

Plant Population Structure of Mt. Jeolyoung in Young-do of Busan

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The purpose of the present investigation was to investigate diversity patterns in a fragmented Young-do forested landscape. It was conducted on sloping 18 plots (twelve 50×50 m plots and six 10×100 m plots). Total 1562 individuals were identified and measured in the 50×50 m plots. These were a total of 68 species of 23 families present in the three sites. Least significant differences (LSD) by post hoc analysis revealed that fragments site A had significantly greater densities than site B. Shannon-Wiener functions differed significantly among forests ($F = 4.12$, $p < 0.05$), with site A forest having significantly higher value (3.401) than the others (2.590 for site B and 2.648 for site C). *Pinus thunbergii* and *Quercus aliena* were dominant on most sites. The *Pinus densiflora* forest of sites A and C is distributed better in the NE exposures compared with the opposite ones. *Ficus erecta* and *Pinus densiflora* largely occupied the southern exposures. The spatial distribution in southern Young-do's littoral forest was very heterogeneous, reflected by most species having low densities and patchy distributions.

Key words – Young-do, Least significant differences, Shannon-Wiener functions

Worldwide, urban areas are expanding both in size and populations. As a result of urban expansion, native vegetation is reduced and fragment a landscape mosaic in which both the amount of impervious surface is increased, and the structure and composition of the remaining vegetation is progressively altered [5,11].

Urbanization adjacent to natural areas and parks often results in simplification of habitats and a community of plant, which lead to fewer species dominated by habitat patch size to species richness, increase of immigration and extinction rates, and have been applied to habitat patch dynamics in fragmented urban areas [16,17].

The destruction and fragmentation of habitat results in the conservation of relatively continuous ecosystems, such as forests, into archipelago of natural habitat surrounded by a 'sea' of urban development [7]. Population in fragmented ecosystems are more likely to become extinct due to the effects associated with size reduction of remnant habitat, greater isolation from neighboring populations, and increased amounts of 'edge' habitat, and this should consequently lead to an overall reduction in biological diversity in the region [8]. The effects of fragmentation have been assessed indirectly by testing for a decline in diversity with decreasing fragment size and/or isolation

[4,6,18].

The purpose of the present investigation was to investigate diversity patterns in a fragmented Young-do forested landscape. It was conducted on sloping 18 plots (twelve 50×50 m plots and six 10×100 m plots) that was representative of the three fragmented forests, where the canopy has well developed. What is the nature of floristic diversity and species richness patterns generally, and what are the effects of habitat fragmentation? We examined trees and understory species separately, to examine the relationship between floristic diversity patterns and plant life forms.

Study area and Methods

The Young-do is located in the southeastern coast of Busan, Korea (35°02'27"N~35°06'00"N, 129°02'05"~129°06'00") (Fig. 1). The three forests in this island are all highly fragmented. The site A is ca. 100 ha in size and situated on the north of the Young-do Island. The north mountain is called in a sense by the name of Bongrae-san or Jeolyoung-san. The topography is flat or gently sloping in the lower and middle altitudes, and rather steep at higher altitude. The site C including the Taejeongdae Forest Reserve on southeast Young-do Island is a typically developed and truly old-growth evergreen broad-leaved forest. The site B is located between Sites A and C.

Within each forest fragment, 4 placed 50×50 m plots

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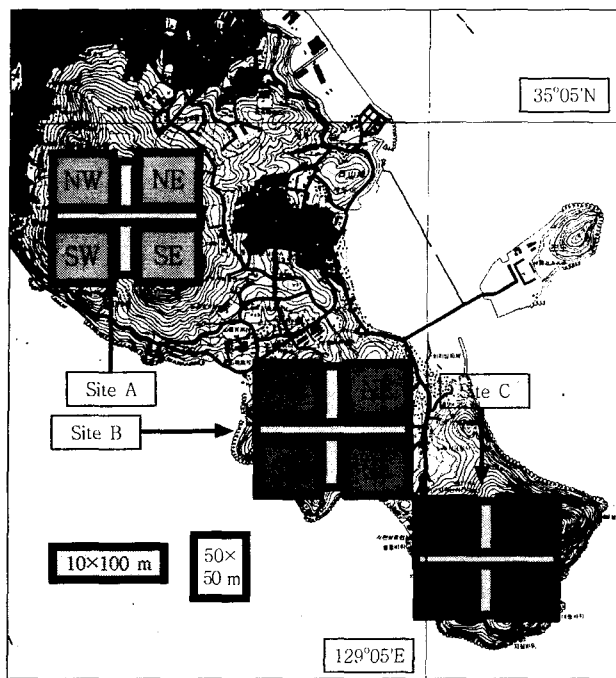


Fig. 1. Location of the regions at Young-do and three forest fragmented sites used in this study.
 NE: North-East plot, NW: North-West plot, SE: South-East plot, SW: South-West plot.

were set up on the site with the most developed canopy and were completely censused for all trees with a diameter at breast height (DBH) ≥ 10 m.

For the second part of this study, 10x100 m plots were completely censused woody vegetation (trees plus shrubs) taller than 1 m. Plots were positioned along 100 traits running from edge to interior. Numbering and measuring the individuals was done systematically, with plants being marked to avoid re-censusing.

Analysis of variance and least significant differences post hoc tests were used with SYSTAT 9 to compare results among forest fragments [15,20].

The Shannon-Weiner index of diversity was used to characterize species richness and abundance [3]. It was calculated as:

$$H' = - \sum_{i=1}^s (p_i)(\ln p_i)$$

where s is the total number of species and p_i is the proportion of all individuals in a sample that belong to the i th species.

Species diversity may be thought of as being composed of two components. The first is the number of species in the community, which ecologists often refer to as species

richness. The second component is species evenness or equitability. Two well-known richness indices are as follows: R1 and R2 indices [10].

$$R1 = \frac{s-1}{\ln(n)}$$

$$R2 = \frac{s}{\sqrt{n}}$$

s : the total number of species in a community, n : the total number of individuals observed.

The common evenness indices used by ecologists are E1-E5[2].

Jaccard's coefficient (J) of similarity for twelve 50x50 m plots was used to compare the number of species shared between plots in different shared fragments.

J = number of shared species between plot A and plot B / number of species in plot A + number of species in plot B.

Environmental species and environmental plot relationships were investigated by detrended canonical correspondence analysis using CANOCO, version 4.0, based on normal data[18].

Result

Overall across the fragments, total 1562 trees were identified and measured in the 50x50 m plots. These were a total of 68 species and 23 families present in the three sites (Table 1). There were 42 understory species in 12 forest plots of three sites. Average density (tree per plot) differed significantly among fragments ($F = 9.96, p < 0.001$). Least significant differences (LSD) post hoc analysis revealed that fragments site A had significantly greater than densities than site B (Fig. 2). Mean number of species per plot differed significantly among the three fragments ($F = 7.75, p < 0.01$). Post hoc LSD tests showed that site A and site C had a significantly greater mean number of species per region than site B. Mean number of families per site varied between 12 (site B) and 20 (site A), giving a total of 23 over all sites. Shannon-Wiener functions differed significantly among forests ($F = 4.12, p < 0.05$), with site A forest having significantly higher value (3.401) than the others (2.590 for site B and 2.648 for site C) (Table 1). The richness indices R1 and R2 decrease from Site A to site B. The evenness indices except E2 were not shown a significant differences among three sites.

Table 1. Richness and abundance parameters for four plots (50×50 m) in three coastal forest fragments

		Site A	Site B	Site C	Total
No. of trees		521	306	735	1562
No. of species		62	22	37	68
No. of families		20	12	17	23
Mean no. of trees per plot		130.3	76.5	183.8	***
Mean no. of species per plot		15.5	5.5	9.3	**
Mean no. of families per plot		5.0	3.0	3.8	*
Shannon-Weiner index		3.401	2.590	2.648	*
Richness index	R1	9.751	3.669	5.455	**
	R2	2.716	1.258	1.365	*
Evenness index	E1	0.824	0.838	0.733	ns
	E2	0.484	0.606	0.382	*
	E3	0.475	0.587	0.365	ns
	E4	0.547	0.752	0.569	ns
	E5	0.532	0.732	0.536	ns

*, **, and ***: Significant at the 0.05, 0.01, and 0.001 levels, respectively.

ns : Nonsignificant.

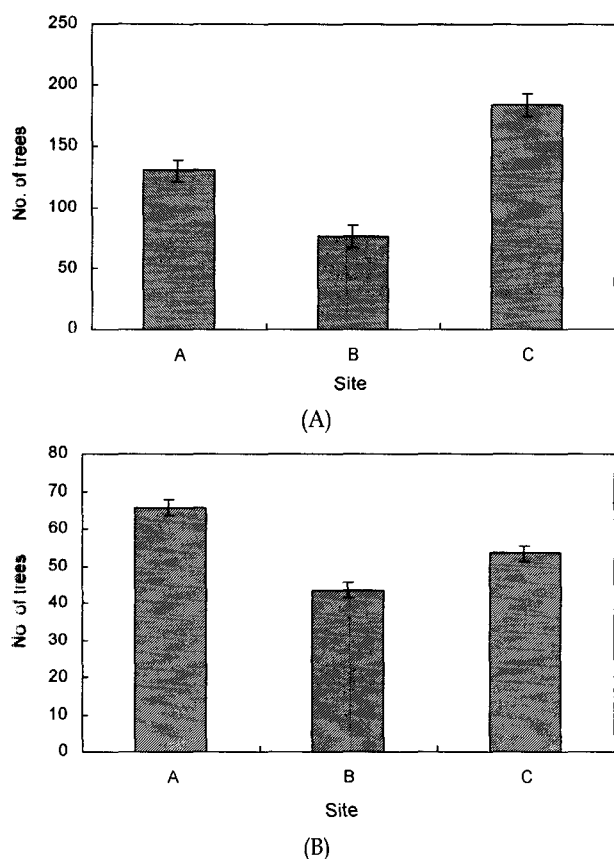


Fig. 2. The mean number of individuals at three sites: (A) per 50×50 m plot and (B) per 10×100 m plot.

In the 10×100 m plots, 331 individuals of which were woody vegetation (height>1 m) and 209 individuals of which were understory (diameter<10 cm DBH) woody were

identified and measured (Table 2). Those samples represented a total of 33 species in 11 taxonomic families. Excluding >10 cm DBH trees, there were 17 species in 8 families. The average woody understory density (stems per plot) differed significantly among fragments ($F = 7.66$, $p < 0.05$). Post hoc analysis showed that fragment site A had significantly greater density than sites B and C ($p < 0.05$). The mean number of woody and understory species per plot differed significantly among the three fragments ($F = 7.72$ for woody species, $F = 6.69$ for understory species, respectively, $p < 0.05$). Mean number of families per plot also same trend and differed significantly among fragments ($F = 5.59$, $F = 6.07$, respectively, $p < 0.05$). Shannon-Wiener values varied between 3.380 (site A) and 2.807 (site C). Site A had the highest richness indices R1 and R2. The evenness indices were not shown a significant differences among three sites.

Species abundance patterns in the three Young-do Island fragments mirror the right tail of a lognormal distribution, both for tree in the 50×50 m plots and understory woody vegetation in the 10×100 m plots (Fig. 3). More than two-thirds of tree species and understory species of the two sites (A and B) are found in the first three abundance classes of the log-distribution (<4 years), while fewer than 6% were found in each of the final 16~30 abundance class. The distribution for all forests dramatically dropped off to a long right tail. However, 28% of the site C including the Taejeongdae Forest Reserve is found in the final class of the log-distribution.

Table 2. Richness and abundance parameters in 10×100 m long transect in three coastal forest fragments

		Site A	Site B	Site C	Total
All woody individuals, height > 1 m					
No. of individuals		137	87	107	331
No. of species		25	14	21	33
No. of families		9	5	7	11
Mean no. of trees per plot		68.5	43.5	53.5	*
Mean no. of species per plot		12.5	7.0	10.5	*
Mean no. of families per plot		4.5	2.5	3.5	ns
Shannon-Weiner index		3.380	3.081	2.807	*
Richness index	R1	10.110	5.770	4.623	***
	R2	2.562	1.734	1.303	*
Evenness index	E1	0.804	0.860	0.825	ns
	E2	0.438	0.605	0.552	ns
	E3	0.430	0.594	0.537	ns
	E4	0.529	0.749	0.648	ns
	E5	0.512	0.737	0.625	ns
individuals < 10 cm DBH					
No. of individuals		83	64	62	209
No. of species		14	10	11	17
No. of families		6	4	4	8
Mean no. of trees per plot		41.5	32.5	31.0	*
Mean no. of species per plot		7.0	5.0	5.5	*
Mean no. of families per plot		3.0	2.0	2.0	*
Shannon-Weiner index		3.208	2.787	2.697	*
Richness index	R1	8.917	6.300	4.385	*
	R2	2.283	1.612	1.289	*
Evenness index	E1	0.787	0.797	0.809	ns
	E2	0.419	0.492	0.530	ns
	E3	0.409	0.476	0.512	ns
	E4	0.554	0.608	0.660	ns
	E5	0.535	0.582	0.635	ns

Asterisks and ns are the same as Table 1.

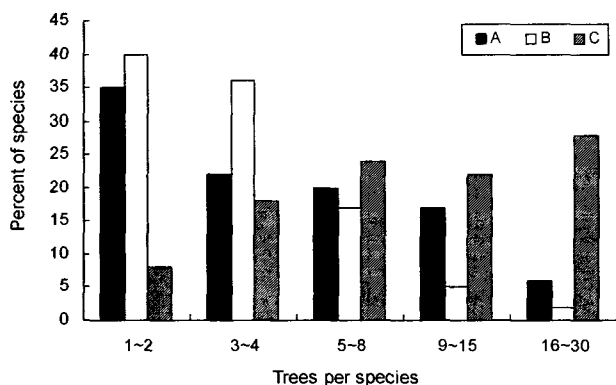


Fig. 3. The distribution of tree species per site (four 50×50 m plots and two 10×100 m plots per site) in three forest fragments.

A total of 5 tree species occurred at an abundance of 10 trees per plot or greater in at least one fragment, and 7 at

an abundance of 20 trees per plot or greater, and 4 at an abundance of 20 trees per plot or greater (Table 3).

Two pine species were typical on almost all sites; *Pinus thunbergii* and *Quercus aliena*, thus they were the dominant habitat type on most sites. The most common species in the site A forest *Pinus densiflora* (Pinaceae), according for 17.1% of the individuals sampled in 50×50 m plots and 24.5% in 10×100 m plots.

In marked contrast, the most common tree species in the site B and C fragments were *Rhus verniciflua* and *Camellia japonica* accounted for 21.7% and 16.8%, respectively.

Mean Jaccard's coefficient of similarity between fragments pairs was compared by the two-sample t-test (Table 4). The Jaccard's coefficient showed three distinct groups, although SW of site C (C-SW) and four plots of site A were not well separated from each other.

Table 3. Major tree species exceeding 10 (+), 20 (++) and 30 (+++) individuals per plot in three forest fragments

Species (Family)	Site A	Site B	Site C
<i>Pinus densiflora</i> Sieb. & Zucc. (Pinaceae)	+	+	+++
<i>Pinus thunbergii</i> Parlatores (Pinaceae)	++	++	+++
<i>Larix leptolepis</i> Gordon (Pinaceae)	+		++
<i>Chamaecyparis obtuse</i> Endlicher (Cupressaceae)	++		++
<i>Camellia japonica</i> L. (Theaceae)	+	++	+++
<i>Alnus firma</i> Sieb. & Zucc. (Betulaceae)	+		+
<i>Betula schmidtii</i> Regal (Betulaceae)	+		++
<i>Corylus heterophylla</i> Fischer (Betulaceae)	+		+
<i>Daphniphyllum macropodium</i> Miquel (Euphorbiaceae)		+	+
<i>Melia azedarach</i> var. <i>japonica</i> L. (Meliaceae)		+	++
<i>Quercus aliena</i> Blume (Fagaceae)	+++	++	+
<i>Quercus mongolica</i> Fischer (Fagaceae)	+	+	+
<i>Ligustrum obtusifolium</i> Sieb. & Zucc. (Oleaceae)	++	+	++
<i>Rhus verniciflua</i> Stokes (Anacardiaceae)	+	++	++
<i>Prunus serrulata</i> var. <i>spontanea</i> Wils. (Rosaceae)		+	++
<i>Ficus erecta</i> Thunberg (Moraceae)	+	+	+

Restricting analysis gradually to higher dominant species, the dependency of species variance on environmental factors was still variances a little more (Fig. 4). When we restricted the species to more than 5% in dominance (10 species), the first axis explained 12.8% of the species variation.

To ascertain the relation between the distribution of the plant communities and exposure, exposures of the site of all plant communities were examined, and the percentage of distributions to the directions are shown in Fig. 5. The

Pinus densiflora forest of sites A and C is distributed better in the NE exposures compared with the opposite ones. *Ficus erecta* and *Pinus densiflora* largely occupied the southern exposures at the site C.

Discussion

In the early 1900s a village was established near the north part of site A. During the period of the Korean War in 1950-1953, many people settled the Young-do Island and began to cultivated the low land. At this time, many refuges began to expand domiciles toward the site B because it was gently sloping in the lower altitudes. These villages are currently located within the surrounding areas of the southern part of site A and the northern part of site B resulting in forest fragmentations.

Many studies on plants in fragmented habitats have focused primarily on the relationship between species diversity and fragment size and isolation[4,6,19]. In general, those or these their studies indicate that larger fragments have greater diversity than smaller fragments[9]. However, differences in diversity cannot always be attributed to fragmentation per se; this relationship is often a result of greater environmental heterogeneity in larger fragments, and that the influence of successional stage and site history can be more important than fragment size[6]. Other problems limit the utility of these studies as well: sample sizes are often small[19], inappropriate controls are used by necessity[12], and juvenile trees are usually considered an indication of future canopy composition, an

Table 4. Jaccard's coefficient of similarity (below diagonal) and t-tests (above diagonal) among forest plots

Plot	A-NE	A-NW	A-SE	A-SW	B-NE	B-NW	B-SE	B-SW	C-NE	C-NW	C-SE	C-SW
A-NE	-	ns	ns	ns	***	***	***	***	*	*	*	*
A-NW	0.996	-	ns	ns	***	***	***	***	*	ns	*	*
A-SE	0.984	0.970	-	ns	***	***	***	***	*	ns	ns	*
A-SW	0.970	0.991	0.975	-	***	***	***	***	*	*	*	*
B-NE	0.614	0.723	0.707	0.699	-	ns	ns	ns	**	**	*	ns
B-NW	0.726	0.704	0.694	0.745	0.971	-	ns	ns	***	**	***	**
B-SE	0.794	0.767	0.799	0.681	0.980	0.978	-	ns	***	**	***	**
B-SW	0.879	0.684	0.742	0.795	0.976	0.985	0.986	-	**	*	**	**
C-NE	0.808	0.879	0.886	0.769	0.825	0.667	0.778	0.771	-	ns	ns	ns
C-NW	0.891	0.911	0.908	0.913	0.739	0.683	0.790	0.763	0.992	-	ns	ns
C-SE	0.884	0.903	0.882	0.796	0.884	0.794	0.783	0.768	0.980	0.998	-	ns
C-SW	0.905	0.921	0.903	0.917	0.833	0.750	0.794	0.768	0.968	0.997	0.996	-

A-: site A, B-: site B, C-: site C.
NE, NW, SE, and SW are the same as in Fig. 1.
Asterisks and ns are the same as Table 1.

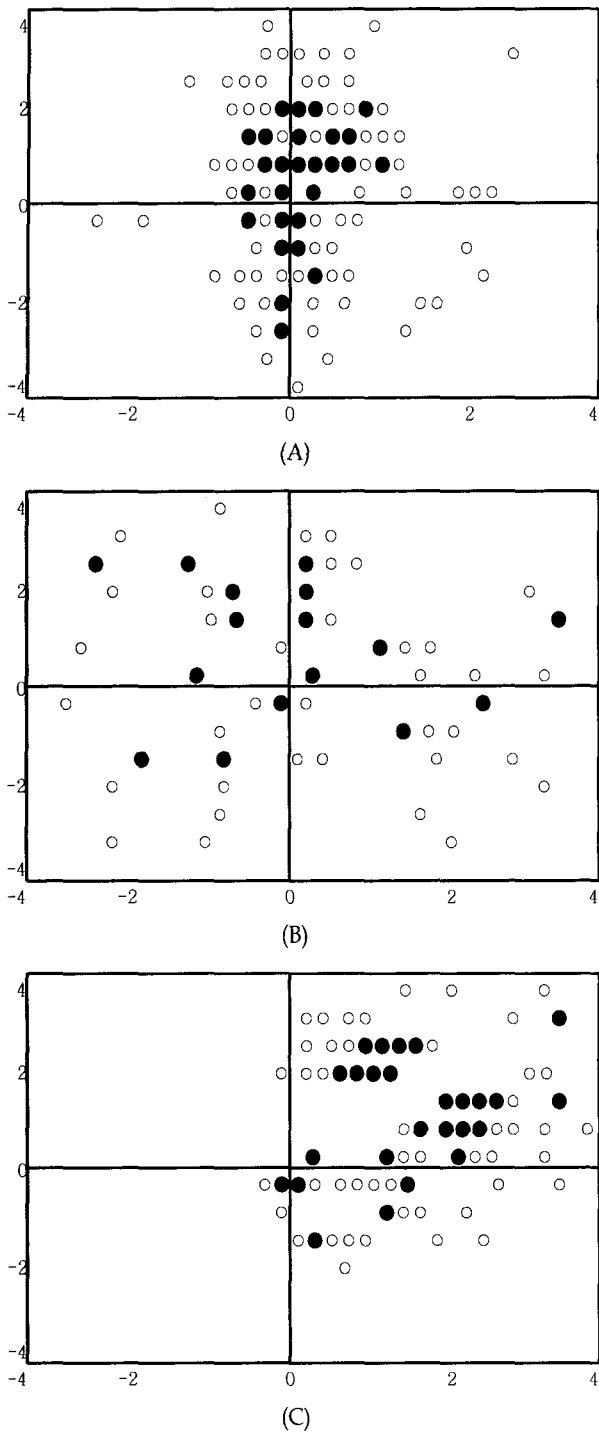


Fig. 4. Detrended canonical correspondence analysis coordination diagram showing understory species scores (○) and plot scores (●) by basal area. (A): Site A, (B): Site B, (C): Site C.

inference that does not allow for differential mortality rates among species[13]. Moreover, none of these studies provide direct evidence supporting the principal prediction that has emerged from theoretical work on habitat frag-

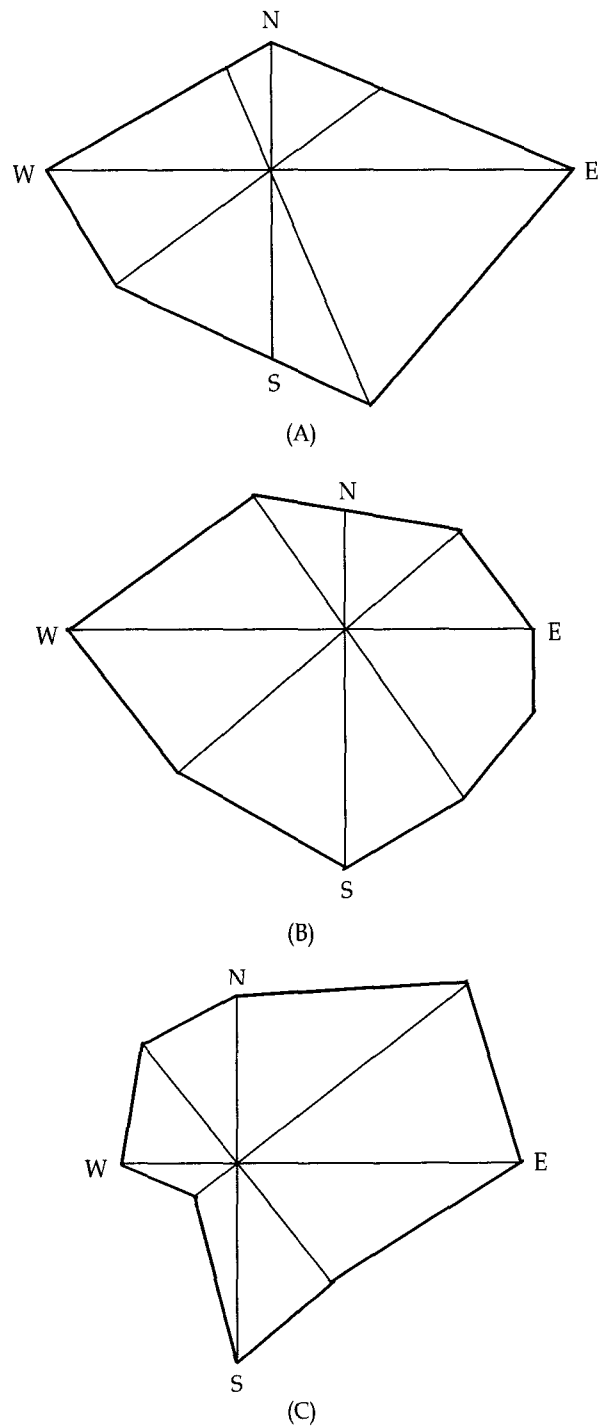


Fig. 5. Distribution diagrams of the plant communities showing the percentage occurrences of each site along directions of slope exposure. (A): Site A, (B): Site B, (C): Site C.

mentation that populations are more likely to become extinct in fragmented habitats[15].

In this study, fragment size was not related directly to estimates of recruitment for several tree species. However,

smaller habitat that is consisted of a greater proportion of edge habitat that is unsuitable for outcrossing mating system species than inbreeding species and larger fragments[1]. Accurately determining the distance into forests that is unsuitable for all species is not yet possible and would require better projections for populations using measures of mortality and survivorship over multiple years. Still, there is a marked reduction in recruitment at site near edges. For example, although fragments are usually not square-shaped, two 10×100 m plots for each site is more diversity than four 50×50 m plots for each site.

A total of 68 tree species occurred at an abundance of fifteen in at least one fragments (Table 1). Among understory species, 33 species were found at abundance of 87 individuals or more (Table 2).

Considering just the most common species, the community comparison of the fragments is strikingly different (Fig. 5). The site A is primarily a *Pinus thunbergii* - *Quercus aliena* forest, whereas the site C fragments are all dominant by *Pinus thunbergii* - *Camellia japonica*. Three rare species appeared in the only site A: *Eurya emarginata*, *Styrax japonica*, and *Chionanthus retusa*. No unique species was found in site B and C.

The spatial distribution in southern Young-do Island's coastal littoral forest is very heterogeneous, reflected by most species having low densities and patchy distributions. In addition there were significant differences among the three forest fragments in this study in terms of Shannon-Weiner index of diversity, number of trees, species richness, family richness, species evenness and species composition.

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초록 : 영도 절영산에서의 식물 집단 구조

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영도 절영산과 단절된 산림지 3곳에 대한 식물종, 목본류의 다양성 양상을 조사하기 위해 18 plot(12개 50×50 m plot와 6곳 10×100 m plots)를 설정하였다. 50×50 m plots에는 총 68종이 동정되고 목본류의 개체는 1562개였다. 최소 유의성 차이(LSD)에서 A지점(절영산)이 B지점(낮은 구릉지역)보다 높았다. Shannon-Wiener의 다양성 지수에서 세 지역간 유의한 차이가 있었다(F = 4.12, p<0.05). 곰솔-갈참나무군락이 대부분 지역에서 우점하였다. 절영산과 태종대 지역에서 곰솔군락이 다른 방향보다 NE방향에 잘 분포하였다. 천선과 나무-곰솔군락은 C지역의 남쪽 plot에 잘 분포하였다. 영도 절영산과 해안 지역에 대한 수목의 공간적 분포는 이질적이며 패치(patchy)구조를 나타내었다.