

Research Journal of Pharmaceutical, Biological and Chemical Sciences

Spatial Distribution Pattern of the Populations of *Pleurospermum camtschaticum* at Mt. Geomum and Mt. Ahop.

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ABSTRACT

The spatial distribution of plant populations is an important feature of population structure and it determines the population's ecological preferences. *Pleurospermum camtschaticum* Hoffmann is an herbaceous and has reputed Chinese medicinal value. It has been investigated the population density and spatial distribution of this species in Korea during 2014. The spatial pattern of *P. camtschaticum* was analyzed according to several patchiness indexes, population uniformity or aggregation under different sizes of plots by dispersion indices, and spatial autocorrelation. Most natural plots of *P. camtschaticum* were not uniformly distributed in the forest community. The small plots (2 m x 2 m, to 8 m x 16 m) of *P. camtschaticum* were uniformly distributed in the forest community and large plots (16 m x 16 m and 16 m x 32 m) were aggregately distributed. Significant aggregations by Moran's *I* of *P. camtschaticum* were partially observed within III classes (6 m). Dissimilarity among pairs of individuals could found by more than 12.0 m. In conclusion, the geographic distribution of *P. camtschaticum* is not even with varying degrees of size of plots and human activities give rise to density effects in the plots at both Mt. Geomum and Mt. Ahop in Korea.

Keywords: *Pleurospermum camtschaticum*, spatial distribution, patchiness indexes, Moran's.

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INTRODUCTION

Analysis of the spatial distribution pattern of a plant population is helpful to determine the population's ecological preferences, biological characteristics and relationships with environmental factors (Zhang *et al.*, 2012). Therefore, the analysis of the spatial distribution pattern of plant populations has always been a major focus for ecological research [1]. The spatial distribution pattern of plant populations exhibits scale dependence, e.g. a species may show an aggregated distribution at one spatial scale and may change to a random or uniform distribution at a different scale [2].

Many botanists, ecologists, and geographers alike have long been interested in studying plant distribution patterns as they provide insight into the processes that facilitate diversification and speciation in plants and the factors that lead to reproductive isolation between closely related plant populations. The investigation of spatial pattern has become a specialized area of study in plant ecology and an imposing array of methods has developed over the last 50 years [3].

Each plant community was considered as a discrete patch occupied by individuals of different species from a limited regional pool because all species were assumed to be in competition with each other. The spatial prediction of species distributions from survey data has recently been recognized as a significant component of conservation planning [4, 5]. Quantitative examination of spatially explicit data in ecology is broadly categorized as "spatial analysis" [6, 7]. The analysis of the spatial pattern of individuals of a particular species has long been a concern of ecologists [8].

Many ecologists have adopted several different major schools of spatial analysis from other disciplines [9]. The first of these comes from geography, and its methods include the use of statistics (e.g., Moran's *I*) to measure spatial autocorrelation [10]. It measures the extent to which the occurrence of an event in a real unit constrains, or makes more probable, the occurrence of an event in a neighboring areal unit.

Pleurospermum camtschaticum Hoffmann is an herbaceous and a member of the *Pleurospermum* genus in the family Umbelliferae. *P. camtschaticum* is a perennial growing to 1.5 m (5ft). It is in flower from Jun to July, and the seeds ripen from Jul to August. The flowers are hermaphrodite (have both male and female organs) and are pollinated by Insects. *P. camtschaticum* usually grows on stream banks in forests or mountain ravines. This species has reputed medicinal value. Chinese material previously recorded as *Pleurospermum austriacum* Linnaeus is referable to *Pleurospermum uralense* [11]. Methods that are commonly used to describe dispersion of *P. camtschaticum* populations are no reported similar researches. So, it is necessary to do this study in temperature region where this species is native to East Asia.

In this report, the several statistical tools of percentage distribution and population structure of the geographical areas are used to study the spatial distribution of *P. camtschaticum* in Busan. Mt. Geomum and Mt. Ahop locate in south of the Korean. A sample of a large (more than 300 individuals) natural population of *P. camtschaticum* collected at both mountains and was used in this study. It is expected to provide useful experimental conditions because of the large undisturbed and isolated site. The purpose of this paper was to describe a statistical analysis for detecting a species association, which is valid even when the assumption of within- species spatial randomness is violated. The purpose of this study is addressed: is there a spatial structure within four populations of *P. camtschaticum*? and 2) if so, what is the spatial pattern and is it the same for all populations?

MATERIALS AND METHODS

Study area

This study was carried out on two populations of *P. camtschaticum*, located at Mt. Ahop (346.5 m) (35°16'N/129°11'E) and Mt. Geomum (543 m) (35°17'N/129°10'E) respectively, at Busan-ci in Korea. Mt. Geomum and Mt. Ahop is about 20 km away. In this region the mean annual temperature is 14.7°C with the maximum temperature being 29.4°C in August and the minimum -0.6°C in January. Mean annual precipitation is about 1519.1 mm with most rain falling period between June and August.

Sampling procedure

55 quadrats in size at Mt. Geomum and 35 quadrats at Mt. Ahop were randomly chosen for each combination of site x habitat, so that, overall, 90 quadrats were sampled for the complete experiment. The number of events per unit area are counted and divided by area of each square to get a measure of the intensity of each quadrat. We randomly located quadrates in each plot which we established populations. The quadrat sizes were 2 m x 2 m, 2 m x 4 m, 4 m x 4 m, 4 m x 8 m, 8 m x 8 m, 8 m x 16 m, 16 m x 16 m, and 16 m x 32 m. We mapped all plants to estimate *P. camtschaticum* density per plot.

Index calculation and data analysis

The spatial pattern of *P. camtschaticum* was analyzed according to the Nearest Neighbor Rule [12, 13] with Microsoft Excel 2010.

Average viewing distance (r_A) was calculated as follows:

$$r_A = \sum_{i=1}^N r_i / N \quad (i = 1, 2, 3 \dots N)$$

Where r_i is the distance from the individual to its nearest neighbor. N is the total number of individuals within the quadrat.

The expectation value of mean distance of individuals within a quadrat (r_B) was calculated as follows:

$$r_B = 1/2\sqrt{D}$$

Where D is population density and D is the number of individuals per plot size.

$$R = r_A/r_B$$

When $R > 1$, it is a uniform distribution, $R = 1$, it is a random distribution, $R < 1$, it is an aggregated distribution. The significance index of the deviation of R that departs from the number of "1" is calculated from the following formula [13].

$$C_R = \frac{r_A - r_B}{\delta_{r_B}}$$

$$\delta_{r_B} = 0.2613/\sqrt{ND}$$

When $C_R > 1.96$, the level of the significance index of the deviation of R is 5%, and When $C_R > 2.58$, the level is 1%.

Many spatial dispersal parameters were calculated the degree of population aggregation under different sizes of plots by dispersion indices: index of clumping or the index of dispersion (C), aggregation index (CI), mean crowding (M^*), patchiness index (PAI), negative binominal distribution index K , Ca indicators (Ca is the name of one index) [9] and Morisita index (IM) were calculated with Microsoft Excel 2010. The formulae are as follows:

$$\text{Index of dispersion: } C = S^2/m$$

$$\text{Aggregation index } CI = \frac{S^2}{m} - 1$$

$$\text{Mean crowding } M^* = m + \frac{S^2}{m} - 1 = m + CI = m + C - 1 - 1$$

$$\text{Patchiness index } PAI = \frac{m}{\frac{S^2}{m} - 1} = \frac{M^*}{m}$$

$$\text{Aggregation intensity } PI = k = m^2 / (S^2 - m) = \frac{m}{CI} = \frac{m}{c-1}$$

$$\text{Ca indicators } Ca = 1/k$$

$$IM = \frac{n \sum m(m-1)}{nm(nm-1)}$$

Where S^2 is variance and m is mean density of *P. camtschaticum*.

When $C, M^*, PAI > 1$, it means aggregately distributed, when $C, M^*, PAI < 1$, it means uniformly distributed, when $CI, PA, Ca > 0$, it means aggregately distributed, and when $CI, PA, Ca < 0$ it means uniformly distributed.

The mean aggregation number to find the reason for the aggregation of *P. camtschaticum* was calculated [14].

$$\delta = mr/2k$$

Where r is the value of chi-square when $2k$ is the degree of freedom and k is the aggregation intensity.

Green index (GI) is a modification of the index of cluster size that is independent of n [15].

Spatial structure

When a plant population or community is sampled, the samples have a spatial relationship with each other. To a certain extent, samples that are close to each other are more likely to be similar. Numerical simulations of previous analyses were performed to investigate the significant differences at various distance scales, i.e., 1.0 m, 1.5 m, 2.0 m, and so on. However, no significant population structure was found within the 2.0 m distance classes by means of Moran's I , and a significant population structure was revealed beyond 2.0 m. Thus, the distance classes are 0-2.0 m (class I), 2.0-4.0 m (class II), 4.0-6.0 m (class III), 6.0-8.0 m (class IV), 8.0-10.0 m (class V), 10.0-12.0 m (class VI), 12.0-14.0 m (class VII), 14.0-16.0 m (class VIII), 16.0-18.0 m (class IX), and 18.0-20.0 m (class IX). The codes of classes are the same as in the distance classes and are listed Table 1.

The spatial structure was quantified by Moran's I , a coefficient of spatial autocorrelation (SA) [10]. As applied in this study, Moran's I quantifies the similarity of pairs of spatially adjacent individuals relative to the population sample as a whole. The value of I ranges between +1 (completely positive autocorrelation, i.e., paired individuals have identical values) and -1 (completely negative autocorrelation). Each plant was assigned a value depending on the presence or absence of a specific individual. If the i th plant was a homozygote for the individual of interest, the assigned p_i value was 1, while if the individual was absent, the value 0 was assigned [16].

Pairs of sampled individuals were classified according to the Euclidian distance, d_{ij} , so that class k included d_{ij} satisfying $k - 1 < d_{ij} < k + 1$, where k ranges from 1 to 10. The interval for each distance class was 1.5 m. Moran's I statistic for class k was calculated as follows:

$$I(k) = \frac{n \sum_i \sum_{j(i \neq j)} W_{ij} Z_i Z_j}{S \sum Z_i^2}$$

where Z_i is $p_i - p$ (p is the average of p_i); W_{ij} is 1 if the distance between the i th and j th plants is classified into class k ; otherwise, W_{ij} is 0; n is the number of all samples and S is the sum of $W_{ij} \{ \sum_i \sum_{j(i \neq j)} W_{ij} \}$ in class k . Under the randomization hypothesis, $I(k)$ has the expected value $u_1 = -1/(n - 1)$ for all k . Its variance, u_2 , has been given, for example, in Sokal and Oden [10]. Thus, if an individual is randomly distributed for class k , the normalized $I(k)$ for the standard normal deviation (SND) for the plant genotype, $g(k) = \{I(k) - u_1\} / u_2^{1/2}$, asymptotically has a standard normal distribution. Hence, SND $g(k)$ values exceeding 1.96, 2.58, and 3.27 are significant at the probability levels of 0.05, 0.01, and 0.001, respectively.

RESULTS

The spatial pattern of individuals

Population densities (D) at Mt. Geomum varied from 0.441 to 4.500, with a mean of 2.259 (Table 1). Population densities (D) at Mt. Ahop varied from 0.445 to 3.250, with a mean of 1.936. The mean D value of Mt. Geomum area (2.259) is higher than Mt. Ahop area (1.936). There was not shown significant difference between both mountain areas. The values (R) of spatial distance (the rate of observed distance-to-expected distance) among the nearest individuals were higher than 1 and the significant index of CR was > 2.58. If by this parameter, the small plots (2 m x 2 m, 2 m x 4 m, 4 m x 4 m, 4 m x 8 m, 8 m x 8 m, and 8 m x 16 m) of *P. camtschaticum* at Mt. Geomum were uniformly distributed in the forest community (Table 1). However, *P. camtschaticum* were aggregately distributed in two large plots (16 m x 16 m and 16 m x 32 m). *P. camtschaticum* at Mt. Ahop were aggregately distributed in three large plots (8 m x 16 m, 16 m x 16 m, and 16 m x 32 m).

Table 1: Spatial patterns of *Pleurospermum camtschaticum* individuals at different sampling quadrat sizes in Mt. Geomum and Mt. Ahop

Location	Quadrat size (m x m)	Density	R	CR	Distribution pattern
Mt. Geomum	2 x 2	4.500	2.430	11.612	Uniform
	2 x 4	4.250	2.369	15.271	Uniform
	4 x 4	3.063	2.263	16.920	Uniform
	4 x 8	2.281	2.350	22.078	Uniform
	8 x 8	1.594	1.325	6.283	Uniform
	8 x 16	1.156	1.134	3.085	Uniform
	16 x 16	0.789	0.995	-0.124	Aggregation
	16 x 32	0.441	0.967	-0.960	Aggregation
Mt. Ahop	2 x 2	3.250	1.591	5.763	Uniform
	2 x 4	3.125	1.558	5.342	Uniform
	4 x 4	2.500	1.281	3.397	Uniform
	4 x 8	2.781	1.111	2.007	Uniform
	8 x 8	1.516	1.323	6.089	Uniform
	8 x 16	1.164	0.997	-0.068	Aggregation
	16 x 16	0.703	0.666	-8.578	Aggregation
	16 x 32	0.445	0.405	-17.193	Aggregation

The degree of population aggregation

The values dispersion index (C) at Mt. Geomum and Mt. Ahop were lower than 1 except three large plots (8 m x 16 m, 16 m x 16 m, and 16 m x 32 m) (Table 2). Thus aggregation indices (CI) were negative at Mt. Geomum and Mt. Ahop, which indicate a uniform distribution. The mean crowding (M*) and patchiness index (PAI) showed positive values. In Mt. Geomum and Mt. Ahop, the three indices, C, M*, PAI were <1 and their values of PI and Ca except two plots were also shown smaller than zero, thus it means uniform distributed. In *P. camtschaticum*, the two indices, C, PAI were >1 and their values of PI and Ca except four small plots were also shown greater than zero, thus it means aggregately distributed. The most individuals of *P. camtschaticum* were clustered and the distribution pattern of the *P. camtschaticum* was quadrat-sampling dependent.

Morisita index (IM) is related to the patchiness index (PAI) and showed an overly steep slope at the plot 16 m x 16 m in Mt. Geomum and at the plot 16 m x 16 m in Mt. Ahop. When the area was smaller than 16 m x 16 m, the degree of aggregation increased significantly with increasing quadrat sizes, while the patchiness indices did not change from the plot 8 m x 16 m to 16 m x 32 m. Green indices varied between 0.0001 to 0.004 (Fig. 1).

The mean aggregation number (δ) analysis showed that the reasons for aggregation of *P. camtschaticum* differed in quadrats with different plot sizes (Fig. 2).

Table 2: Changes in gathering strength of *Pleurospermum camtschaticum* at different sampling quadrat sizes

Population	Quadrat size (m x m)	No. Quadrat	Aggregation indices						
			C	CI	M*	PAI	PI	Ca	IM
Mt. Geomum	2 x 2	15	0.632	-0.368	0.173	0.320	-1.471	-0.680	0.358
	2 x 4	12	0.563	-0.437	0.120	0.216	-1.275	-0.782	0.228
	4 x 4	10	0.549	-0.454	0.146	0.243	-1.320	-0.757	0.253
	4 x 8	8	0.548	-0.452	0.048	0.096	-1.106	-0.904	0.097
	8 x 8	6	0.819	-0.181	0.338	0.651	-2.865	-0.349	0.663
	8 x 16	4	1.090	0.090	0.613	1.173	5.786	0.173	1.188
	16 x 16	2	1.060	0.060	0.562	1.119	8.408	0.119	1.130
Mt. Ahop	16 x 32	1	1.097	0.097	0.709	1.158	6.311	0.158	1.167
	2 x 2	15	0.650	-0.350	0.169	0.325	-1.482	-0.675	0.382
	2 x 4	10	0.618	-0.382	0.077	1.167	-1.204	-0.833	0.183
	4 x 4	8	0.634	-0.366	0.075	0.107	-1.206	-0.829	0.182
	4 x 8	6	0.542	-0.458	0.005	0.011	-1.011	-0.989	0.011
	8 x 8	5	0.519	-0.481	0.017	0.034	-1.035	-0.966	0.035
	8 x 16	3	1.134	0.134	0.596	1.289	3.461	0.289	1.295
Mt. Ahop	16 x 16	2	1.015	0.015	0.623	1.025	40.769	0.029	1.027
	16 x 32	1	1.017	0.017	0.664	1.027	37.493	0.027	1.033

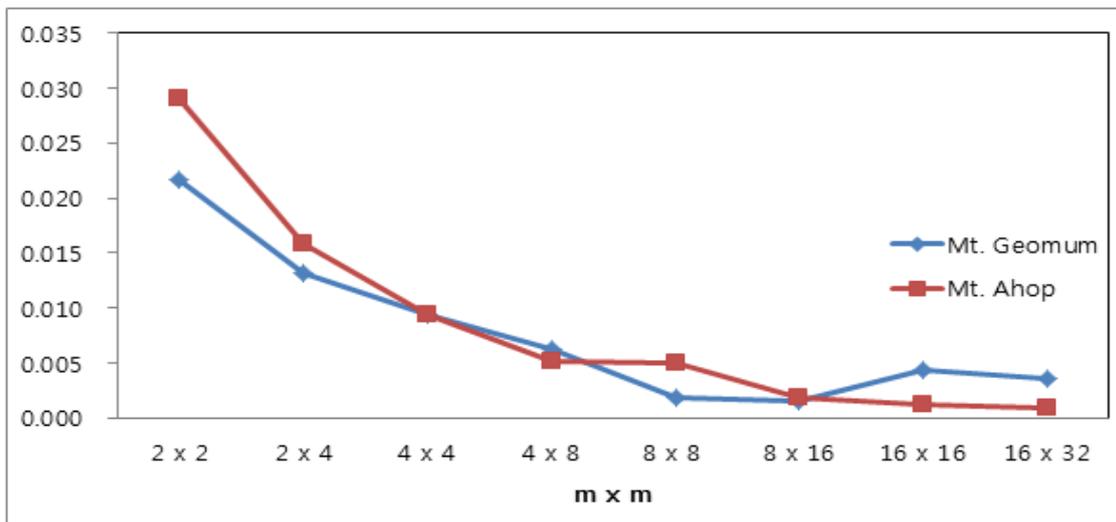


Figure 1: The curves of patchiness in two areas of *Pleurospermum camtschaticum* using values of Green index.

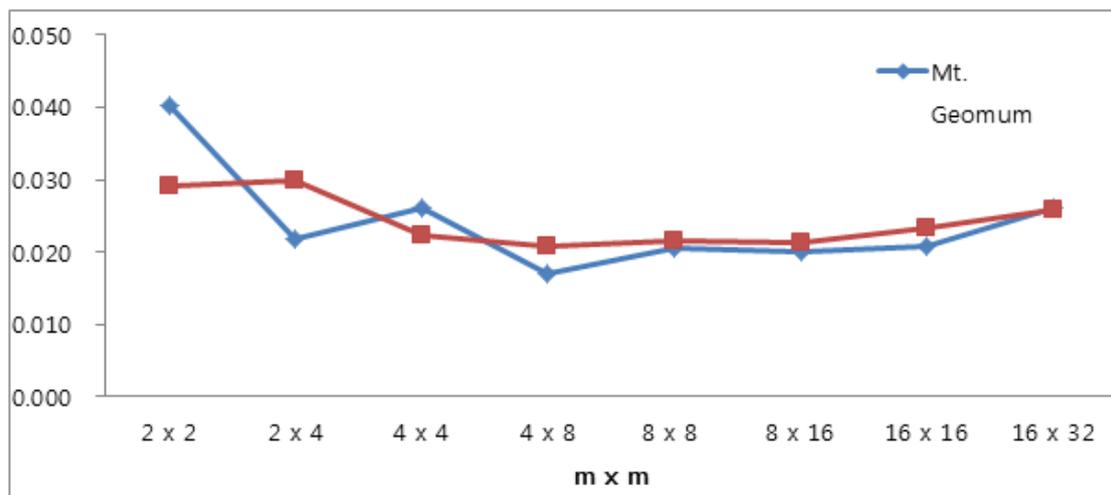


Figure 2: The changes in the mean aggregation numbers for two areas.

Analysis of spatial autocorrelation

The spatial autocoefficient, Moran's *I* is presented in Table 3. Separate counts for each type of joined individuals and for each distance class of separation were tested for significant deviation from random expectations by calculating the SND. Moran's *I* of *P. camtschaticum* significantly differed from the expected value in only 12 of 20 cases (30%). Five of these values (41.7%) were negative, indicating a partial dissimilarity among pairs of individuals in the 10 distance classes. Seven of the significant values (58.3%) were positive, indicating similarity among individuals in the first 3 distance classes, i.e., pairs of individuals can separate by more than 6.0 m. Namely, significant aggregations were partially observed within III classes. As a matter of course, the negative SND values at classes VI, VII, VIII, IX and X. Thus, dissimilarity among pairs of individuals could found by more than 12.0 m.

Table 3: Spatial autocorrelation coefficients (Moran's *I*) among two populations of *Pleurospermum camtschaticum* for ten distance classes

Population	I	II	III	IV	V	VI	VII	VIII	IX	X
Mt. Geomum	0.726***	0.783***	0.212*	0.207	0.181	-0.070	-0.157	-0.261*	-0.316*	-0.398**
Mt. Ahop	0.473**	0.388*	0.310*	0.195	0.222*	0.074	-0.044	-0.174	-0.338**	-0.453**

*: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$.

The comparison of Moran's *I* values to a logistic regression indicated that a highly significant percentage of individual dispersion in *P. camtschaticum* populations at Mt. Geomum and Mt. Ahop could be explained by isolation by distance.

DISCUSSION

When $R = 1$, it is a random distribution; $R < 1$, it is an aggregation; $R > 1$, it is a uniform distribution [13]. According to this rule, individuals within short distance plots of *P. camtschaticum* at Mt. Geomum and Mt. Ahop are uniform distribution (Table 1). However, According to dispersion indices of Lord [9], many plots are not uniform distribution (Table 2) and not consistent with the rule. $R = r_A / r_B$ [12]. N for r_A is total numbers of within the plot and r_B is concerned with plot size. Although, a large plot has large N , the plot size is not N . As D is the number of individuals per plot size, the nearest neighbor rule by Clark and Evans (1954) is good for spatial pattern. 11 plots (68.8%) among total 16 plots showed were uniform distributed (Table 1). In only 6 plots, the three indices, C , M^* , PAI were >1 , and PI and $Ca > 0$, thus it means aggregately distributed. Aggregation is mainly caused by the environmental factors [13]. When $\delta > 2$, the aggregation was mainly caused by both species characteristics and environmental factors [13]. All 16 plots had low $\delta < 2$. I recognized that the important environmental factors might be considered competition, growth rate, little decomposition, light, and below-ground resources. The characteristics of the *P. camtschaticum* concerned included primarily their life history, artificial disturbance, and population density. Life history theory seeks to understand the variation in traits such as growth rate, number and size of offspring and life span observed in nature, and to explain them as evolutionary adaptations to environmental conditions [17]. Artificial disturbances are important environmental factors affecting *P. camtschaticum* such as constitutional roads at east area, temple construction at west area, and farming at south area. At the plots which had fewer *P. camtschaticum*, the cluster was mainly determined by *P. camtschaticum* themselves.

One result of spatial autocorrelation is that statistical tests performed give more apparently significant results than the data actually justify because the number of truly independent observations is smaller than the number used in the test [6, 18]. A significant positive value of Moran's *I* indicated that pairs of individuals separated by distances that fell within distance class III had similar individuals, whereas a significant negative value indicated that they had dissimilar individuals (Table 3). The overall significance of individual correlograms was tested using Bonferroni's criteria. The results revealed that patchiness similarity was shared among individuals within up to a scale of a 4.0 m~6.0 m distance. Thus it was looked for the presence of dispersion correlations between neighbors at this scale.

The results from this study are consistent with the supposition that a plant population is subdivided into local demes, or neighborhoods of related individuals [4]. Previous reports on the local distribution of

genetic variability suggested that microenvironmental selection and limited gene flow are the main factors causing substructuring of alleles within a population [19].

In conclusion, *P. camtschaticum* populations within Mt. Geomum and Mt. Ahop were observed a strong spatial structure. Neighboring patches of *P. camtschaticum* are predominantly 4.0 m to 6.0 m apart on average. The present study demonstrates that a spatial structure of *P. camtschaticum* in the Mt. Geomum and Mt. Ahop populations could be explained by isolation by distance, limited gene flow, and topography. However, if the natural populations were disturbed by human activities, the aggregation was occurred in more short distance than a scale of a 4.0 m~6.0 m distance. The results of this study were used as systematic conservation planning which is an effective way to seek and identify efficient and effective types of reserve design to capture or sustain the highest priority biodiversity values and to work with communities in support of local ecosystems. Conservation biology is an objective science when biologists advocate for an inherent value in nature.

ACKNOWLEDGEMENT

This work was supported by Dong-eui University Foundation Grant (2013AA074)

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