

Utility of taxonomic unit and life form in the analysis of plant diversity patterns in a temperate meadow steppe, China

Utilidad de la unidad taxonómica y forma de vida en el análisis de los modelos de diversidad de plantas en una estepa de pradera templada, China

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Abstract. Rapid and precise assessment of biodiversity is a central issue in conservation biology and biodiversity science. Higher taxonomic units and life form-based morphospecies were utilised to assess plant diversity patterns at the habitat scale in temperate meadow steppe, Songnen Plain, China. Patch area, taxonomic composition (families and genera) and life form (based on Raunkiaer's life forms, and stem and root growth forms) were recorded in five communities. Taxonomic unit-based hierarchical diversity indices (HDI) and life form-based hierarchical diversity indices (HLDI) were calculated. Twenty-six families, 67 genera, and 87 species were recorded in the five communities. HDI and HLDI were significantly correlated with patch area for all except the *Kochia sieversiana* community. For each community, HDI components showed no significant difference with species in slope, but differed in intercept, whereas HLDI components showed significant differences with species both in slope and intercept. Among the communities, the percentage contribution to HDI was highest for family diversity and lowest for infrageneric species diversity, and the percentage contribution to HLDI by different morphospecies components varied greatly (33.39–66.61%). Genus and family can be used instead of species to analyse plant diversity patterns, but use of life form-based morphospecies requires further study.

Keywords: Plant diversity; Taxonomic units; Life form; Shannon-Wiener index; Hierarchical diversity; *Leymus chinensis* meadow; Songnen Plain.

Abbreviations: RLF, Raunkiaer's life form classification; H, hemicryptophyte; G, geophyte; Th, therophyte; Ch, chamaephyte; SGF, stem growth form; EG, erect grass-like stem; ED, erect dicot stem; BRo, basal rosette stem; SR, semi-rosette stem; PG, prostrate or climbing stem; CG, caespitose stem; RGF, root growth form; R, rhizomatous root; BR, bushy root; TR, taproot; B, bulbous root; Lk: *Leymus chinensis*-*Kalimeris integrifolia* community; Lc: *Leymus chinensis* community; Pc: *Phragmites communis* community; Cv: *Chloris virgata* community; Ks: *Kochia sieversiana* community.

Resumen. La medición rápida y precisa de la biodiversidad es un tema central en la biología de la conservación y la ciencia de la biodiversidad. Se utilizaron unidades taxonómicas superiores y morfoespecies basadas en su forma de vida para determinar modelos de diversidad vegetal a escala de hábitat en una estepa de pradera templada, Planicie Songnen, China. El área del parche, la composición taxonómica (familia y género) y la forma de vida (basada en las formas de vida de Raunkiaer, y las formas de crecimiento de la raíz y el tallo) se determinaron en cinco comunidades. Se calcularon además los índices de diversidad jerárquicos basados en la unidad taxonómica (HDI) y los índices de diversidad jerárquicos basados en la forma de vida (HLDI). Veintiséis familias, 67 géneros, y 87 especies fueron registradas en las cinco comunidades. HDI y HLDI se correlacionaron significativamente con el área del parche en todas las comunidades, excepto la comunidad de *Kochia sieversiana*. Para cada comunidad, los componentes de HDI no mostraron diferencias significativas con la especie en la pendiente, pero difirieron en la intercepta, mientras que los componentes de HLDI mostraron diferencias significativas con la especie tanto en la pendiente como en la intercepta. Entre las comunidades, la contribución porcentual a HDI fue la más alta para la diversidad de familia, y la más baja para la diversidad de especies infragenérica, y la contribución porcentual a HLDI por los diferentes componentes de las morfoespecies varió ampliamente (33.39–66.61%). El género y la familia pueden ser usados en lugar de la especie para analizar los modelos de la diversidad vegetal, pero el uso de morfoespecies basadas en la forma de vida requiere estudio adicional.

Palabras clave: Diversidad vegetal; Unidades taxonómicas; Forma de vida; Índice de Shannon-Wiener; Diversidad jerárquica; Pradera de *Leymus chinensis*; Planicie Songnen.

Abreviaturas: RLF, clasificación de las formas de vida de Raunkiaer; H, hemicriptófito; G, geófito; Th, terófito; Ch, caméfito; SGF, forma de crecimiento de tallo; EG, tallo erecto semejante al de una gramínea; ED, tallo erecto de dicotiledónea; BRo, tallo de roseta basal; SR, tallo de semi-roseta; PG, tallo postrado o trepador; CG, tallo cespitoso; RGF, forma de crecimiento radical; R, tallo rizomatoso; BR, raíz arbustiva; TR, raíz pivotante; B, bulbo; Lk: comunidad de *Leymus chinensis*-*Kalimeris integrifolia*; Lc: Comunidad de *Leymus chinensis*; Pc: Comunidad de *Phragmites communis*; Cv: Comunidad de *Chloris virgata*; Ks: comunidad de *Kochia sieversiana*.

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INTRODUCTION

Rapid and precise assessment of biodiversity is a central issue in conservation biology and biodiversity science (Biaggini et al., 2007). Because identification of the relative abundance of species is a tedious and time-consuming task and requires advanced taxonomic knowledge, more rapid ways of obtaining the same data are desirable. The most common approach is to use higher taxonomic units, such as family and genus, as a surrogate for species, which is time- and labour-saving, highly accurate and easily recognisable (Gaston & Williams, 1993; Williams & Gaston, 1994; Anderson, 1995; Williams et al., 1997). In recent decades, this approach has been applied extensively in the study of species richness patterns at regional and geographic scales (Balmford et al.; 1996a, 1996b; Doerries & van Dover, 2003; Heino & Soininen, 2007; Shokri & Gladstone, 2009; Mazaris et al., 2010).

However, the use of higher taxonomic units is not the only approach to assess species diversity. The morphospecies method is an additional technique that has been used widely in assessment of species diversity in invertebrate communities (Oliver & Beattie 1993, 1996). The life form of plant species is classified on the basis of external morphology, and can be classified into different morphospecies to provide important information about species composition and community structure (Li & Yang 2002, 2003a, 2003b, 2004). To date, use of taxonomic units and life form in a morphospecies approach as a surrogate for species has been rarely applied for analysis of plant diversity patterns at the habitat scale.

The Shannon-Wiener index is often employed to describe the diversity of a biotic community. A taxon-based hierarchical diversity index (HDI) was developed from the Shannon-Wiener index to partition the total species diversity at different taxonomic levels, and quantify the percentage contribution of the different components (Pielou, 1978). Previously, the HDI was used to study the diversity of animal communities (Godfrey, 1978; Kaesler et al., 1978; Osborne et al., 1980). However, Osborne et al. (1980) argued that the ecological meaning of the HDI was unclear, and developed a trophic-based hierarchical index (HTDI) for a lotic community. In the present study, we developed a life form-based hierarchical index (HLDI) to analyse species diversity patterns within a plant community.

Leymus chinensis meadow steppe is a soil-climax vegetation type on the Songnen Plain, China, characterised by a complex vertical structure and species composition, and is distributed on open plains and lowlands in sodic meadow soil, saline-alkaline soil or complexes of these soil types. Due to the influence of soil properties and human disturbance, the plant communities that occur within the *L. chinensis* meadow are patchily distributed and form patches of different areas and shapes (Zheng & Li 1993; Li et al., 2002; Han et al., 2007). In the present study, we recorded information on the composition of plant taxa and life

forms in 144 patches of five representative communities in the *L. chinensis* meadow steppe. This was to test the applicability of higher taxonomic units and life form-based morphospecies as a surrogate for species in the HDI and HLDI. The aim was to identify the best surrogate for species for analysis of plant diversity patterns at the habitat scale in order to establish a rapid assessment method for plant diversity conservation, and offer a reference for the restoration and management of a degraded grassland ecosystem.

MATERIALS AND METHODS

Study area and site selection. *Leymus chinensis* meadow steppe is the dominant vegetation type on the Songnen Plain (40° 30' – 46° 05' N, 122° 12' – 126° 20' E), which is located at the eastern limit of the Eurasian Steppe in the North Temperate Zone of China. The plain has a continental monsoon climate featuring four distinct seasons. The mean annual temperature is 4–5 °C, the mean temperature for the warmest month (July) is 26.8–28.1 °C and for the coldest month (January) is –22 to –28 °C. The mean annual precipitation and evaporation range from 350 to 400 mm and from 1800 to 2000 mm, respectively. The non-frost period is 140–150 d and the maximum depth of frozen earth is about 2 m. The landform mainly includes fixed dunes, open plains and low-lying wetlands with an altitude ranging from 137.8 to 144.8 m (Zhang et al., 2011). The natural vegetation is represented by *Phragmites communis* swamp in shallow lakes, halophytic meadow (*Salsola* spp. or *Kochia sieversiana*) around the alkali lakes, *L. chinensis* meadow on the open, flat plain, *Stipa baicalensis* meadow on the highland, and elm woodland and shrub communities on the top of fixed dunes (Li & Wang, 1998; Han et al., 2007, 2009; Yang et al., 2008). The zonal soil is chernozem, which is distributed in highlands, and the azonal soil is sodic meadows and saline-alkaline soils distributed on the open plain, lowland and lake shores.

The study site was situated in the *L. chinensis* meadow steppe near the Ecological Research Station of Northeast Normal University in Songnen grassland (44° 42' – 44° 45' N, 123° 35' – 123° 46' E), Changling County, Jilin Province, China. The area of the study site was about 2,250 ha. The dominant communities consisted of *L. chinensis* community, *L. chinensis*-herb community, *P. communis* community, *Chloris virgata* community and *K. sieversiana* community, which were patchily distributed in patches of different areas and shapes (Han et al., 2009).

Vegetation survey. A field survey was conducted in early September 2015. A series of isolated patches of *L. chinensis*-*Kalimeris integrifolia* community (representative of the *L. chinensis*-herb community), *L. chinensis* community, *P. communis* community, *C. virgata* community and *K. sieversiana* community were selected within the *L. chinensis* meadow steppe. The patches were of uniform appearance within the same commu-

nity. The dimensions of these patches were measured with an extendable ruler depending on whether the patch was circular, triangular, diamond or trapezoidal in shape to estimate the patch area. Quadrats (each 1 m²) were placed at equal intervals along the longest axis of each patch. Monodominant stands were eliminated in order to include as many herbaceous species in the patch as possible. The number of quadrats per patch varied from 3 to 8 depending on the patch area and community heterogeneity. The cover of each species was estimated using the Braun-Blanquet scale (r, +, 1, 2, 3, 4 and 5) and plant height was measured with an extendable ruler. A total of 144 patches in the five communities were sampled (Table 1).

Plant life form classification. According to the results of previous research on plant life forms in this region (Li, 1979; Li & Yang, 2002, 2003a, 2003b, 2004), we developed three life form classification systems on the basis of different classification standards. First, on the basis of the degree of protection afforded by the perennating buds, we used a modified Raunkiaer's life form classification (RLF) to define four major morphospecies categories, namely hemicryptophyte (H), geophyte (G), therophyte (Th) and chamaephyte (Ch). Second, on the basis of stem morphology and leaf arrangement, we used a stem growth form (SGF) classification to define six morphospecies categories, which comprised erect grass-like stem (EG), erect dicot stem (ED), basal rosette stem (BRo), semi-rosette stem (SR), prostrate or climbing stem (PG) and caespitose stem (CG). The EG category was characterised by an erect, unbranched stem and was mainly composed of Poaceae and Cyperaceae species; ED was characterised by an erect stem with well-developed lateral branches, and mainly comprised dicotyledonous herbs; BRo was characterised by a large rosette of leaves from which flowering stems bearing few very reduced leaves arose; SR was similar in morphology to BRo at early growth stages, but the flowering stem bore well-developed stem-leaves or branches and became the main stem at a later growth stage; PG lacked an erect stem, and instead the stem was either prostrate or climbing by means of twining

stems or tendrils, and no adventitious buds were present on the stem; CG was characterised by many ramets born from a very short rhizome or free tillers arising from the stem base. Finally, on the basis of root morphology, we devised a root growth form (RGF) classification to define four morphospecies, namely rhizomatous root (R), bushy root (BR), taproot (TR) and bulbous root (B). The R category was characterised by a horizontal underground rhizome for clonal reproduction; BR was characterised by many fibrous roots and either lacked a taproot or the taproot died at an early growth stage; in contrast to BR, in TR the taproot and lateral roots were both well developed; B was characterised by an underground bulb, and mainly comprised *Allium* species.

Analysis of taxon and life form diversity. Shannon-Wiener's diversity index (H') was employed to estimate taxonomic and life-form diversity, using the formula:

$$H' = - \sum_{i=1}^S (P_i \lg P_i)$$

where S is the number of species (genus, family, RLF, SGF or RGF), $P_i = N_i/N$, and N and N_i are the total number of individuals of all species (genus, family, RLF, SGF or RGF) and the i th species (genus, family, RLF, SGF or RGF), respectively. The HDI and HLDI were calculated using the approach of Pielou (1988). The formula for calculation of the HDI was as follows:

$$\text{HDI} = H'(F) + H'_F(G) + H'_{FG}(S),$$

where $H'(F)$ is the family diversity, $H'_F(G)$ is the generic diversity within a family, and $H'_{FG}(S)$ is the species diversity within a genus. The total generic diversity was calculated by the formula $H'(G) = H'(F) + H'_F(G)$.

The formulas for calculation of the HLDI were as follows: $\text{HLDI}_1 = H'(RLF) + H'_{RLF}(S)$, $\text{HLDI}_2 = H'(SGF) + H'_{SGF}(S)$, and $\text{HLDI}_3 = H'(RGF) + H'_{RGF}(S)$, where HLDI_1 , HLDI_2 and

Table 1. Patch characteristics of five communities in a *Leymus chinensis* meadow steppe.

Tabla 1. Características del parche en cinco comunidades en una estepa de pradera de *Leymus chinensis*.

Community type ^A	Number of patches	Patch area (m ²)			
		Min.	Max.	Mean ± SD	Total
Lk	33	6.8	1068	184.38 ± 242.88	6084.42
Lc	35	1.2	816	160.13 ± 189.09	5604.46
Pc	30	2	162	60.18 ± 47.36	1703.62
Cv	26	1.5	212	61.87 ± 63.64	1608.74
Ks	20	6	226.87	64.07 ± 66.69	1281.47
Total	144				16282.71

^A Lk: *Leymus chinensis*-*Kalimeris integrifolia*; Lc: *L. chinensis*; Pc: *Phragmites communis*; Cv: *Chloris virgata*; Ks: *Kochia sieversiana*.

Table 2. Number of taxa and species richness in different life form-based morphospecies of five communities in meadow steppe.
Tabla 2. Número de clasificaciones taxonómicas y riqueza de especies en diferentes morfoespecies basados en su forma de vida de 5 comunidades en una estepa de pradera de *Leymus chinensis*.

		Community type ^B					Total
		Lk	Lc	Pc	Cv	Ks	
Taxon (Number)							
Family		22	21	14	7	7	26
Genera		55	51	36	15	12	67
Species		71	63	42	17	15	87
Species/Family ratio		3.23	3	3	2.43	2.14	3.35
Species/Genera ratio		1.29	1.24	1.17	1.13	1.25	1.3
Life form (Species richness)							
RLF ^A	Ch	3	2	2	—	—	3
	G	20	13	9	3	4	23
	H	43	39	23	10	7	51
	Th	5	9	8	4	4	10
SGF ^A	BRo	7	4	2	1	1	8
	CG	8	8	8	4	4	12
	ED	33	29	18	7	6	38
	EG	11	10	8	5	2	14
	PG	4	6	5	—	2	6
RGF ^A	SR	8	6	1	—	—	9
	B	2	1	1	—	—	2
	BR	13	11	10	5	5	17
	R	21	17	8	4	2	24
	TR	35	34	23	8	8	44

^A RLF, Raunkiaer's life form classification; SGF, stem growth form; RGF, root growth form.

H, hemicryptophyte; G, geophyte; Th, therophyte; Ch, chamaephyte. EG, erect grass-like stem; ED, erect dicot stem; BRo, basal rosette stem; SR, semi-rosette stem; PG, prostrate or climbing stem; CG, caespitose stem. R, rhizomatous root; BR, bushy root; TR, taproot; B, bulbous root.

^B Lk: *Leymus chinensis*–*Kalimeris integrifolia*; Lc: *L. chinensis*; Pc: *Phragmites communis*; Cv: *Chloris virgata*; Ks: *Kochia sieversiana*.

HLDI₃ are hierarchical diversity indices based on RLF, SGF and RGF morphospecies, respectively; $H(\text{RLF})$, $H(\text{SGF})$ and $H(\text{RGF})$ are the morphospecies diversity based on RLF, SGF and RGF, respectively; and $H'_{\text{RLF}}(S)$, $H'_{\text{SGF}}(S)$ and $H'_{\text{RGF}}(S)$ are the species diversity within morphospecies. The average percentage contributions of the different components to HDI and HLDI were estimated for each community type. After a preliminary test for homogeneity of the variances, Duncan's multiple range test was employed to analyse differences in contributions among the five communities at the significance level $\alpha = 0.05$.

Applicability of taxon and life form in analysis of plant diversity patterns. First, we applied linear regression to analyse the relationship between the taxonomic and life-form diversity indices and patch area after logarithmic (lg) transformation.

Second, we tested the significance of all regression equations by analysis of variance at the significance levels $\alpha = 0.05$, 0.01 or 0.001. Third, we tested the significance of differences in the slope and intercept between the regression equations for higher taxonomic units and life forms and those of species by analysis of covariance (Quinn & Keough, 2002) at the significance level $\alpha = 0.05$. If the slopes of two regression lines showed a significant difference, the two lines were considered to be uncorrelated. If two regression lines showed no significant difference in slope, we further explored the difference in the intercepts. If the intercepts showed no significant difference, the two lines were considered to be identical; if the intercepts differed significantly, the two lines were different but significantly correlated.

All data were analysed using SPSS 13.0 (SPSS, Chicago, IL, USA).

RESULTS

Taxonomic and life-form composition of communities.

A total of 26 families, 67 genera and 87 species were recorded in the 144 patches in the five communities. The highest numbers of species, genera and families occurred in the *L. chinensis*-*K. integrifolia* community, whereas the lowest numbers occurred in the *K. sieversiana* community. The highest numbers of monospecific families and monospecific genera were present in the *L. chinensis*-*K. integrifolia* community (3.33- and 4.89-fold more than the lowest numbers, which were present in the *K. sieversiana* community). In terms of species richness represented by life form-based morphospecies, the highest species richness among RLF morphospecies was observed in H, followed by G, Th, and was lowest in Ch (Table 2). The highest species richness among SGF morphospecies was observed in ED, followed by EG, CG, SR, BRo, and lowest in PG. The highest species richness among RGF morphospecies was observed in TR, followed by R, BR, and lowest in B in each community (Table 2).

Patterns in diversity indices of taxon and life form according to patch area. The HDI of the five communities showed a significant linear correlation ($P < 0.05$) with

patch area after logarithmic transformation, except for the *K. sieversiana* community. In the five communities, no significant differences ($P > 0.05$) were observed between $H'(G)$ and $H'(S)$ both in slope and intercept of the regression equations, and between $H'(F)$, $H'_F(G)$ and $H'(S)$ in slope, but a significant difference ($P < 0.05$) between $H'(F)$, $H'_F(G)$ and $H'(S)$ in intercept was observed. In terms of HLDI, only $H'(SGF)$ and $H'_{SGF}(S)$ of the *L. chinensis*-*K. integrifolia* community, and the *L. chinensis* and *P. communis* communities showed a significant correlation ($P < 0.05$) with patch area. The HLDI of all communities, except that of *K. sieversiana*, showed a significant difference ($P < 0.05$) with $H'(S)$ both in slope and intercept most of the times (Table 3).

Contributions of different components to HDI and HLDI. The percentage contributions of taxonomic and life-form components to HDI and HLDI were similar and showed no significant differences among the five communities. The percentage contribution to HDI was highest for $H'(F)$ (57.3–75.6%) and lowest in $H'_{FG}(S)$ (1.98–5.41%). The percentage contribution to HLDI by the different components was similar and ranged from 33.39% to 66.61% among the five communities ($P < 0.05$) (Fig. 1).

Table 3. Parameters of the linear regression equations between diversity indexes of taxon and life form (dependent variables) and patch area (independent variables) of five communities in a *Leymus chinensis* meadow steppe. All variables were log transformed. The significance of the difference between $H'(S)$ and each of the other indices was tested with Duncan's multiple range test at $\alpha = 0.05$. Slope and intercept values followed by the same letter within a column do not differ significantly.

Tabla 3. Parámetros de las ecuaciones de regresión lineal entre índices de diversidad de la taxonomía y forma de vida (variables dependientes) y el área del parche (variable independiente) de cinco comunidades en una estepa de pradera de *Leymus chinensis*. Todas las variables fueron transformadas a logaritmo. La significancia de la diferencia entre $H'(S)$ y cada uno de los otros índices fue evaluada con la prueba de rango múltiple de Duncan a $\alpha = 0,05$. Los valores de la pendiente y la intercepta seguidas por la misma letra dentro de una columna no difieren significativamente.

Index	<i>Leymus chinensis</i> - <i>Kalimeris integrifolia</i>			<i>Leymus chinensis</i>			<i>Phragmites communis</i>			<i>Chloris virgata</i>			<i>Kochia sieversiana</i>		
	Slope	Intercept	r	Slope	Intercept	r	Slope	Intercept	r	Slope	Intercept	r	Slope	Intercept	r
HDI															
$H'(S)$	0.12 a	-0.14 a	0.93***	0.16 a	-0.29 a	0.84***	0.13 a	-0.25 a	0.73***	0.09 a	-0.28 a	0.86***	0.06 a	-0.22 a	0.63**
$H'(G)$	0.11 a	-0.14 a	0.90***	0.16 a	-0.28 a	0.83***	0.12 a	-0.25 a	0.73***	0.08 a	-0.26 a	0.84***	0.03 a	-0.21 a	0.47 NS
$H'(F)$	0.12 a	-0.35 b	0.78***	0.18 a	-0.54 b	0.78***	0.15 a	-0.53 b	0.59***	0.07 a	-0.48 b	0.44*	0.02 a	-0.31 b	0.21 NS
$H'_F(G)$	0.11 a	-0.59 b	0.59***	0.13 a	-0.68 b	0.55***	0.11 a	-0.62 b	0.49**	0.11 a	-0.71 b	0.50*	0.07 a	-0.94 b	0.16 NS
$H'_{FG}(S)$	0.69 b	-2.85 b	0.50**	0.87 b	-3.67 b	0.62***	0.56 b	-3.20 b	0.34 NS	0.83 b	-3.61 b	0.53**	0.85 b	-3.35 b	0.39 NS
HLDI															
$H'(RLF)$	-0.01 b	-0.36 b	0.12 NS	0.06 b	-0.49 b	0.26 NS	0.13a	-0.62 b	0.76***	0.06 a	-0.59 b	0.43*	0.09 a	-0.67 b	0.42 NS
$H'_{RLF}(S)$	0.19 b	-0.46 b	0.87***	0.25 b	-0.69 b	0.85***	0.12a	-0.49 b	0.50**	0.12 b	-0.57 b	0.70***	0.05 a	-0.43 b	0.43 NS
$H'(SGF)$	0.07 b	-0.39 b	0.53**	0.07 b	-0.41 b	0.51**	0.08b	-0.41 b	0.72***	0.03 b	-0.43 b	0.31 NS	0.04 a	-0.44 b	0.20 NS
$H'_{SGF}(S)$	0.17 b	-0.48 b	0.90***	0.29 b	-0.86 b	0.87***	0.21b	-0.78 b	0.55**	0.21 b	-0.85 b	0.73***	0.09 a	-0.65 b	0.28 NS
$H'(RGF)$	0.01 b	-0.33 b	0.13 NS	0.05 b	-0.44 b	0.38*	0.01b	-0.36 b	0.14 NS	0.03 b	-0.41 b	0.30 NS	0.08 a	-0.63 b	0.48 NS
$H'_{RGF}(S)$	0.19 b	-0.52 b	0.91***	0.27 b	-0.75 b	0.89***	0.28b	-0.82 b	0.72**	0.22 b	-0.86 b	0.75***	0.05 a	-0.45 b	0.30 NS

* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, NS, not significant.

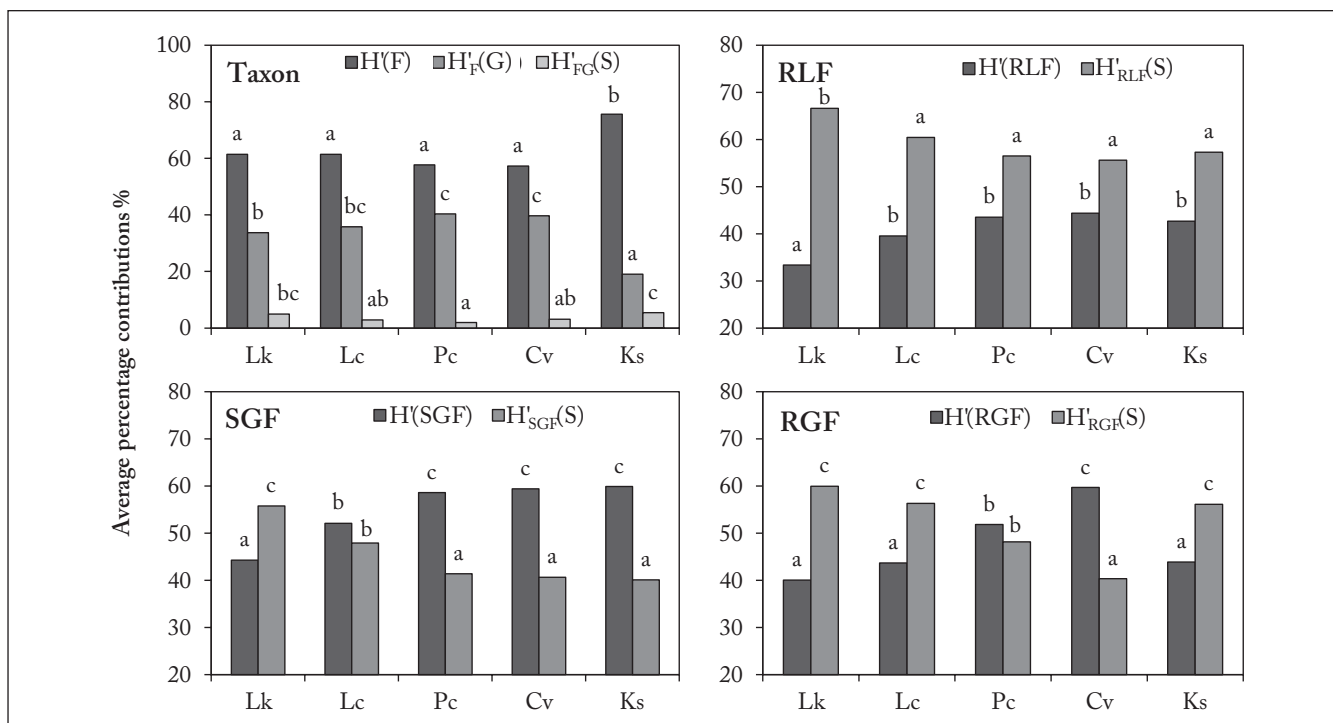


Fig. 1. Average percentage contributions of different components to HDI and HLDI of five communities in a *Leymus chinensis* meadow. Communities with the same letter within the same index do not differ at $P=0.05$ with Duncan's multiple range test. Lk: *Leymus chinensis-Kalimeris integrifolia*; Lc: *L. chinensis*; Pc: *Phragmites communis*; Cv: *Chloris virgata*; Ks: *Kochia sieversiana*.

Fig. 1. Contribuciones porcentuales promedio de diferentes componentes a HDI y HLDI de cinco comunidades en una pradera de *Leymus chinensis*. Las comunidades con la misma letra dentro del mismo índice no difieren a $P=0,05$ con la prueba de rango múltiple de Duncan. Lk: *Leymus chinensis-Kalimeris integrifolia*; Lc: *L. chinensis*; Pc: *Phragmites communis*; Cv: *Chloris virgata*; Ks: *Kochia sieversiana*.

DISCUSSION

Applicability of Shannon-Wiener index for analysis of taxonomic and life-form diversity. The applicability of the Shannon-Wiener index to biotic communities has been discussed frequently (Hill, 1973; Magurran, 1988; Ma & Liu, 1994). On the basis of Pielou's method, the Shannon-Wiener index is used for calculation of the HDI. However, some authors argue that the HDI based on higher taxonomic units is meaningless, because the measurement of species diversity is still uncertain, even with higher taxonomic units (Magurran, 1988). Osborne et al. (1980) argued that the HTDI should be considered for lotic community analysis, which has a definite ecological meaning. Harper (1977) suggested that plant growth form should be considered in plant community analysis. With regard to our current results, the HDI and HLDI both showed very similar patterns (positive linear relationships) in relation to patch area, except for the *K. sieversiana* community, which indicated that the Shannon-Wiener index was sensitive enough to estimate the patterns of taxonomic and life-form diversity at the habitat scale.

Applicability of higher taxonomic units and life form as a surrogate for species. In recent decades, family and genus were used in many studies as surrogates for species to describe diversity patterns at regional or geographical scale (Balmford et al., 1996a, 1996b; Grelle, 2002; Heino & Soininen, 2007; Mazaris et al., 2010). However, in some studies, no relationship between the number of families and species richness was observed (Prance, 1994; Vanderklift et al., 1998). Our results demonstrated that no significant difference existed between genus and species, both in the regression slope and intercept, in each community. In addition, no significant differences between family and species in the slope but significant differences in the intercept were observed for each community. Thus both genus and family could be used as a surrogate of species to analyse plant diversity patterns at the local community level in a *L. chinensis* meadow.

Many studies have analysed morphospecies diversity in invertebrate communities (Oliver & Beattie, 1996; Cotes et al., 2009; Derraik et al., 2010). Similarly, different plant life forms are classified as "morphospecies" for rapid assessment of plant diversity patterns. Life form-based morphospecies were classified on the basis of stem or root morphology and were easily

recognisable even if the observer has no formal training in plant taxonomy. The present results indicated that the HLDI showed a significant difference with species for each of the five communities, especially in species-rich communities such as the *L. chinensis*–*K. integrifolia* and the *L. chinensis* communities. This may be because the number of life form categories was too low and consequently the morphospecies showed a high level of variation.

Determinants of the applicability of different components in HDI and HLDI. In the present study, a modified hierarchical diversity approach was employed to partition species diversity in order to quantify the contribution of different taxonomic units and life forms. In terms of higher taxonomic units (family and genus), a lower $H'_{FG}(S)$ would cause a smaller difference between $H'(G)$ and $H'(S)$. Our results demonstrated that the contributions of species ($H'_{FG}(S)$) to HDI were rather low in the five communities (mean 3.66%) (Fig. 1). As a result, genus was the best surrogate for species. Similarly, a lower $H'_F(G)$ would cause a smaller difference between $H'(F)$ and $H'(S)$. The mean contribution of genus ($H'_F(G)$) was about 33.71%, which led to strong differences between the family and species diversity patterns. In terms of different life forms, the contribution of RLF-based morphospecies ($H'(RLF)$) to $HLDI_1$, SGF-based morphospecies to $HLDI_2$, and RGF-based morphospecies to $HLDI_3$ was on average 47.79%, and that of species within morphospecies was on average 52.21%. Thus the life form-based morphospecies showed a significant difference with species in diversity patterns. Classification of life form-based morphospecies into more-detailed categories, such as caespitose-H or rosette-H, is needed to improve the sensitivity of the morphospecies classification.

Osborne et al. (1980) demonstrated that the contribution of family to HDI was about 60%, that of genus was 30–40%, and that of different trophic components to HTDI was about 50% in a lotic community, which is similar to our present results. Accordingly, we hypothesised that a contribution of 50–55% may be the threshold that determines the applicability of life form-based morphospecies. Furthermore, in the present study no significant differences in the contributions of different components to HDI and HLDI were observed among the five communities. We also hypothesised that the percentage contribution of different components to total species diversity was relatively stable. Of course, these hypotheses need further testing in additional taxa and at a larger spatial scale. However, it is likely that higher taxonomic units such as family and genus are applicable as a surrogate for species in a community that contains a large number of monospecific genera and monospecific families. With regard to temperate meadow steppe, identification to family and genus level is adequate to reflect plant diversity patterns but more detailed categories are needed for classification of life form-based morphospecies to be applicable in analyses of diversity patterns.

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APPENDIX

Composition of taxon and life forms and the species importance value in five communities.
Importance value = $100 \times (\text{relative coverage} + \text{relative height}) / 2$.

Species	Family	Life form			Importance value (mean \pm SD)				
		RLF	SGF	RGF	Lk	Lc	Pc	Cv	Ks
<i>Leymus chinensis</i>	Poaceae	H	EG	R	9.95 \pm 4.51	16.78 \pm 10.79	8.25 \pm 6.34	3.94 \pm 2.75	4.19 \pm 4.61
<i>Phragmites communis</i>	Poaceae	H	EG	R	5.52 \pm 3.22	10.74 \pm 5.50	22.42 \pm 8.12	12.93 \pm 6.07	
<i>Arundinella hirta</i>	Poaceae	H	EG	R	4.96 \pm 1.91	1.90 \pm 2.41			
<i>Setaria viridis</i>	Poaceae	Th	CG	BR	4.89 \pm 4.09	6.56 \pm 3.71	10.21 \pm 4.00	0.31	7.79 \pm 4.51
<i>Calamagrostis rigidula</i>	Poaceae	H	EG	R	3.28 \pm 2.45	3.28 \pm 2.98	1.13 \pm 2.41		
<i>C. epygjos</i>	Poaceae	H	EG	R	0.56 \pm 1.06	0.96 \pm 2.55	1.13 \pm 1.18		
<i>Chloris virgata</i>	Poaceae	Th	CG	BR	1.14 \pm 2.74	2.17 \pm 2.17	7.48 \pm 6.77	30.92 \pm 7.01	17.72 \pm 5.25
<i>Hierochloa glabra</i>	Poaceae	H	CG	R	0.99 \pm 1.49	0.62 \pm 2.04	0.21		
<i>Hemarthria sibirica</i>	Poaceae	H	EG	R	0.88 \pm 1.74	0.14			
<i>Spodiopogon sibirica</i>	Poaceae	H	EG	R	0.86 \pm 2.20				
<i>Celestogenes squarrosa</i>	Poaceae	H	EG	BR	0.47 \pm 1.83	0.79 \pm 1.70			
<i>Elymus davouricus</i>	Poaceae	H	EG	R	0.13 \pm 3.00				
<i>Eragrostis pilosa</i>	Poaceae	H	CG	BR		0.14 \pm 0.77			
<i>Puccinellia chinampoensis</i>	Poaceae	H	CG	BR			1.87 \pm 3.43	7.72 \pm 3.84	3.52 \pm 8.87
<i>P. tenuifolia</i>	Poaceae	H	CG	BR			0.61 \pm 3.42	1.32 \pm 1.32	1.66 \pm 3.60
<i>Echinochloa crusgalli</i>	Poaceae	H	EG	BR			0.53 \pm 5.23	0.57	0.78
<i>Kalimeris integrifolia</i>	Compositae	H	ED	TR	8.04 \pm 2.77	1.89 \pm 2.45	1.52 \pm 3.76		
<i>Artemisia scoparia</i>	Compositae	H	ED	TR	5.57 \pm 2.86	7.18 \pm 3.95	7.75 \pm 4.11	4.73 \pm 4.06	10.61 \pm 3.94
<i>A. mongolica</i>	Compositae	H	ED	R	2.54 \pm 1.39	1.07 \pm 2.13			
<i>A. anethifolia</i>	Compositae	H	ED	TR	1.25 \pm 1.86	0.88 \pm 1.46	2.87 \pm 2.90	10.75 \pm 3.53	8.91 \pm 6.06
<i>A. argyi</i> var. <i>gracilis</i>	Compositae	H	ED	R	0.91 \pm 2.33	0.24 \pm 0.76			
<i>A. gemelinii</i>	Compositae	Ch	ED	TR	0.51 \pm 3.35				
<i>A. laciniana</i>	Compositae	H	SR	R	0.10 \pm 0.92	0.08			
<i>Inula japonica</i>	Compositae	G	EG	BR	2.02 \pm 1.31	0.43 \pm 0.63	0.28 \pm 1.12		
<i>Heteropappus altaicus</i>	Compositae	H	ED	TR	1.08 \pm 2.94	0.97 \pm 1.73	0.2		
<i>Saussurea glomerata</i>	Compositae	H	ED	TR	0.89 \pm 1.19	0.03			
<i>Scorzonera albicaulis</i>	Compositae	G	SR	TR	0.89 \pm 0.78	0.59 \pm 1.49			
<i>Taraxacum sinicum</i>	Compositae	H	BRo	TR	0.85 \pm 0.62	0.84 \pm 0.60	0.32 \pm 1.10		
<i>T. mongolicum</i>	Compositae	H	BRo	TR	0.07 \pm 0.69				
<i>Sonchus brachyotus</i>	Compositae	H	EG	TR	0.78 \pm 2.65	2.64 \pm 4.27	2.34 \pm 3.60	0.13	
<i>Turczaninowia fastigiatus</i>	Compositae	H	SR	BR	0.41 \pm 0.82				
<i>Ixeris chinensis</i>	Compositae	H	SR	BR	0.33 \pm 0.57	0.71 \pm 0.57	0.13		
<i>Vicia amoena</i>	Compositae	G	ED	R	0.10 \pm 2.34				
<i>Cirsium setosum</i>	Compositae	H	ED	R	0.07 \pm 1.59			0.83 \pm 0.55	
<i>Senecio embraceus</i>	Compositae	H	SR	BR	0.06 \pm 0.55	0.10 \pm 0.09			
<i>Xanthium strumarium</i>	Compositae	Th	ED	TR		0.24 \pm 0.70	0.27 \pm 1.10		
<i>Lespedeza haburica</i>	Fabaceae	Ch	ED	TR	4.39 \pm 2.17	4.16 \pm 2.88	0.65 \pm 0.89		
<i>L. hedyaroides</i>	Fabaceae	Ch	ED	TR	2.83 \pm 2.72	1.40 \pm 1.62	0.61 \pm 1.29		
<i>Midicago ruthenica</i>	Fabaceae	H	ED	TR	3.01 \pm 1.58	2.45 \pm 1.77	0.33 \pm 0.31		
<i>Astragalus adsurgens</i>	Fabaceae	H	ED	TR	1.56 \pm 1.29	0.62 \pm 1.04	0.27		
<i>A. complanatus</i>	Fabaceae	H	PG	TR		0.21 \pm 0.10	0.11		
<i>A. scaberrimus</i>	Fabaceae	H	PG	TR		0.05			

<i>Amblytropis multiflora</i>	Fabaceae	H	BRo	TR	0.41 ± 0.63	1.34 ± 1.38	0.38 ± 4.75		
<i>Melilotus suaveolens</i>	Fabaceae	H	ED	TR	0.13 ± 3.05	1.18 ± 9.55	1.10 ± 4.07		
<i>Lathyrus quinquenervius</i>	Fabaceae	G	ED	TR	0.06 ± 1.45				
<i>Kummerowia striata</i>	Fabaceae	Th	ED	TR		0.09			
<i>Kochia sieversiana</i>	Chenopodiaceae	Th	ED	TR	1.71 ± 1.30	4.26 ± 6.17	8.02 ± 3.57	16.25 ± 3.27	27.15 ± 7.45
<i>Suaeda glauca</i>	Chenopodiaceae	Th	ED	TR	0.69 ± 3.37	2.13 ± 2.63	5.99 ± 4.39	5.75 ± 5.46	3.85 ± 3.28
<i>Salsola collina</i>	Chenopodiaceae	Th	ED	TR	0.31 ± 1.78	0.61 ± 5.39	0.39 ± 3.20		
<i>Chenopodium aristatum</i>	Chenopodiaceae	Th	ED	TR		0.16 ± 2.05	0.08		
<i>Potentilla flagellaris</i>	Rosaceae	H	PG	BR	2.80 ± 0.97	1.21 ± 1.49	0.49 ± 2.14		
<i>P. chinensis</i>	Rosaceae	H	SR	TR		0.14 ± 0.49			
<i>Sanguisorba tenuifolia</i>	Rosaceae	G	SR	TR	1.97 ± 1.70				
<i>S. officinalis</i>	Rosaceae	H	SR	TR	0.68 ± 1.97	0.14			
<i>Cynantrum chinense</i>	Asclepiadaceae	G	PG	TR	0.72 ± 2.47	4.10 ± 4.07	4.67 ± 3.28		0.44 ± 1.07
<i>C. sibiricum</i>	Asclepiadaceae	G	PG	R	0.56 ± 2.05	2.01 ± 2.39	0.48 ± 0.55		0.19
<i>C. paniculatum</i>	Asclepiadaceae	G	ED	BR	0.54 ± 1.12				
<i>Scutellaria scordifolia</i>	Lamiaceae	G	ED	TR	1.11 ± 0.76	0.90 ± 2.30			
<i>Stachys chinensis</i>	Lamiaceae	H	ED	TR	0.19 ± 1.74				
<i>Leonurus japonica</i>	Lamiaceae	H	ED	TR	0.14 ± 3.25	0.24 ± 1.81			
<i>Allium odorum</i>	Liliaceae	G	CG	B	3.80 ± 1.86	3.80 ± 2.37	0.90 ± 3.37		
<i>A. schoenoprasum</i>	Liliaceae	G	CG	B	0.10 ± 2.37				
<i>Anemarrhena asphodeloides</i>	Liliaceae	G	BRo	R	0.11 ± 2.39				
<i>Carex duriuscula</i>	Cyperaceae	H	CG	R	1.77 ± 0.96	0.53 ± 1.14	0.63 ± 1.10		
<i>Eleocharis intersita</i>	Cyperaceae	G	EG	R		0.09			
<i>Scirpus planiculmis</i>	Cyperaceae	G	EG	R			0.48 ± 2.04	0.63	
<i>Iris lectea</i>	Iridaceae	H	CG	BR	0.57 ± 1.16	0.16 ± 0.19	0.21		
<i>I. dichotoma</i>	Iridaceae	G	SR	BR	0.22 ± 1.25				
<i>Polygala tenuifolia</i>	Polygalaceae	H	ED	TR	0.29 ± 2.93	0.12			
<i>P. sibirica</i>	Polygalaceae	H	ED	TR	0.04 ± 0.81	0.15 ± 0.46			
<i>Thalictrum simplex</i>	Ranunculaceae	G	ED	BR	3.72 ± 1.88	0.38 ± 1.98	0.51 ± 7.74		
<i>T. squarrosa</i>	Ranunculaceae	G	ED	BR	1.34 ± 2.68	0.92 ± 1.61			
<i>Viola prionantha</i>	Violaceae	H	BRo	R	0.62 ± 0.51				
<i>V. dissecta</i>	Violaceae	H	BRo	R	0.20 ± 0.83	0.09 ± 0.26			
<i>Messerschmidia sibirica</i>	Boraginaceae	G	ED	TR	0.85 ± 1.38	2.34 ± 2.38	2.63 ± 2.23	1.09 ± 1.10	1.50 ± 1.80
<i>Polygonum sibirica</i>	Polygonaceae	G	ED	TR	0.85 ± 0.91		1.25 ± 2.73	1.73 ± 2.17	0.92 ± 0.58
<i>Siler divaricatum</i>	Umbelliferae	H	ED	TR	0.42 ± 0.79	0.60 ± 1.78			
<i>Gelium verum</i>	Rubiaceae	G	ED	R	0.35 ± 1.27	0.21 ± 0.67			
<i>Adenophora stenophylla</i>	Campanulaceae	G	ED	TR	0.32 ± 1.33				
<i>Calystegia japonica</i>	Convolvulaceae	G	PG	TR	0.28 ± 1.15	0.57 ± 1.40	0.11		
<i>Thesium chinensis</i>	Santalaceae	H	CG	TR	0.13 ± 1.18				
<i>Plantago depressa</i>	Plantaginaceae	H	BRo	TR	0.07 ± 0.39	0.18 ± 0.35			10.77 ± 7.62
<i>Lysimachia barystachys</i>	Primulaceae	H	ED	R	0.04 ± 0.94	0.05			
<i>Hibiscus trionum</i>	Malvaceae	Th	ED	TR		0.33 ± 0.48			
<i>Equisetum arvense</i>	Equisetaceae	G	CG	R		0.11			
<i>Draba nemorosa</i>	Cruciferae	Th	ED	TR			0.18		
<i>Limonium bicolor</i>	Plumbaginaceae	H	BRo	TR				0.39	

RLF, Raunkiaer's life form classification; SGF, stem growth form; RGF, root growth form.

H, hemicryptophyte; G, geophyte; Th, therophyte; Ch, chamaephyte. EG, erect grass-like stem; ED, erect dicot stem; BRo, basal rosette stem; SR, semi-rosette stem; PG, prostrate or climbing stem; CG, caespitose stem. R, rhizomatous root; BR, bushy root; TR, taproot; B, bulbous root.

Lk: *Leymus chinensis*-*Kalimeris integrifolia*; Lc: *L. chinensis*; Pc: *Phragmites communis*; Cv: *Chloris virgata*; Ks: *Kochia sieversiana*.