

Spatial Distribution Patterns and Population Structure of *Doellingeria scabra* at Mt. Maebong in Korea

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Doellingeria scabra Thunb. (syn. *Aster scaber* Thunb.), a perennial herb in the family Asteraceae, is frequently found in the wild mountain regions of Korea. This aim of this work was to measure the characteristics of patchiness of *D. scabra* in a local population on Mt. Maebong in Taebaek-ci, Gangwon-do. The spatial distribution pattern of this species was estimated by analyzing ecological data by methods including the index of dispersion, Lloyd's mean crowding, and Morisita's index. The mean population density of the *D. scabra* population was 2.94. The *D. scabra* individuals were uniformly or randomly distributed in small-scale plots and were aggregately distributed in two large-scale plots (16×32 m² and 32×32 m²). The mean crowding (M^*) was 0.916. The mean patchiness index (PAI) was 0.796. Morisita's coefficient tended to decrease the density of the population as the plot size increased. The expected value of Eberhardt's index (I_E) in the local population was 2.623. Moran's I of *D. scabra* significantly differed from the expected value in 6 of 8 cases (75.0%). The first five classes were positive, with four showing statistical significance, indicating similarity among individuals in the first four distance classes (I - IV, 8 m). The results presented here could provide a theoretical basis for the conservation of *D. scabra* (Korean: *chamchwi*) and for the rehabilitation and sustainable management of forest ecosystems on Mt. Maebong, as well as on other mountains.

Key words : *Doellingeria scabra*, mean crowding, Mt. Maebong, patchiness index, spatial distribution

Introduction

The distribution pattern of plant individuals in space as an outcome of possible regulatory mechanisms involved within the community, has attracted the attention of numerous workers [8, 10]. Pattern in a population can be defined as a quantitative description of the horizontal distribution of individuals of a species within a community [23]. How can we measure dispersion in populations? Spatial statistics provides the quantitative description of natural variables distributed in space and time and now it is the most rapidly growing field in ecology [8, 22]. A typical approach again involves quadrat sampling. By counting the number of individuals within each sampling plot, we can see how the density of individuals changes from one part of the habitat to another. The spatial distribution pattern of plant pop-

ulations 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 [28].

There are three major components in any framework for statistical modelling in plant ecology [2]. There needs to be an ecological model, a data model, and a statistical model. The ecological model consists of the ecological knowledge and theory to be used or tested in the study. The data model consists of the decisions made regarding how the data are collected and how the data will be measured or estimated. The statistical model involves the choice of statistical method, error function and significance tests.

Doellingeria scabra (syn. *Aster scaber* Thunb.) is a perennial herb in the family Asteraceae from Eurasia which includes eastern Russia, China, Japan, and Korea. It is frequently found in wild mountain regions of Korea. It is known for its distinctive fragrance and taste, and is frequently used in Korean cuisine. Known among locals for its medicinal use, studies show it contains many beneficial compounds. Its Korean name is *chamchwi* (true *chwi*), and it is often simply referred to as *chwinamul* by the Korean locals [3].

Ultra high performance liquid chromatography (UHPLC)

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analysis of the leaf extract revealed that myricetin (4850.45 $\mu\text{g/g}$) was the most dominant flavonols, compared to quercetin and kaempferol [27]. Caffeic acid was the dominant phenolic compound in *D. scabra* leaf extracts, it constituted about 104.20 $\mu\text{g/g}$, followed by gentisic acid (84.50 $\mu\text{g/g}$), gallic acid (61.05 $\mu\text{g/g}$) and homogentisic acid (55.65 $\mu\text{g/g}$) [27].

Here we studied a spatial analysis of *D. scabra* communities subjected to interpecific aggregation and interaction strength. The present study used the point pattern analysis method to investigate the variation in the spatial distribution pattern of *D. scabra* at different spatial scales and spatial autocorrelation at different plots in a $16 \times 32 \text{ m}^2$ spatial scales at the Mountain Maebong in Korea.

Materials and Methods

Surveyed regions

This study was carried out on the populations of *D. scabra*, located at Mt. Maebong (1,303 m) ($37^{\circ}07'30''\text{N}/128^{\circ}34'30''\text{E}$) in Taebaek-ci, Gangwon-do Province in Korea. The elevation of community of *D. scabra* ranges from 500 to 650 m. The site is characterized by a temperate climate with a little hot in summer and cold winter. Mean annual temperature ranges from -9.7°C (January) to 25.5°C (August) with 8.7°C , and mean annual precipitation ranges from 19.2 (December) to 287.3 mm (August) with 1324.3 mm.

Sampling procedure

In May 2018 *D. scabra* plants with a meta-population ready were selected with the aim of studying their spatial distribution. Total 84 quadrats were sampled for the complete experiment at Mt. Maebong. Spatial ecologists use artificial sampling units (so-called quadrats) to determine abundance or density of species. 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 was established in demes of *D. scabra*. Numerical simulations of previous analyses and spatial autocorrelation (SA) were performed to investigate the significant differences at various distance scales, i.e., 1.0 m, 1.5 m, 2.0 m, 2.5 m and so on. However, no significant population structure was found within the 2.0 m distance. Thus, the quadrat sizes were $2 \times 2 \text{ m}^2$, $2 \times 4 \text{ m}^2$, $4 \times 4 \text{ m}^2$, $4 \times 8 \text{ m}^2$, $8 \times 8 \text{ m}^2$, $8 \times 16 \text{ m}^2$, $16 \times 16 \text{ m}^2$, and $16 \times 32 \text{ m}^2$.

Index calculation and data analysis

The distance from an individual to its nearest neighbor,

irrespective of direction, provides the basis for this measure of spacing. The spatial pattern of *D. scabra* was analyzed according to the Nearest Neighbor Rule [4].

Average viewing distance (γ_A) was calculated as follows:

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

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

The expectation value of mean distance of individuals within a quadrat (γ_B) was calculated as follows: $r_B = 1/2\sqrt{D}$

Where D is population density and the number of individuals per plot size. The mean of all those quadrat counts yields the population density, expressed in numbers of individuals per quadrat area.

$$R = \gamma_A / \gamma_B$$

The significance index of the deviation of R that departs from the number of "1" is calculated from the following formula [15].

$$C_R = \frac{r_A - r_B}{\delta_{rB}} \quad \delta_{rB} = 0.2613 / \sqrt{ND}$$

One test for spatial pattern and associated index of dispersion that can be used on random-point-to-nearest-organism distances was suggested by Eberhardt [7] and analyzed further by Hines and Hines [13]: $I_E = (s/m)^2 + 1$

Where I_E = Eberhardt's index of dispersion for point-to-organism distances, s = observed standard deviation of distances, m = mean of point-to-organism distances. 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). Dispersion of a population can be classified through a calculation of the variance mean ratio [19].

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

When $C = 1$ is random dispersion, <1 regular and >1 aggregated. Departure from a random distribution can be tested by calculating the index of dispersion (ID), where n denotes the number of samples:

$$ID = (n-1)s^2/m$$

ID is approximately distributed as χ^2 with $n-1$ degrees of freedom. Values of ID which fall outside a confidence interval bounded with $n-1$ degrees of freedom and selected probability levels of 0.95 and 0.05, for instance, would indicate a significant departure from a random distribution. This index can be tested by Z value as follows:

$$Z = \sqrt{2ID} - \sqrt{(2v-1)}, v = n-1$$

If $1.96 \geq Z \geq -1.96$, the spatial distribution would be random but if $Z < -1.96$ or $Z > 1.96$, it would be uniform and aggregated, respectively [20].

Mean crowding (M^*), patchiness index (PAI), negative binomial distribution index K , Ca indicators (Ca is the name of one index) [17] and Morisita index (IM) were calculated with Microsoft Excel 2014. The formulae are as follows:

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

Mean crowding

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

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

Aggregation intensity

$$PI = k = \frac{m^2}{(S^2 - m)} = \frac{m}{CI} = \frac{m}{C-1}$$

Ca indicators $Ca = 1/k$

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

Where S^2 is variance and m is mean density of plants.

The mean aggregation number to find the reason for the aggregation of *D. scabra* was calculated [1].

$$\delta = mr/2k$$

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 [11].

Spatial autocorrelation

When a plant population or community is sampled, the samples have a spatial relationship with each other. The concepts of autocorrelation and auto-covariance are derived from the familiar statistical concepts of covariance and

correlation. For two variables, x and y , their covariance is related to the expected value of their product: $Cov(x, y) = E(x - E(x)) \times E(y - E(y)) = E(xy) - E(x) \times E(y)$.

Their correlation is: $\rho(x, y) = Cov(x, y) / \sqrt{Var(x)Var(y)}$.

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), and 14.0-16.0 m (class VIII). 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) [24]. 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 [25].

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 3.0 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 [9]. Thus, if an individual is randomly distributed for class k , the normalized $I(k)$ for

Table 1. Spatial patterns of *Doellingeria scabra* individuals at different sampling quadrat sizes in Mt. Maebong

Quadrat size (m×m)	Density	R	CR	I_E	Distribution pattern
2×2	9.750	2.329	15.876	3.704	Uniform
2×4	6.001	2.520	20.150	2.216	Uniform
4×4	2.563	2.092	13.379	2.559	Uniform
4×8	1.938	1.870	13.110	2.499	Uniform
8×8	1.469	2.028	19.067	2.505	Uniform
8×16	0.930	1.596	12.432	2.513	Uniform
16×16	0.543	0.985	-0.339	2.468	Aggregated
16×32	0.350	0.960	-1.032	2.519	Aggregated
Mean	2.943	1.798	11.580	2.623	-

Table 2. Changes in gathering strength of *Doellingeria scabra* at different sampling quadrat sizes

Quadrat size (m×m)	Aggregation or dispersion indices				Distribution pattern
	C	ID	Z	PI	
2×2	0.649	24.667	-1.636	-1.073	Uniform
2×4	0.641	30.148	-1.879	-1.417	Uniform
4×4	0.988	39.503	0.004	-51.949	Uniform
4×8	0.992	60.532	0.003	-85.246	Uniform
8×8	1.259	117.104	1.702	3.228	Uniform
8×16	1.271	149.944	1.988	2.899	Aggregation
16×16	1.250	172.458	1.990	2.664	Aggregation
16×32	1.290	229.693	2.592	2.926	Aggregation
Mean	1.043	103.006	0.560	-15.996	-

the standard normal deviation (SND) for the plant genotype, $g(k) = \{I(k) - u\} / u^{1/2}$, asymptotically has a standard normal distribution [5]. 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 optimum sample size is the smallest number of sample units that would satisfy the objectives of the sampling program and achieve the desired precision of estimates. Each type of joined individuals and for each distance class of separation were tested for significant deviation from random expectations by calculating the standard normal deviation. No significant population structure of *D. scabra* was found within the 2.0 m quadrat sizes. Population densities (D) of *D. scabra* populations at Mt. Maebong varied from 0.35 to 2.97, with a mean of 2.94 (Table 1). Small quadrat sizes such as 2×2 m², 2×4 m², and 4×4 m² have relatively high D values (>2), whereas larger or wider quadrat sizes such as 8×16 m², 16×16 m², and 16×32 m² have, comparatively, very low D values (<1). 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 six scale plots (2×2 m², 2×4 m², 4×4 m², 4×8 m², 8×8 m², and 8×16 m²) of *D. scabra* at Mt. Maebong were uniformly distributed in the forest community. However, *D. scabra* was aggregately distributed in two large scale plots (16×32 m² and 32×32 m²). Eberhardt's index of dispersion for point-to-organism distances (I_E) varied from 2.216 (2×4 m) to 3.704 (2×2 m²), with a mean of 2.623.

The values dispersion index (C) of *D. scabra* at Mt. Maebong were lower at four scale plots (2×2 m², 2×4 m², 4×4 m², and 4×8 m²) than 1 except four large scale plots

(8×8 m², 8×16 m², 16×16 m², and 16×32 m²) (Table 2). Departure from a random distribution can be tested by calculating the index of dispersion (ID). In this Model, values of ID ranged from 24.67 to 229.69. Large scale plots were considerably greater than those of small scale plots, indicating that large scales plots tend to be aggregated. This ID index can be tested by Z value. If $1.96 \geq Z \geq -1.96$, the spatial distribution would be random. Thus, the six scale plots (2×2 m², 2×4 m², 4×4 m², 4×8 m², 8×8 m², and 8×16 m²) of *D. scabra* at Mt. Maebong were random distributed in the forest community. Two large plots (16×16 m² and 16×32 m²) were aggregated ($Z > 1.96$). Aggregation intensity (PI) ranged from -85.246 to 3.228 and it was not strong.

The mean crowding (M^*) was 0.92 (Table 3). The mean patchiness index (PAI) was 0.796. Both were showed positive values for all plots. The mean Morisita index (IM) was 0.82. The values of δ were showed an overly steep slope at the plot 4×4 m² (Fig. 1). The values of Morisita's coefficient showed a tendency to decrease as the plot size increased (Fig. 2).

The spatial auto coefficient, Moran's I is presented in Table 4. Separate counts for each type of joined individuals

Table 3. Clouding or patchiness indices of *Doellingeria scabra* at different sampling quadrat sizes

Quadrat size (m×m)	No. Quadrat	Clouding or patchiness indices		
		M^*	PAI	IM
2×2	32	0.026	0.068	0.073
2×4	16	0.150	0.294	0.307
4×4	12	0.633	0.981	1.019
4×8	8	1.007	0.007	1.021
8×8	6	0.647	0.988	0.999
8×16	4	1.096	1.310	1.327
16×16	4	1.056	1.345	1.359
16×32	2	0.916	1.376	0.480
Mean	10.5	0.691	0.796	0.823

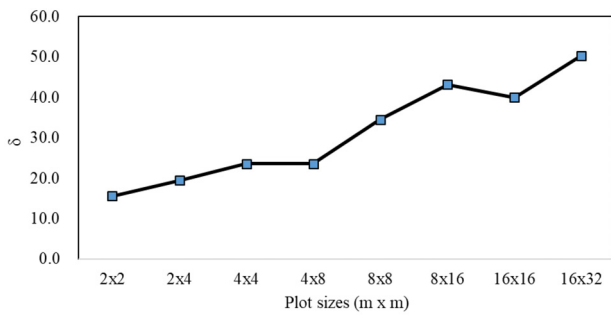


Fig. 1. The mean aggregation number to find the reason for the aggregation of *Doellingeria scabra*.

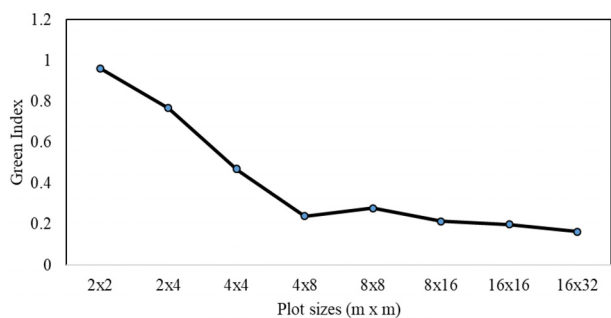


Fig. 2. The curves of patchiness in two areas of *Doellingeria scabra* using values of Green index.

and for each distance class of separation were tested for significant deviation from random expectations by calculating the SND. Moran's *I* of *D. scabra* significantly differed from the expected value in 6 of 8 cases (75.0%). The first five classes were positive. Four of them showed significance, indicating similarity among individuals in the first four distance classes (I-IV), i.e., pairs of individuals can separate by more than 8.0 m. Three of these values (37.5%) were negative, indicating a partial dissimilarity among pairs of individuals at the VI distance class scales (10-12 m).

Discussion

Thus, two large plots (16x16 m² and 16x32 m²) of *D. scabra* at Mt. Maebong were clustered based on the Nearest Neighbor Rule (Table 1). The result of one plot (8x16 m²) in Table 2 was inconsistent with the previous results (Nearest Neighbor Rule). One of the reasons is in uneven

collection and distribution pattern of the *D. scabra* was quadrat-sampling dependent. As Morisita's coefficient estimates spatial distribution pattern using the mean and variance of each sampling date separately, so this index is more perfect than dispersion index [19]. The detailed knowledge of dispersion in different time intervals during growing season would be useful for research strategies more than management programs.

The comparison of Moran's *I* values to a logistic regression indicated that a highly significant percentage of individual dispersion in *D. scabra* populations at Mt. Maebong could be explained by isolation by distance (Table 4).

The expected value of *I_E* in a random population is 2.62 (Table 1). *I_E* values for all quadrates are larger than 1.27. Under the hypothesis, *D. scabra* is clumping. Clumped dispersion is often due to an uneven distribution of nutrients or other resources in the environment. Species interactions can be intra- or interspecific. The former is usually negative due to conspecific competition for the same resources [14], while the latter can be negative (interspecific competition), positive (facilitation) or neutral.

Although positive interspecific interactions are not rare, the positive interaction often occurs because one species ameliorates a physical, physiological or trophic stress that otherwise compromises the fitness of a resource exploiter [16]. Also during extreme events which drive much of the gap formation in plant communities, species interactions take place and more importantly influence the survival of individuals [26]. In a high density plots, interspecies competition is maintained within a certain distance (Table 1). However, in less dense plots, *D. scabra* could co-aggregate with each other to compete with other species.

*M** was proposed by Lloyd to indicate the possible effect of mutual interference or competition among individuals [19]. As an index, mean crowding is highly dependent upon both the degree of clumping and population density. Patch-based measures of pattern include size, number, and density of patches [12]. Useful edge information may include perimeter of individual patches, total perimeter of all patches of a particular class, the frequency of specific patch adjacencies, and various edge metric that incorporate the contrast (degree

Table 4. Spatial autocorrelation coefficients (Moran's *I*) among plots of *Doellingeria scabra* for eight distance classes

I	II	III	IV	V	VI	VII	VIII
0.486***	0.403***	0.292*	0.274*	0.113	-0.053	-0.166*	-0.234**

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

of dissimilarity) between the patch and its neighbors. However, different spatial patterns may also reflect differential abilities of species to survive intra and interspecific competition during succession [9]. The effects of density-dependent mortality may be revealed by comparing the change in spatial pattern of different life-history stages [18, 21].

Conclusion, M^* and PAI showed positive values for all plots. When the three indices C , M^* , PAI were <1 and their values of PI were also shown smaller than zero, it means uniform distributed. In *D. scabra*, the two indices, C , PAI were >1 and their values of PI were also shown greater than zero, thus it means aggregately distributed. In many near neighbor plants of *D. scabra* at Mt. Maebong, density between neighboring individuals was high and similarity was high. Whereas, two large plots ($16 \times 16 \text{ m}^2$ and $16 \times 32 \text{ m}^2$) of *D. scabra* were clustered each other and aggregation. This plant is distributed in low mountains and is easy to collect. The genetic resources can be secured by preserving the sizes of the effective group of this plant. According to the results of this study, the size of the *D. scabra* population should be at least $8 \times 8 \text{ m}^2$.

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초록 : 한국 매봉산 참취의 공간적 분포 양상과 집단 구조

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참취, *Doellingeria scabra* Thunb. (이전의 학명: *Aster scaber* Thunb.)는 국화과의 다년생 초본으로 한국의 야생 산지에서 흔히 찾을 수 있다. 본 연구는 강원도 태백시 매봉산에 분포하는 참취의 국지적 집단에 대해 패치 특성을 측정하고자 하였다. 이 종의 공간적 분포를 평가하기 위해 분산의 지수, Lloyd 평균 군집도, Morisita 지수 등을 통해 자료를 분석했다. 참취 집단의 평균 밀도는 2.94이었다. 참취는 작은 규모의 플롯에서는 일정한 분포 또는 임의 분포를 하였고, 두 개의 큰 규모 플롯(16×32 m²와 32×32 m²)에서는 응집 형태로 분포했다. 평균 밀집도(M*)는 0.916이었다. 평균 patchiness index (PAI)는 0.796이었다. Morisita의 계수는 플롯 크기가 커짐에 따라 감소하는 경향을 보였다. 이 집단에서 Eberhardt 지수(IE)의 예상 값은 2.623이었다. 참취의 Moran's I 값에서 처음 5개 구간은 양의 값이었다. 그 중 4개는 유의성을 나타내어 개체간 유사성은 8 m 이내에서 발생한다고 볼 수 있다. 본 연구는 매봉의 참취군락뿐만 아니라 다른 산의 산림 생태계 내 참취 군락의 지속 가능한 유지 및 복원에 대한 이론적 근거를 제공할 수 있다.