS} valuea was 0.216. The majority of the deviation from equilibrium resided among individuals within populations (F_{IS}). The deficiency of heterozygotes for the artificial populations was slightly higher than the value (F_{IS} = 0.243) for the natural populations.

Analysis of fixation indices, calculated for all polymorphic loci in each population, showed a substantial deficiency of heterozygotes relative to Hardy-Weinberg expectations (Table 3). For example, 88.3% of fixation indices were positive (235/266), and 64 of those departed significant from zero ($p < 0.05$). In contrast, of only 31 negative indices, no one was departed significantly from zero ($p < 0.05$).

On a per locus basis, the proportion of total genetic variation due to differences among populations (G_{ST}) ranged from 0.022 for *Skd-2* to 0.124 for *Idh-2* with a mean of 0.065, indicating that about 7% of the total allozyme variation was among populations. Thus, the majority of genetic variance (93%) resided within populations. The mean G_{ST} values of the ten natural populations and the nine artificial populations were 0.051 and 0.095, respectively. The level of artificial

Table 3. Wright's fixation indices for nineteen populations of *A. juribrissin*.

Pop	*Adh –2*	*Mdh – 2*	*Mdh – 3*	*Pgd – 1*	*Pgd – 2*	*Pgm – 2*	*Idh –2*	*Fe –1*	*Fe – 2*
Natural populations									
N1	0.630**	0.292	–0.038	0.336	0.353	–	0. 479*	0.053	0.337
N2	0.710**	0.365*	–	0.331	–0.166	–	0.592**	0.80	0.337
N3	–	0.376*	–	0.244	–	–	0.502**	0.133	0.332
N4	0.605**	0.374*	–	0.228	–0.035	–	*	0.071	–0.041
N5	0.632**	0.373	–	0.265	0.052	–	0.379**	0.246	–0.020
N6	–	0.313	–	0.260	0.229	–	–	0.251	0.391
N7	0.570**	0.132	–0.036	0.076	0.094	–	0.239	0.212	0.362*
N8	0.605**	0.222	–	0.179	–0.019	–	0.476**	0.199	0.421*
N9	–	0.445*	–	0.233	0.362*	0.274	0.471*	0.386*	0.118
N10	0.293	0.371*	–	0.348	0.038	–0.032	0.197	0.346	0.228
							0.421*		
Artificial populations									
A1	–	0.332	–	0.361	–	–	0.611**	0.053	0.390*
A2	–	0.282	–	0.229	–0.068	–0.090	*	0.133	–0.019
A3	0.514**	–	–	0.278	0.123	0.237	0.627**	0.310	–0.021
A4	–	0.123	–	0.302	0.152	–0.070	*	0.205	0.195
A5	0.615**	–0.019	–	0.261	–	–0.073	0.257	0.119	0.470*
A6	1.000**	0.268	–	0.149	–	–	0.479**	0.138	0.351
A7	*	0.282	0.261	–0.131	–	–	0.362*	0.133	–
A8	0.513**	0.336	0.346	0.144	–	–	–	–	–
A9	0.563**	0.415*	–	0.297	–0.145	–0.035	0.267	0.476	0.471*
	–0.032						–		
							–		

Pop	*Me*	*Acp –1*	*Skd –1*	*Skd – 2*	*Got*	*Lap*	*Sod*	*Per – 1*	*Per –2*
Natural populations									
N1	0.439*	0.221	0.192	0.369*	0.252	0.276	–0.019	–0.180	–
N2	0.191	0.215	0.263	0.307	0.241	0.211	0.517**	0.221	–
N3	0.283	0.166	0.377	0.160	0.308	0.272	0.437*	–0.250	–
N4	0.195	0.271	0.214	0.427*	0.347	0.353	0.346	0.342	–
N5	–0.056	0.346	0.350	0.536**	0.308	0.119	0.440	0.151	–0.019
N6	0.260	0.196	0.195	0.367*	0.318	0.376	–	0.173	–
N7	–	0.140	0.170	0.160	0.343*	0.329	0.311	0.218	–
N8	–0.121	0.293	0.311	0.356	0.401*	0.518	0.351	–0.017	–
N9	0.308	0.313	0.351	–0.036	0.293	0.276	0.351	–	–
N10	0.369	0.247	0.213	–	0.226	0.358*	0.654***	–0.146	–
Artificial populations									
A1	0.292	0.253	0.271	0.211	0.385*	0.356	0.470*	0.263	–
A2	0.337	0.248	0.313	0.274	0.349	0.358	–	–0.196	–
A3	0.324	0.269	0.271	0.356	0.207	0.471	–	–0.279	–
A4	0.375*	0.127	0.427*	0.211	0.260	0.355	–	–	–
A5	0.109	0.369	0.163	0.466**	0.268	0.346	0.424*	0.265	–
A6	0.239	0.159	0.312	0.305	0.256	0.375	0.508**	–0.262	–
A7	–	0.276	0.220	0.423**	0.239	0.304	0.115	0.287	–
A8	–	–	0.360*	0.477**	0.229	0.232	0.303	0.078	–
A9	0.198	0.518	0.293	0.438*	0.171	0.354	0.271	0.211	–

* = $p < 0.05$; ** = $p < 0.01$; *** = $p < 0.001$.

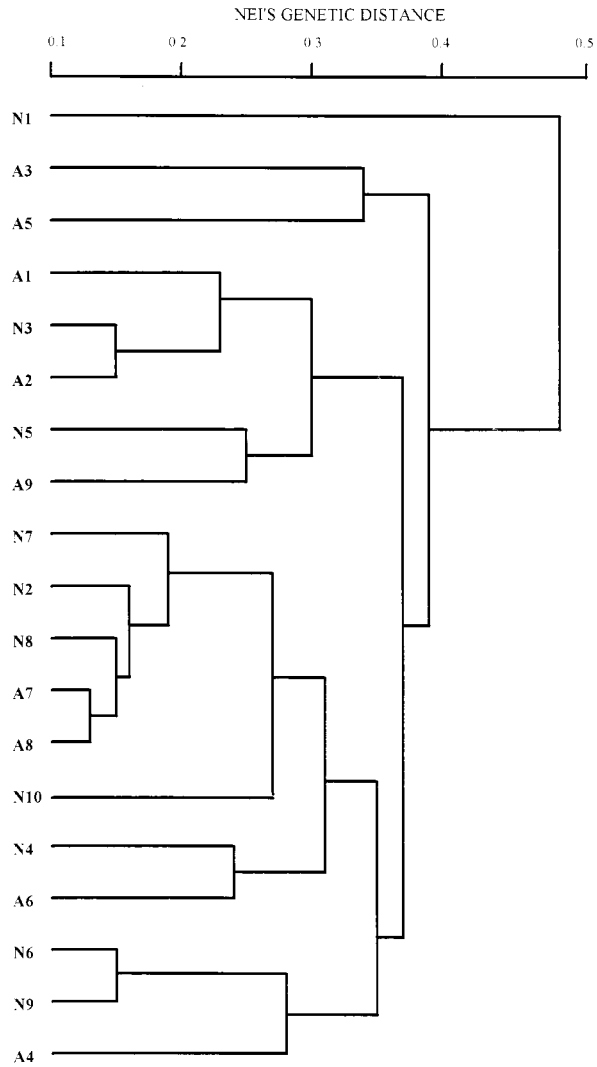

Figure 2. A dendrogram showing the phylogenetic relationships among the nineteen populations of *A. julibrissin*, based on data of genetic distances obtained by starch gel electrophoresis.

population differentiation was almost twofold higher than that of natural population differentiation. The similar trend is observed in the absolute population differentiation (D_m) between natural populations (0.016) and artificial populations (0.028). Genetic identity values among pairs populations range from 0.845 to 0.992. The similarity among populations can be seen in the UPGMA dendrogram, where total populations cluster at a below genetic distance of 0.429 (figure. 2). The indirect estimate of gene flow based on mean G_{ST} was high (Nm = 3.60), and estimate of gene flow based on private alleles was relative high (Nm = 2.30). The correlation coefficient between genetic distance and geographical distance was significantly different from zero using the Mantel's test for all populations (r = 0.30), and about 91% of the variation in genetic distance seemed to be caused by unknown factors other than geographic distance.

DISCUSSION

Levels of allozyme diversity

A. julibrissin maintains relatively high levels of allozyme variation compared to the average plant species. For example, its mean genetic diversity at 0.224 is higher than that of angiosperms (0.169), long-lived woody perennial species (0.177), outcrossing-animal species (0.211), but low than species with widespread geographic ranges (0.251) (HAMRICK & GODT 1989). The same trend is observed in other genetic variation. For most other long-lived and woody species, percentage of polymorphic loci (P_S) is 65%, mean number of alleles per locus (A_S) is 2.22, and effective number of alleles per locus (A_{ES}) is 1.24 (HAMRICK & GODT 1989). For *A. julibrissin*, P_S is 72%, A_S is 2.78, and A_{ES} is 1.43. This high genetic variation is also shown in population levels. For long-lived, woody species, mean percentage of polymorphic loci (P_P) is 49.3%, A_P is 1.76, and A_{EP} is 1.20 (HAMRICK & GODT 1989). Within *A. julibrissin* populations, P_P is 56.4%, A_P is 1.95, and A_{EP} is 1.44. These comparisons suggest that the genetic diversity levels of *A. julibrissin* are higher than its associates. *A. julibrissin* maintains more diversity in populations than the average plant species. It is somewhat surprising when we consider the fact that no specialized seed dispersal mechanism is known, flowers are visited by insects, and the present-day populations of this species are discontinuous and isolated. Furthermore some of population sizes are recolonization.

One of the most notable features of the family (Fabaceae or Leguminosae) is the high percentage of polymorphic loci per population and genetic diversity (SCHNABEL & HAMRICK 1990). The high levels of genetic diversity of this family (Fabaceae) are reported in herbaceous as well as woody species. For example, for everlasting pea (*Lathyrus latifolius*), P_S is 81%, P_P is 54%, H_{ES} is 0.207, and H_{EP} is 0.169 (GODT & HAMRICK 1991). For Mexican beans (*Phaseolus coccineus*), H_{ES} and A_S are 0.319 and 3.0, respectively (WALL & WALL 1975). For honey locust (*Gleditisia triacanthos*), P_S is 81%, P_P is 62%, H_{ES} is 0.221, and H_{EP} is 0.198 (SCHNABEL & HAMRICK 1990). For *Gleditisia japonica* var. *koraiensis* in Korea, P_S is 64.7%, P_P is 52.9%, H_{ES} is 0.247, and H_{EP} is 0.206 (HUH *et al.* 1999).

The relatively high level of genetic variation found in A. julibrissin is consistent with several aspects of its biology. First, geographic range has been shown to be

strongly associated with the level of variation maintained within populations and at the species level (HAMRICK & GODT 1989). Widely distributed species tend to maintain more variation than more narrowly distributed species. Second, the breeding system of a species is an important determinant of variability at both the species and population level. A. julibrissin is dominantly outcrossing, insect-pollinated species. This combination is well known to be associated with high levels of allozyme variation (BROWN 1979, GOTTLIEB 1981, HAMRICK & GODT 1989). Third, long-lived perennial species, like *A. julibrissin,* generally maintains relatively higher levels of variation than annuals and short-lived perennials (HAMRICK & GODT 1989). The observation of annuals rings in *A. julibrissin* examined revealed that the stems were at least 30–45 years old. As individuals of *A. julibrissin* are long-lived, opportunities for the accumulation of mutations should be high (LEDIG 1986).

The comparison of natural populations and artificial populations

Populations of long-lived woody plants, composed of cohorts established at different times and spaces, can be genetically differentiated both temporally, if any, and spatially (LINHART *et al.* 1981, SCHNABEL & HAMRICK 1990). In the present study, significant differences in four genetic parameters except genetic diversity were little between artificial populations and natural populations (Table 1). We tested data submitted to the hypothesis test for whether genetic diversity in plantation populations have less variability than that of natural populations. The variance ratio is severely ($F = 503.9$, $df = 18$). The similar results were observed in other woody angiosperms such as two oak species (HOKANSON *et al.* 1993) and a tropical forest tree (HALL 1994). However, what is the reason for genetic diversity in the artificial populations to be low when compared to natural populations? The life history characteristics of *A. julibrissin* would lead one to predict the change of genetic diversity. It should be noted that the number of age classes comprised in two groups of populations examined is quite different. Artificial populations organized of 10–15 different age classes, while natural populations consist of 30–45 year old plants and a few juveniles of this populations were transferred to artificial populations directly or indirectly via botanical gardens to artificial populations because it is different to transfer adult individuals. Some natural population sizes in Korea have a tendency to decrease gradually because Korean Government transplanted silk trees in forest to the Seoul Olympic park, public garden, Buddhist temples, and amusement parks. In exactly ten years ago, sudden forest attacks occurred in the spring of 1988 for the purpose of ornament around the Seoul Olympic Gymnasium. Regardless of growth rate, however, populations undergoing bottlenecks tend lose low frequency alleles, reducing polymorphism and the number of alleles per polymorphic locus (GODT & HAMRICK 1991). Genetic diversity found between two different age groups, if any, may be due to difference among cohorts as well as to genetic change within a cohort formed along with aging. Considering this point, why are the levels of genetic diversity in adults (natural) populations? We think partly that one plausible explanation can be considered here. Like long lived woody plants, *A. julibrissin* maintains higher levels of genetic diversity with a relatively high evolutionary potential (HAMRICK & GODT 1989), and thus appears to be less susceptible to environmental stresses and stochastic events than the majority of woody angiosperms examined to date. If this is true, it is speculated that reproductive events, initial reproductive process, and/or selective force, etc. may be homogeneous in time. For example mean genetic identity between populations ($I = 0.995$) was somewhat above the mean identity ($I = 0.945$) reported by GOTTLIEB (1981) for 22 species. These factors may be part contribute to a similar genetic architecture in populations between artificial and natural groups.

No specialized seed dispersal mechanisms were known in *A. julibrissin.* The observed high, significant, and positive F_{IS} value (0.242) indicates that homozygotes were significantly in excess. Especially, the F_{IS} value in the artificial populations was higher than the value in the natural populations. If significant deficiencies of heterozygosity for each polymorphic locus are present, this indirectly indicates the existence of inbreeding as a result of family clustering. Generally, seedling stages are expected to have higher levels of inbreeding than found in adults. This level of inbreeding can result from a variety of causes because *A. julibrissin* is bisexual and insect-pollinated species: positive assortive mating (*i.e.*, preferential mating among similar genotypes) (CROW & FELSENSTEIN 1968); selection for homozygotes; family structure within a restricted neighborhood, and causing mating among relatives (LEVIN & KERSTER 1971).

The significant deficiency of heterozygotes found in artificial populations may partly be due to the fact that there has been selection favoring homozygotes among artificial populations (LINHART *et al.* 1981). This might suggest that selection against homozygotes operated in the progeny populations throughout the life cycle. This allowed few inbred progenies to survive to

the adult stage, resulting in more outcrossed adult trees (LIENGSIRI *et al.* 1998). Selection in favor in favor of heterozygotes typically occurs in more extreme environments. Artificial populations are most located at urban areas and more drier than forest populations, with poorer soils, leading to more xeric conditions which might promote selection in favor of heterozygotes (LIENGSIRI *et al.* 1998). The silvics and the reproductive strategy of *A. julibrissin* could explain the observed inbreeding level. Because *A. julibrissin* is polygamous species, it is expected that all of the inbreeding detected is due to consanguineous and selfing mating. In addition previous studies of families Fabaceae (HOKANSON *et al.* 1993) and Minosoideae (HALL *et al.* 1994) showed that the levels of gene flow in seed and seedling populations were considerably higher than in adults populations. In the present study, artificial population differentiation was twice as high in natural population differentiation. NEI *et al.* (1975) have shown that the reduction in average heterozygosity per locus depends not only on the size of the population bottleneck, but also on the subsequent rate of population growth. If population growth is reduced, reduction in average heterozygosity is large, even given a small number of founder (LOVELESS & HAMRICK 1984).

The UPGMA and correlation analysis showed very weak correspondence between genetic distance and geographic distance ($r = 0.30$). Only the most isolated population N1 could be explained by the Holocene paleoclimatic history of the Korean Peninsula. *A. julibrissin* is a lon-lived species originally inhabiting southern China or western Japan (HEINS *et al.* 1987). It is inferred that gene flow from population N1 of *A. julibrissin* went freely into mainland Korea without restriction when Cheju Island (population N1) was part of Korea.

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