

Spatial Distribution Pattern of the Populations of *Camellia japonica* in Busan

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The spatial distribution of geographical distances at five natural populations of *Camellia japonica* in Busan, Korea was studied. The four plots (Mollundae, Gadeok-do, Du-do, and Jwiseum) of *C. japonica* were uniformly distributed in the forest community and only one plot (Amnam-dong) was aggregatedly distributed in the forest community. Morisita index is related to the patchiness index showed that the plot 20 m × 50 m had an overly steep slope when the area was larger than 20 m × 20 m, which indicated that the degree of aggregation increased significantly with increasing quadrat sizes, while the patchiness indices did not change from the plot 5 m × 10 m to 10 m × 10 m. The spatial structure was quantified by Moran's *I*, a coefficient of spatial autocorrelation. Ten of the significant values (76.9%) were positive, indicating similarity among individuals in the first 4 distance classes (80 m), i.e., pairs of individuals with dissimilarity characteristics can separate by more than 100 m.

Key words : Moran's *I*, patchiness index, quadrat, spatial distribution

Introduction

In recent decades, there was much increase in the statistical tools used in spatial ecology [13]. Botanists, ecologists, geographers and plant evolutionary biologists have long recognized that plants are not distributed at random within communities but are rather clustered in distinct patches [8, 20]. Environmental heterogeneity is usually cited as playing a critical role in determining the spatial structure, but colonization patterns and stochastic events affecting establishment and mortality are also important [18]. More recently, plant evolutionary biologists have demonstrated that genetic variations in plant populations are also nonrandomly distributed [6]. This nonrandom distribution of genetic variation is often referred to as the genetic structure of a population [9]. The genetic structure is an integral part of the process of population genetics [5]. Population structure interacts with a number of factors: microenvironmental heterogeneity, mortality due to stochastic events [19], and mating systems that feature limited dispersal of seed or pollen [5].

Of the several methods of describing the spatial distribution of plant community the simplest way is percentage distribution of individuals over the geographical areas. Another methodology usually adopted is to list the geographical areas of a given class into rank order which enables comparison of ranking from individual to individual. 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 *Camellia japonica* in Busan.

In theory, genetic differentiation over short distances may occur either as a result of spatially variable selection or localized genetic drift, provided that gene flow is sufficiently restricted [14]. Indirect evidence for genetic correlations between neighboring plants has been obtained from data on mating systems [5]. Localized seed and pollen dispersals produce family clusters within these populations [7]. Several studies have revealed decreased seed set and seed survivorship from mating between genetically similar near-neighbors, which has been interpreted as inbreeding depression [10].

In the wild, *C. japonica* is found in mainland China (Shandong, east Zhejiang), Taiwan, southern Korea and southern Japan. *C. japonica* is sometimes called the rose of winter, it belongs to the Theaceae family. An edible oil is obtained from the seeds of this species. The leaves are a tea substitute. The dried flowers used as a vegetable or mixed

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with gelatinous-rice to make a Japanese food called 'mochi'.

Saha-gu and Gangseo-gu locate in south of the Korean, and at the western part of the North Pacific Ocean. A sample of a large (more than 300 individuals) natural population of wild species *C. japonica* collected at Saha-gu and Gangseo-gu in Korea was used in this study.

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 to find if there a spatial structure within four populations of *C. japonica* and 2) if so, what is the spatial pattern and if it is the same for all populations?

Materials and Methods

Study area

We conducted the spatial analysis in the communities of *Camellia japonica* at Saha-gu and Gangseo-gu in Busan-si (Fig. 1). This area is on the southern margin of Busan. It has a temperate climate with a little hot and long summer. 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

We established nine plots with an area of 20 m × 160 m

each around four populations at Saha-gu and one population at Gangseo-gu in Busan, 2014. We randomly located quadrates in each plot which we established populations. The quadrat sizes were 5 m × 5 m, 5 m × 10 m, 10 m × 10 m, 10 m × 20 m, 20 m × 20 m, and 20 m × 50 m. We mapped all plants to estimate population density.

Index calculation and data analysis

The spatial pattern of *C. japonica* was analyzed according to the Nearest Neighbor Rule [3, 11] 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 for-

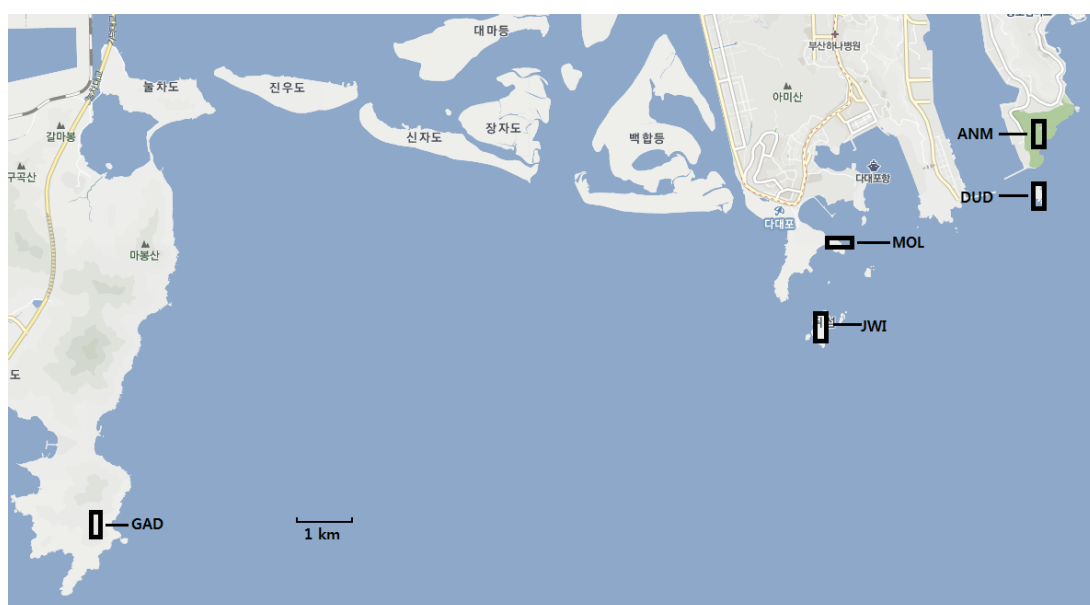


Fig. 1. The five studied populations of *Camellia japonica* in Busan, Korea. ANM: Annam-dong, DUD: Du-dong, JWI: Jwiseum, GAD: Gadeok-do

mula [11].

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

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

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%.

We 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 binomial distribution index K, Ca indicators (Ca is the name of one index) [12] and Morisita index (IM) were calculated with Microsoft Excel 2010. The formulae are as follows:

Index of dispersion: $C = S^2/m$

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

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

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

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

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 *C. japonica*

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.

We used the mean aggregation number to find the reason for the aggregation of *C. japonica* [1].

$$\delta = mr/2k$$

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

Spatial structure

Numerical simulations of previous analyses were performed to investigate the significant differences at various distance scales, i.e., 10.0, 20.0 m, and so on. However, no significant population structure was found within the 20.0 m distance classes by means of Moran's I, and a significant population structure was revealed beyond 20.0-m. Thus, the

Table 1. Spatial patterns of *Camellia japonica* individuals at five populations in Busan

Population	Density	R	C_R	Distribution pattern
Mollundae	0.087	1.605	0.129	Uniform
Gadeok-do	0.190	1.600	5.217	Uniform
Amnam-dong	0.155	0.880	-1.453	Aggregation
Du-do	0.115	2.180	7.217	Uniform
Jwiseum	0.104	1.400	3.748	Uniform
Mean	0.130	1.533	2.972	Uniform

R and C_R were shown in text.

distance classes are 0-20.0 m (class I), 20.0-40.0 m (class II), 40.0-60.0 m (class III), 60.0-80.0 m (class IV), 80.0-100.0 m (class V), 100.0-120.0 m (class VI), 120.0-140.0 m (class VII), and 140.0-160.0 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) [15, 16]. 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 pi value was 1, while if the individual was absent, the value 0 was assigned.

Pairs of sampled individuals were classified according to the Euclidian distance, dij, so that class k included dij satisfying $k - 1 < dij < k + 1$, where k ranges from 1 to 7. The interval for each distance class was 20 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); 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 (1978a). 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 [3]. 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) varied from 0.097 to 0.190, with a mean of 0.130 (Table 1). The values of spatial distance (the rete of observed distance-to-expected distance) among the nearest individuals were higher than 1 but Amnam-dong was lower than 1. The four plots (Mollundae, Gadeok-do, Du-do, and Jwiseum) of *C. japonica* were uniformly distributed in the forest community and only one plot (Amnam-dong) was aggregately distributed in the forest community (Table 1).

The degree of population aggregation

Dispersion index (C) were higher than 1 except for three quadrats (5 m × 5 m, 5 m × 10 m, and 10 m × 10 m) of Amnam-dong (Table 2). As the sizes of quadrat were greater,

the values of *C. japonica* were high. Thus aggregation indices were positive except for plots which indicate a clumped distribution. The values of PI and Ca were shown greater than zero. The values of PAI except three quadrats of Amnam-dong were greater than 1 (Table 2). Thus, the most individuals of *C. japonica* were clustered and the distribution pattern of the *C. japonica* was quadrat-sampling dependent. When the sampling quadrat in Amnam-dong was smaller than 10 m × 10 m, *C. japonica* were aggregately distributed, and when the sampling quadrat was greater than 10 m × 10 m, the aggregation index showed the trend of being uniformly distributed for *C. japonica*. The mean crowding (M^*) and aggregation intensity (Ca) indicator were higher with a big quadrat.

Morisita index (IM) related to the patchiness index (PAI) showed that the plot 20 m × 50 m had an overly steep slope when the area was larger than 20 m × 20 m, which indicated

Table 2. Changes in gathering strength of *Camellia japonica* at different sampling quadrat sizes

Location	Quadrat size (m × m)	Sample size	Aggregation indices						
			C	CI	M^*	PAI	PI	Ca	IM
Mollundae	5 × 5	12	1.225	0.225	4.781	1.049	0.781	1.281	1.076
	5 × 10	10	1.090	0.090	5.790	1.016	0.989	1.012	1.034
	10 × 10	8	1.056	0.056	13.181	1.004	0.963	1.039	1.014
	10 × 20	7	2.437	1.437	28.723	1.053	0.170	5.901	1.058
	20 × 20	5	3.310	2.310	53.110	1.046	0.091	10.938	1.050
	20 × 50	3	5.391	4.391	81.724	1.057	0.034	29.048	1.061
Gadeok-do	5 × 5	10	1.520	0.520	5.520	1.104	0.474	2.110	1.127
	5 × 10	10	1.429	0.429	5.529	1.084	0.541	1.847	1.106
	10 × 10	8	1.663	0.663	16.288	1.042	0.370	2.702	1.051
	10 × 20	6	1.743	0.743	32.243	1.024	0.333	3.008	1.029
	20 × 20	4	2.667	1.667	54.417	1.032	0.141	7.094	1.037
	20 × 50	3	4.421	3.421	91.980	1.001	0.256	3.910	1.015
Amnam-dong	5 × 5	12	0.574	-0.427	3.624	12.204	0.985	0.082	0.917
	5 × 10	10	0.683	-0.317	5.483	0.945	3.404	0.294	1.049
	10 × 10	8	0.958	-0.042	15.333	0.997	1.172	0.853	1.006
	10 × 20	6	2.132	1.132	40.798	1.029	0.221	4.519	1.033
	20 × 20	4	2.304	1.304	54.554	1.025	0.189	5.289	1.029
	20 × 50	2	3.818	2.818	87.818	1.033	0.089	14.563	1.036
Du-do	5 × 5	12	1.067	0.067	3.400	1.020	1.194	0.838	1.055
	5 × 10	10	1.505	0.505	8.405	1.034	0.468	2.139	1.078
	10 × 10	8	2.758	1.758	18.258	1.107	0.133	7.544	1.115
	10 × 20	6	2.389	1.389	31.056	1.047	0.176	5.676	1.053
	20 × 20	4	2.527	1.527	57.027	1.028	0.157	6.368	1.032
	20 × 50	2	4.466	3.466	86.466	1.042	0.050	19.932	1.046
Jwiseum	5 × 5	12	1.096	0.096	3.459	1.028	1.107	0.904	1.057
	5 × 10	10	1.168	0.168	7.568	1.023	1.228	0.814	1.037
	10 × 10	8	1.211	0.211	14.336	1.015	0.716	1.396	1.024
	10 × 20	6	1.952	0.952	28.095	1.035	0.265	3.773	1.041
	20 × 20	4	2.949	1.949	50.149	1.040	0.115	8.678	1.049
	20 × 50	2	4.642	3.642	82.975	1.050	0.046	21.531	1.050

Aggregation indices were shown in text.

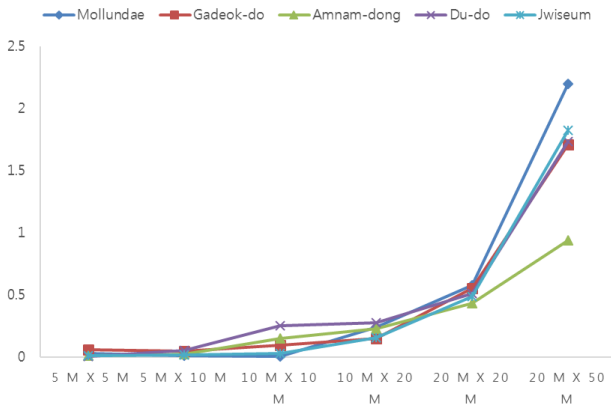


Fig. 2. The curves of patchiness in four populations of *Camellia japonica* using values of Green index.

that the degree of aggregation increased significantly with increasing quadrat sizes, while the patchiness indices did not change from the plot 5 m × 10 m to 10 m × 10 m (Fig. 2).

The mean aggregation number analysis showed that the reasons for aggregation of *C. japonica* differed in quadrats with different plot sizes (Table 3). The cluster at 5 m × 5 m quadrat was determined by environmental factors. When the sizes were greater than 10 m × 10 m quadrat, the clusters were determined by both species characteristics and environmental factors.

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 *C. japonica* significantly differed from the expected value in only 13 of 35 cases (37.1%). Thirteen of these values (37.1%) were negative, indicating a partial dissimilarity among pairs of individuals in the seven distance classes. Ten of the significant values (76.9%) were positive, indicating similarity among individuals in the first four distance classes, i.e., pairs of individuals can separate by

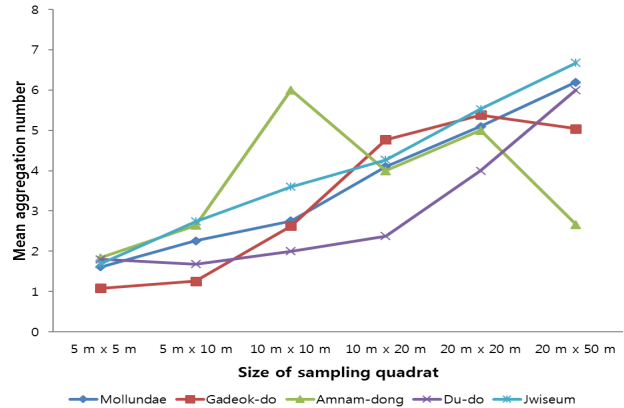


Fig. 3. The changes in the mean aggregation numbers for five populations.

more than 100 m. Namely, significant aggregations were partially observed within IV classes. As a matter of course, the negative SND values at classes IV, V, and VI. Thus, dissimilarity among pairs of individuals could be found by more than 100 m.

The comparison of Moran's *I* values to a logistic regression indicated that a highly significant percentage of individual dispersion in *C. cammelia* populations of the Saha-gu and Gangseo-gu could be explained by isolation by distance.

Discussion

When the value of δ is less than 2, the aggregation is mainly caused by the environmental factors [11]. When δ is higher than 2, the aggregation is mainly caused by both species characteristics and environmental factors [11]. We recognized that the important environmental factors might be considered competition, growth rate, little decomposition, light, and below-ground resources. The characteristics of the *C. japonica* 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 offsprings and life span observed in na-

Table 3. Spatial autocorrelation coefficients (Moran's *I*) among five populations of *Camellia japonica* for seven distance classes

Population	I	II	III	IV	V	VI	VII
Mollundae	0.237*	0.111	0.059	0.176	-0.256**	-0.106	-0.144
Gadeok-do	0.249**	0.243**	0.221*	0.028	-0.131	-0.192	-0.209*
Amnam-dong	0.194	0.152	0.179	0.028	-0.035	-0.030	-0.091
Du-do	0.387***	0.317**	0.257**	0.260**	-0.228*	-0.025	-0.128
Jwiseum	0.411***	0.340*	0.181	0.126	0.012	0.029	-0.031

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

ture, and to explain them as evolutionary adaptations to environmental conditions [17]. The cluster was determined by environmental factors when the sampling quadrat was smaller than 10 m × 10 m (<2). Artificial disturbance such as constitutional roads is an important environmental factor affecting *C. japonica* in Amnam-dong. At the plots which had fewer *C. japonica*, the cluster was mainly determined by *C. japonica* themselves; the mean value of the aggregation index changed irregularly with the variation in plot sizes.

A significant positive value of Moran's *I* indicated that pairs of individuals separated by distances that fell within distance class IV had similar individuals, whereas a significant negative value indicated that they had dissimilar individuals. 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 an 80 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, 7]. 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 [5].

The community of *C. japonica* at Gadeok-do is the Busan Natural Monument No. 38. There are some communities of the Korean Natural Monuments of *C. japonica*. No. 66 (Daecheon-do, Ungjin-gun, Gyeonggi-do), No. 161 (Baekryeonsa, Gangjin-gun, Jeon-nam), No. 169 (Marhang-ri, Seocheon-gun, Chung-nam), No. 184 (Seonsa, Gochang-gun, Jeon-buk), No. 489 (Okrhongsa, Gwangyang-ci, Jeon-nam). *C. japonica* is one of very important resource of East Asia. The camellia in Europe was brought details of over 30 varieties back from Asia. Camellias were introduced into Europe during the 18th century and had already been cultivated in the Orient for thousands of years.

In conclusion, *C. japonica* populations within the Saha-gu and Gangseo-gu were observed a strong spatial structure. Neighboring patches of *C. japonica* were predominantly 80 to 100 m apart on average. The present study demonstrates that a spatial structure of *C. japonica* in the Saha-gu and Gangseo-gu populations could be explained by isolation by distance, limited gene flow, and topography. 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.

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초록 : 부산 사하구 동백나무 집단의 공간적 분포 양상

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부산광역시 사하구 동백나무 네 집단과 강서구 가덕도의 동백나무 한 집단 분포지에 대한 지리적 거리에 의한 공간적 분포 양상을 연구하였다. 네 프룻(물운대, 두도, 쥐섬, 가덕도)은 군집에서 균질한 분포 양상을 나타내었으나 한 플룻(암남동)은 응집 형태를 나타내었다. 모리시타 지수는 패치 지수와 유관하며 20 m × 20 m 프룻보다 큰 20 m × 50 m 프룻으로 값이 급격한 증가를 나타내었는데 이는 방형구가 커지면 응집의 정도가 유의하게 증가한다는 것을 의미한다. 반면 패치지수는 5 m × 10 m에서 10 m × 10 m까지는 큰 변화가 없었다. 공간적 상관관계 계수인 Moran's I에 의해 유의한 공간 구조를 정량화하였다. 유의한 개체간 유사도(76.9%)는 처음 4거리 등급(80 m)에서 유사성을 보였으며 100 m거리를 초과하면 비유사성 특성을 지닌 개체들의 쌍은 분리될 수 있다.