β-diversity Patterns of Plant Community in Fragmented Habitat in a Degenerated Meadow in Songnen Plain, China

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Abstract: A number of isolated islands of *Leymus chinensis* + herbosa community were investigated in fragmented habitat islands, by Braun-Blanquet field survey approach, in a degenerated meadow in the Songnen Plain, China in 2007. These islands were classified as large, medium, and small scales on the basis of the island area (100–1000m^2, large island; 50–100m^2, middle island; 10–50m^2, small island). Each scale of the investigation involved eight islands. The responses of β-diversity patterns of plant taxon to the habitat fragmentation at local community and metacommunity levels were analyzed on different scales of 24 isolated islands. The results indicated that at the local community level, there were 57 species belonging to 20 families and 49 genera in large islands, 49 species belonging to 16 families and 40 genera in middle islands, and 27 species belonging to eight families and 23 genera in small islands. β-diversity indexes for species, genus and family in large, middle, and small islands varied greatly, and the highest value of the indexes was not noted in the largest island. However, the average of the data obtained at the three scales showed that across large islands, Whittaker indexes were low and Bray-Curtis similarity indexes were high, while across small islands, Whittaker indexes were high and Bray-Curtis similarity indexes were low. At the metacommunity level, Whittaker indexes for species and genus showed a great significantly negative double logarithmic correlation ($p<0.01$) with the island area, whereas the Bray-Curtis indexes for species, genus and family showed a great significantly positive double logarithmic correlation ($p<0.01$) with the island area. At both local community and metacommunity levels, turnovers of species and genus could respond more sensitively to spatial changes of plant diversity patterns than that of family. Hence, the species and the genus could be used for the analysis of β-diversity patterns of plant community.

Keywords: habitat fragmentation; local community; metacommunity; plant taxon; β-diversity

1 Introduction

Understanding spatial patterns of species diversity is fundamental to both community ecology and conservation biology (Plotkin and Helene, 2002; Freestone and Brian, 2006). Whittaker (1960; 1972) classified species diversity into the following three categories: α-diversity, the species richness within a habitat; β-diversity, the change in species composition between habitats; and γ-diversity, the species diversity over a large region. He defined β-diversity as the difference in species composition along a habitat gradient, that is, species turnover. However, later, researchers argued that the similarity of species composition among communities (even in the absence of an environmental gradient) was a better indicator of habitat heterogeneity (Hewitt et al., 2005). Therefore, the definition of β-diversity includes two components, namely, the difference and the similarity of species composition between habitats. Based on the concept of species turnover, the metacommunity theory suggested that local extinction and colonization promotes high variation in the species composition among patchy habitats, eventually resulting in high total species richness (Caswell and Cohen, 1991).

Regional diversity patterns are a result of local processes, underlying environmental heterogeneity and species dispersal among local communities (Lennon et al., 2001; Ellingsen and John, 2002). Therefore, studying

the spatial patterns of β-diversity at the local community level is critical for a better understanding of the biodiversity pattern in a region and at the landscape scale in general (Condit et al., 2002). Despite the fact that it is comparatively more important than the study of α-diversity spatial patterns, such as species-area relationship (SAR), β-diversity has received relatively less attention in empirical literature (Harrison et al., 1992). Most studies have focused on a single taxon (Stevens and Michael, 2002; Kiflawi and Matthew, 2004; Kendi et al., 2005), however, these patterns may also vary among taxa. In conservation biology, higher taxonomic units, such as genus and family, were mainly studied for the prediction of α-diversity patterns along environmental gradients (Gaston and Williams, 1993), and they were also studied at a wider geographic scale or a global scale for identifying the biodiversity hot spots (Gaston et al., 1995). However, β-diversity pattern analysis has not yet been applied for such purpose.

The Songnen Plain is an important farming and pasture region, being of considerable importance in theoretical studies in terms of farm production (Li and Wang, 1998). Recently, there has been serious habitat fragmentation in the plain because of excessive human exploitation. The once-continuous habitats of the landscape have fragmented into habitat islands of different sizes. The presence of such habitat islands limits the biodiversity in the region. An environment gradient is defined not only by the geographical factors such as latitude or salinity and alkalinity, but also by temporal changes, competition intensity, etc. We therefore defined the area of these islands in terms of the ecological distance between them and analyzed the change in the taxon turnovers among the islands and the relationship between taxon composition similarity and the island area on the basis of the second definition of β-diversity. The objective of this study is to understand the spatial patterns of β-diversity at the local community level, develop a new perspective, and find an effective approach for the estimation of β-diversity, thus providing reference for the restoration and the scientific management of degenerated meadow.

2 Study Site and Methods

2.1 Study site

The Songnen Plain is located at the eastern end of the Eurasian steppes, which is an alluvial plain by the Songhua River and the Nenjiang River and belongs to the north temperate zone, has a continental monsoon climate zone, and is surrounded by mountains on three sides. The Songliao watershed is on the south of the plain. The annual precipitation and evaporation in the plain range from 350mm to 400mm and from 1,800mm to 2,000mm, respectively. Maximum precipitation and evaporation are observed between April and May. The average annual temperature is 4℃−5℃ (Han et al., 2007). The soil type in this region is mainly sodic soil and saline-alkali soil (Li and Zheng, 1995; Li et al., 2001).

Our study site is located in a natural mowing grassland in *Leymus chinensis* meadow in Changling County, Jilin Province of China. In 2004, the study site, with an area of 50ha, was enclosed with barrier. The *L. chinensis* was the primary constructive species in the meadow before 2004, subsequently the community became fragmented due to excessive human exploitation.

After 3-year of restoring ecological succession, the *Chloris virgata* community, the *Phragmites australis* community, and the halophytic community occupy the largest area. The area with *L. chinensis* + herbosa community was fragmented into many mosaic-like local habitat islands of different sizes and shapes. In general, this community coverage was approximately 50%–80%. The species saturation was reported to be 9 to 21 plants per square meter.

2.2 Vegetation survey

The field survey was conducted in early September 2007. First, we selected a number of isolated patches of *L. chinensis* + herbosa community, which were uniform in appearance and were clearly separated in the *L. chinensis* meadow. Each isolated patch was considered as an isolated island. Next, these islands were classified as large, medium, and small scales on the basis of the island area (100–1,000m^2, large island; 50–100m^2, middle island; 10–50m^2, small island). Each scale of the investigation involved eight islands. The area of each island was obtained by weighting method after drawing the dimensions of the island on the coordinate paper (1:200 scale). The approach of Braun-Blanquet School was used to get the coverage and height of each plant population, which were the original data to calculate the importance value. In the interest of clearer description, the *L. chinensis* + herbosa community was divided into

two levels on the basis of spatial scale in this article: all the communities on an isolated island were referred to the local communities (totally 24), and all local communities were together referred to the metacommunity.

2.3 Data analysis

The β-diversity index can be calculated by two types of data: presence-absence and quantitative (Ma et al., 1995). The Whittaker index was calculated using the presence-absence data, and the Bray-Curtis similarity index was calculated using the quantitative data, namely, importance value (importance value=100*(relative coverage + relative height)/2), to estimate β-diversity among islands.

Whittaker index (βw) is expressed as Equation (1) (Whittaker, 1960; 1972):

$$\beta w = \frac{S}{A} - 1 \qquad (1)$$

where S is the total number of species at different habitat island area scales; A is the average species number. The turnovers of genus and family can be calculated as above.

Bray-Curtis similarity index (S_{jk}) can be calculated by Equation (2) (Bray and Curtis, 1957):

$$S_{jk} = 100 * \left[1 - \frac{\sum\limits_{i=1}^{p} \left| X_{ij} - X_{ik} \right|}{\sum\limits_{i=1}^{p} \left| X_{ij} + X_{ik} \right|} \right] \qquad (2)$$

where X_{ij} (X_{ik}) is the important value of ith species in the jth (kth) island; p is the number of species overall. The similarity indexes of genus and family can be calculated as above.

All data were analyzed using the Excel 2000 and SPSS 13.0 software programs. In the analysis at the local community level, the islands were ordered according to size, from the smallest to the largest; the β-diversity indexes among the adjacent islands and between the smallest and the largest islands were calculated. The β-diversity indexes of three islands scales were calculated as the mean±standard deviation of the β-diversity of eight islands. The same calculation was applied for the metacommunity.

3 Results

3.1 Taxon composition and richness in metacommunity and local communities

In the metacommunity of the 24 habitat islands, there

were 63 species of vascular plants belonging to 20 families and 49 genera. At the local community level, there were 57 species belonging to 20 families and 49 genera in large islands, 49 species belonging to 16 families and 40 genera in medium islands, and 27 species belonging to eight families and 23 genera in small islands. The above results suggested that the species richness of small islands decreased dramatically because of excessive habitat fragmentation.

3.2 β-diversity of plant taxon at local community level

In eight local communities of the small habitat islands, the Whittaker indexes of adjacent islands in terms of the turnovers for the species, genus and family were high between the largest and the smallest islands, while they were low between the islands of 27.8m² and 28.6m². The Bray-Curtis similarity index for the species was high between the islands of 27.7m² and 27.8m², while those for the genus and family were high between the islands of 28.6m² and 41.2m². Moreover, the similarity indexes for the species and genus were low between the largest and the smallest islands, while that for the family was low between the islands of 24.4m² and 27.7m² (Table 1).

In eight local communities of the medium habitat islands, the Whittaker indexes for the species and genus were high between the islands of 51.3m² and 53.0m², and that for the family was high between the islands of 83.3m² and 85.0m². At the same time, the indexes for the species and family were low between the islands of 66.5m² and 72.4m², and the index for genus was low between the islands of 79.1m² and 83.3m². The Bray-Curtis similarity indexes for the species, genus and family were all high between the islands of 66.5m² and 72.4m². The similarity indexes were low between the islands of 51.3m² and 53.0m² for the species, between the largest and the smallest islands for genus, and between the islands of 65.6m² and 66.5m² for family (Table 1).

In eight local communities of the large habitat islands, the Whittaker indexes were high between the largest and the smallest islands for the species, between the islands of 111.1m² and 133.0m² for genus, and between the islands of 522.9m² and 714.9m² for family. And they were low between the islands of 490.9m² and 522.9m² for the species and genus, and between the islands of

$167.5m^2$ and $217.2m^2$, and $217.2m^2$ and $224.8m^2$ for the family. The Bray-Curtis similarity indexes were high between the islands of $217.2m^2$ and $224.8m^2$ for the species and family, and between the islands of $490.9m^2$ and $522.9m^2$ for genus. Moreover, the similarity indexes were low between the largest and the smallest islands for the species and genus, and they were low between the islands of $133.0m^2$ and $167.5m^2$ for family (Table 1).

The average values of both the indexes for the species, genus, and family were analyzed by multiple comparison tests. The results showed that the changes in the indexes of the large islands, except those of the family, were significantly higher than those of the small islands ($p<0.05$). The Bray-Curtis similarity indexes of the small and the medium islands were not significantly different ($p>0.05$), whereas those of the small and large islands differed significantly ($p<0.05$) (Table 1).

The results obtained in this study suggest that there is apparent fluctuation in the turnovers of species, genus, and family with increase in the island size. Meanwhile, even though there was no distinct pattern, the species and genus turnovers were considerably similar across islands of different sizes. Furthermore, in islands of all the three size groups, the Whittaker indexes decreased and the Bray-Curtis similarity indexes increased with taxonomic units (species<genus<family).

3.3 β-diversity patterns of plant taxon with island area at metacommunity level

The relevant statistical analysis of data from 24 islands of the metacommunity was performed (Fig. 1, Table 2). The Whittaker indexes for species and genus increased with a decrease in the island area and this trend was consistent with the form of the linear function ($p<0.01$)

Table 1 *β*-diversity of plant taxon at the local community level among adjacent area in different island scales in fragmented habitat

Island scale	Adjacent island (m²)	Whittaker index			Bray-Curtis similarity index		
		Species	Genera	Family	Species	Genera	Family
Small	11.8–14.3	0.4	0.3	0.4	46.1	58.1	77.1
	14.3–24.4	0.5	0.6	0.4	35.1	35.1	61.6
	24.4–27.7	0.5	0.4	0.4	45.4	45.4	50.9
	27.7–27.8	0.4	0.3	0.2	61.4	61.4	71.5
	27.8–28.6	0.4	0.3	0.0	58.8	58.8	69.3
	28.6–41.2	0.4	0.4	0.1	60.2	62.8	87.0
	41.2–48.8	0.4	0.5	0.1	60.1	60.1	73.6
	48.8–11.8	0.7	0.7	0.5	33.6	33.6	66.4
Medium	51.3–53.0	0.7	0.6	0.2	27.5	41.3	78.4
	53.0–65.6	0.4	0.4	0.3	55.6	62.6	75.6
	65.6–66.5	0.4	0.4	0.3	53.8	53.8	64.1
	66.5–72.4	0.3	0.4	0.2	67.4	67.6	79.4
	72.4–79.1	0.4	0.5	0.2	57.8	58.9	73.7
	79.1–83.3	0.4	0.3	0.3	54.7	54.9	73.6
	83.3–85.0	0.4	0.4	0.4	48.8	50.8	65.2
	85.0–51.3	0.5	0.5	0.3	34.9	37.3	75.7
Large	111.1–133.0	0.3	0.5	0.2	60.3	64.9	81.0
	133.0–167.5	0.3	0.3	0.2	62.1	63.3	74.8
	167.5–217.2	0.3	0.3	0.1	71.6	72.2	84.8
	217.2–224.8	0.3	0.2	0.1	74.1	74.6	87.0
	224.8–490.9	0.3	0.2	0.2	67.8	72.1	80.8
	490.9–522.9	0.2	0.2	0.2	70.4	76.5	84.0
	522.9–714.9	0.3	0.2	0.3	66.7	68.4	86.1
	714.9–111.1	0.4	0.4	0.2	55.5	62.6	78.8
Average	Small	0.3±0.1b	0.3±0.1b	0.2±0.1a	66.1±6.3b	69.3±5.3b	82.2±4.1b
	Medium	0.5±0.1a	0.4±0.1a	0.3±0.1a	50.0±12.9a	53.4±10.2a	73.2±5.7a
	Large	0.5±0.1a	0.5±0.2a	0.3±0.2a	50.1±11.6a	51.9±12.1a	69.7±10.7a

Note: Different small letters in the same column mean significant difference at 0.05 level
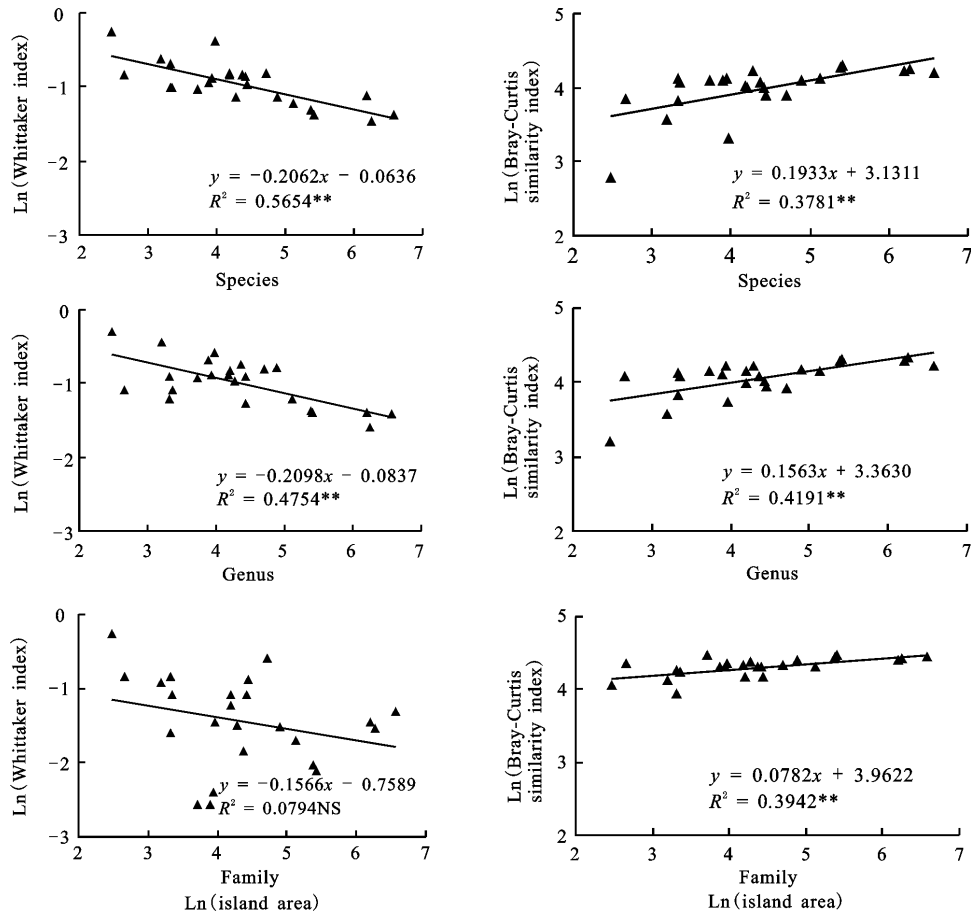
Fig. 1 *β*-diversity patterns of plant taxon in metacommunity of 24 islands among adjacent areas in fragmented habitat

Table 2 ANOVA statistics for variation of *β*-diversity indexes and island area in metacommunity (*n*=24)

	Whittaker index			Bray-Curtis similarity index		
	Species	Genus	Family	Species	Genus	Family
F	28.62	19.94	1.90	13.73	15.87	14.31
P	0.0000	0.0002	0.1823	0.0014	0.0006	0.0010
df	1, 22	1, 22	1, 22	1, 22	1, 22	1, 22

after double logarithmic transformation. However, the relationship between the Whittaker index for family and the island area was not statistically significant ($p > 0.05$). The Bray-Curtis similarity index exhibited an opposite trend, which increased with an increase in the island area. Furthermore, this trend at the species, genus, and family scales was consistent with the form of the power function ($p<0.01$). The above results suggest that the *β*-diversity patterns with respect to species and genus were the same at the levels of local communities and the metacommunity, whereas the *β*-diversity patterns with respect to the family differed significantly at the two scales, and performed unstable.

4 Conclusions and Discussion

β-diversity is very important for the maintenance of regional species diversity and has been under investigation for many years (Condit et al., 2002). The Whittaker index and the Bray-Curtis similarity index reflect two aspects of *β*-diversity, that is, differentiation and similarity, respectively; thus, they exhibited opposite trends. At the local community level, the average of the data obtained at the three scales showed that across large islands, the Whittaker indexes were low and the Bray-Curtis similarity indexes were high, while across small islands, the Whittaker indexes were high and the Bray-

Curtis similarity indexes were low. We believed that such variation in the β-diversity patterns was due to the differences in the sizes of the islands and the associated ecological gradients such as resources types, environment heterogeneity, and competition intensity. On a small island, the species richness was maintained by extinction and colonization that were caused by low-quality resources and high competition intensity; therefore, species co-existence could be achieved only by distribution along different ecological gradients and by sharing the available resources. In the case of small islands, the species turnovers were high owing to frequent immigration and emigration of individuals; on the other hand, in the case of large islands, the species turnovers were low since the habitat heterogeneity within the island was high and different species could coexist through niche overlap. These observations had demonstrated that β-diversity played an important role in the maintenance of regional species richness. Especially in the case of small islands, the taxon richness decreased dramatically because of excessive habitat fragmentation (only 27 species belonging to eight families and 23 genera), hence, the species turnover among islands had an obvious significance.

Plant diversity exhibits ecologically interesting spatial patterns (Koleff and Gaston, 2001). The α-diversity patterns, such as SAR, have been observed to remain more or less similarity, whereas β-diversity patterns have not been reported to be constant. Furthermore, many previous studies have investigated the β-diversity between regions with respect to only a single taxon. This is the first study in which the effect of habitat fragmentation on the β-diversity patterns has been analyzed at three taxonomic scales of species, genus and family. The findings of our study revealed that at the local community level, the two β-diversity indexes showed obvious fluctuations with the island area. Furthermore, the Whittaker indexes decreased and the Bray-Curtis similarity indexes increased with taxonomic units (species<genus<family). However, at the metacommunity level, the two β-diversity indexes for species and genus increased significantly with island area in the linear function after double logarithmic transformation, whereas changes in the Bray-Curtis similarity indexes were significant only for family. Hence, as observed in the case of SAR, the β-diversity with respect to species and genus between fragmented habitat islands also

showed a double logarithmic correlation with the island area, and the two taxonomic units could be taken into account in analyzing the effect of habitat fragmentation on β-diversity. However, since family was a higher taxon and too broad a category for analysis, the results were oversimplified and a large amount of ecological information were lost, consequently, resulting in large deviations.

In conclusion, for understanding the effect of habitat fragmentation on biodiversity, it is important to study the β-diversity between habitat islands. This will, in turn, be crucial for maintaining regional species richness, particularly in the case of small islands. The data on β-diversity patterns in grassland ecosystems can be used for species protection and the scientific management of these ecosystems. For practical purposes, β-diversity patterns can be analyzed with respect to species and genus, however, the inclusion of family is not recommended.

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