Climatic condition effects on the components of plant diversity in the western Iran grasslands using multiplicative partitioning methods

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ABSTRACT

This study aimed to investigate the effects of different climatic conditions (arid vs. semi-arid) on patterns of species richness and plant diversity as well as plant composition in two over-grazed regions. The regions were located in the west of Iran, closed to each other and different in climatic conditions. Based on the aridity index of De Martonne climate classification, Rika (I = 9.94) and Dalab (I = 18.54) were categorized as arid and semi-arid regions, respectively. In each region, we collected plant vegetation data from a nested sampling design consisted of local (80 plots) and regional (8 sites) scales. Patterns of plant diversity and species richness in each region, and similarity of plant composition between the two regions were analyzed using multiplicative partitioning methods, species richness estimator and cluster analysis, respectively. The results showed that diversity components in all scales had significant difference with their expected values (*P*<0.000) resulted in non-random distribution of plant species among and within scales. In addition, the results showed that species richness in Rika region (arid, 89 species) was greater than Dalab region (semi-arid, 76 species). The results of cluster analysis suggested that Rika and Dalab regions had different plant species compositions. Based on our results, the role of seed dispersal might be more prominent in smaller scales (plot and sites) compared to region scale, since the highest possible amount of β-diversity was occurred between regions. Our results suggested that plant diversity in the largest scale (region) had the highest amount of diversity components where the rangeland manager should attend on this scale for conservation of plant diversity.

Keywords: β-diversity, Species richness estimators, Shannon's diversity, Plant composition, Management plans, Climate change.

INTRODUCTION

Study of plant diversity changes at different spatial scales is an important aspect of diversity studies in hierarchical systems (Golodets *et al.* 2011). Since emphasis of conservation biologists has recently shifted from the conservation of single species to the conservation of entire communities (Devictor & Robert 2009), conservationists try to determine the spatial (and temporal) distribution of species within large areas and how abiotic and biotic factors such as animal grazing (Tahmasebi *et al.* 2020), fire disturbance (Moradizadeh *et al.* 2020) and climate change (Erfanzadeh *et al.* 2015), can change these patterns. In addition, study on spatial patterns of plant species is an important issue in vegetation ecology and phytosociology due to important influences of the plant spatial patterns on the functioning of ecosystems (Komac *et al.* 2011). Moreover, biodiversity is defined in various ways, from genetic to landscape levels and, species diversity is the most common approach to relate biodiversity (Ramezani 2019). It is well known that pattern of species diversity in nature is recognized as being scale-dependent (Whittaker *et al.* 2005) and, spatial scaling of diversity patterns helps us to identify the most important sources of diversity in the nature (Sasaki & Yoshihara 2013). It is very important to recognize and conserve diversity at the appropriate scales of interest in order to the preservation of total diversity (γ-diversity)

in a given area (Whittaker *et al.* 2001). It is widely accepted that spatial patterns of species diversity change over multiple spatial scales (Heydari *et al.* 2019). We know that spatial patterns of plant species diversity observed within small areas (e.g. quadrat) may be very different from those found over larger areas such as regions or communities (Erfanzadeh *et al.* 2015).

It could be that distributions of plant species in a region are the result of processes operating at the local and smaller spatial scales (Ricklefs 1987; Huston 1999; Collins *et al.* 2002). Therefore, understanding the diversity patterns in the plant community, determining the impact of biotic and abiotic environmental factors on the species diversity, and recognizing the changes of vegetation after introducing a measure such as grazing required quantifying species diversity at multiple scales (Cabra-García *et al.* 2010). For instance, cessation of grazing may increase plant species diversity in local scale (i.e. plot) but have no significant effect on plant diversity in broader scales, i.e. site or landscape (Erfanzadeh *et al.* 2015).

One way to analyze the pattern of plant distribution at different scales is to employ diversity partitioning methods that partition total diversity into its components. The idea of diversity partitioning is originated by Whittaker (1960), who described alpha (α) and beta (β) as components of the total diversity of gamma (γ), and also linked them, to a spatial scale. Two different perspectives exist for relating β-diversity components directly with α- and γ-diversity components: the multiplicative perspective ($\beta = \gamma/\alpha$) and the additive perspective ($\beta = \gamma-\alpha$). There have been extensive discussions with respect to which perspective is better in partitioning "independent" β-diversity. As a result, both additive and multiplicative partitioning can be extremely useful in studies focusing on species diversity (Ricotta 2010; Veech & Crist 2010). More precisely, the multiplicative partitioning methods has been applied as a useful tool for quantifying diversity components across multiple spatial scales (Wagner *et al.* 2000; Gering *et al.* 2003) and specifically in vegetation studies (e.g. Jost *et al.* 2010; Golodets *et al.* 2011; Rickert *et al.* 2012). In this study, the primary objective was to identify patterns of total plant diversity across different spatial scales in two regions which are closed to each other and different in the climatic conditions. Both regions have being grazed extensive for a long time.

Toward this attempt, we used multiplicative diversity partitioning framework to identify patterns of plant diversity. Secondly, our objective was to compare species richness between the two regions. Therefore, we used diversity estimator and compare its results between the two regions. Finally, we used cluster analysis for comparing the similarity of plant species compositions among the scales for detecting the main resource of composition differentiation. We tried to answer: (1) Which scales had the highest contribution of plant diversity to the total diversity in each region and in the total? In other words, which scale is better for conservation plans of plant diversity? (2) Can change in climatic conditions (arid vs. semi-arid) lead to change in the diversity components and richness of plant species? (3) How is the relationship between β-diversity (coming from multiplicative partitioning methods) and similarity between communities of whole data set (coming from cluster analysis)?

MATERIALS AND METHODS
Study area
The study was conducted in two regions: Rika (extended from 32°53′ to 33°36′ N and from 45°54′ to 46°39′ E) and Dalab (extended from 33°18′ to 33°51′ N and from 45°42′ to 46°49′ E) in the west of Iran. Mean annual temperature and precipitation are 24.1 °C and 339 mm in Rika and 16.7 °C and 495 mm in Dalab, respectively. The climate condition was calculated based on the aridity index of De Martonne climate classification [I = P/(T+10), Jafari *et al.* 2018]; where I is the aridity De Martonne index, P is annual precipitation (mm) and T is mean annual temperature (°C). Based on De Martonne climate classification, the climate condition could be categorized into five classes include: arid (I > 10), semi-arid (10 < I < 19.9), Mediterranean (20 < I < 23.9), semi-humid (24 < I < 27.9) and humid (28 < I < 34.9) (Jafari *et al.* 2018). The climate is arid and semi-arid in Rika (I = 9.94; arid class) and Dalab regions (I = 18.54; semi-arid class), respectively. Rangeland is the main land use type in these regions with the intensive sheep and goat grazing for a long time.

Sites selection and data collection
Vegetation data were collected according to a nested sampling design from two regions of arid (Rika) and semi-arid (Dalab), 8 sites (four sites in each region), and 80 plots (10 plots in each site). During the growing season of 2012, vegetation samplings were carried out in March and May from Rika and Dalab, respectively. The location

of each sampling plot was selected by completely randomized design through Arc GIS 10.6 selection (Faramarzi *et al*. 2010; Erfanzadeh *et al*. 2015) (Fig. 1).

Diversity partitioning

We used multiplicative diversity partitioning to assess plant diversity patterns across multiple spatial scales. The spatial hierarchal method was applied in two levels in each region, including (1) plot scale and (2) site scale. In addition, the analysis was performed for total data coming from both regions. Therefore, the total plant species diversity (through species richness and Shannon index) can be described by the following formula [1] (see also Crist *et al.* 2003) in each region:

[1]: $\gamma = \alpha_1$ (within plots) $\times \beta_1$ (among plots) $\times \beta_2$ (among sites)

We could also define β_3 as a diversity indicating the turnover of species among two regions. Therefore, the aforesaid formula [1] can be improved into formula [2]:

[2]: $\gamma = \alpha_1$ (within plots) $\times \beta_1$ (among plots) $\times \beta_2$ (among sites) $\times \beta_3$ (among regions)
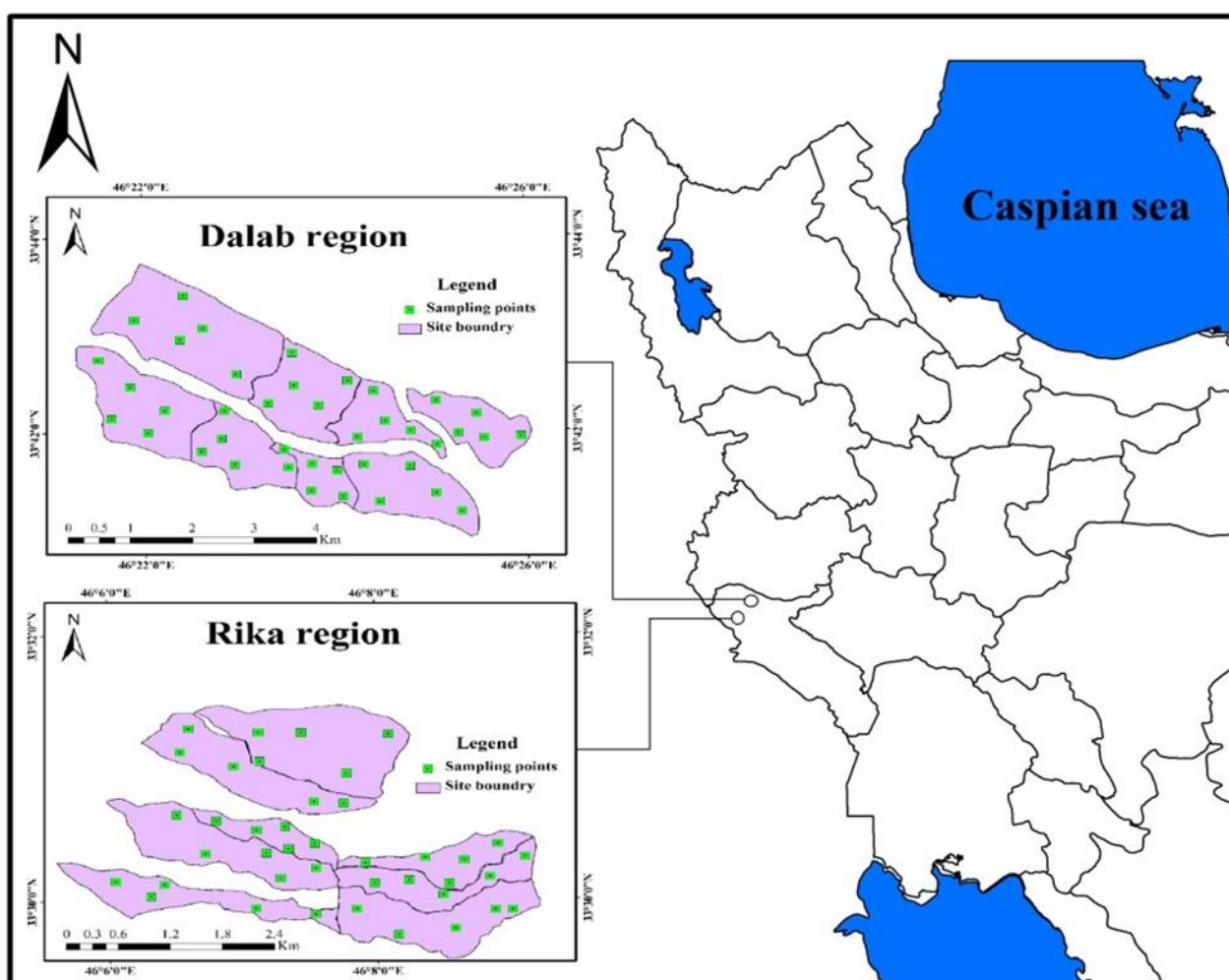

Fig. 1. Map of the study areas; the locations of Dalab and Rika in Ilam province and Iran.

Data Analysis

We tested the significant differences between the spatial partitioning of diversity and expected values of diversity calculated by individual-based randomizations (10,000 permutations; Crist *et al.* 2003), evaluating whether the α- and β-diversity components of diversity differed significantly from a random distribution of individuals among samples (Crist *et al.* 2003). This analysis could be performed for both species richness and Shannon diversity in multiplicative mode, which is appropriate for conservation studies (Jost *et al.* 2010).

β-diversity (estimated using species richness and Shannon index) could range from 1, when two species pools had identical species composition, to 2, when two species pools had no overlap in species composition. However, for the highest scale of the whole region, the β-diversity calculated based species richness and Shannon diversity could range from 1 to 2 because we had two species pools at this level while in plot and site levels it could range from 1 to 10 and 1 to 4, respectively. In the current study, we used species richness and Shannon diversity indices for calculating β-diversity. Species richness is considered as the number of species in each sampling unit, while Shannon diversity is the exponential of Shannon entropy (the traditional Shannon–Wiener index) and is the true diversity, measured as the effective number of species, the number of species in an assemblage with an evenness of 1.0 (Jost 2007, Zamani *et al.* 2019).

In addition, to calculate species richness in each region, data were analyzed using the Estimate S version 8.2 (Colwell 2009) with 1000 randomization runs to compute seven non-parametric species richness estimators (ACE, ICE, Chao1, Chao2, Jack1, Jack2 and Bootstrap) and two estimators based on the extrapolation of species accumulation curves (ESAC) estimators (MMRuns and MMMeans) for both the Dalab and Rika regions to determine which region had greater species richness (Colwell & Coddington 1994; Brose *et al.* 2003; Wu *et al.* 2010). Following the recommendation of recent studies (Colwell & Coddington 1994; Colwell & Coddington 1994; Brose *et al.* 2003; Chiarucci *et al.* 2003; Sodhi *et al.* 2005; O'Dea & Whittaker 2007), the mean of nine estimators was used and the results of two regions were compared with paired *t*-test in R version 3.0.2 (R Development Core Team 2013).

Hierarchical cluster analysis of the species occurrences was used for clustering all data set coming from both regions using the Bray–Curtis similarity index and Ward's methods. This analysis was carried out using program PC-ORD (McCune & Mefford 2006).

RESULTS
General community patterns
We recorded 3805 plant individuals representing 114 plant species from 27 families in all sites (three species could not be identified due to the very early stage of growth). Nearly half of the species were from three families of Poaceae, Asteraceae, and Fabaceae with 25, 24 and 15 species, respectively (Fig. 2).
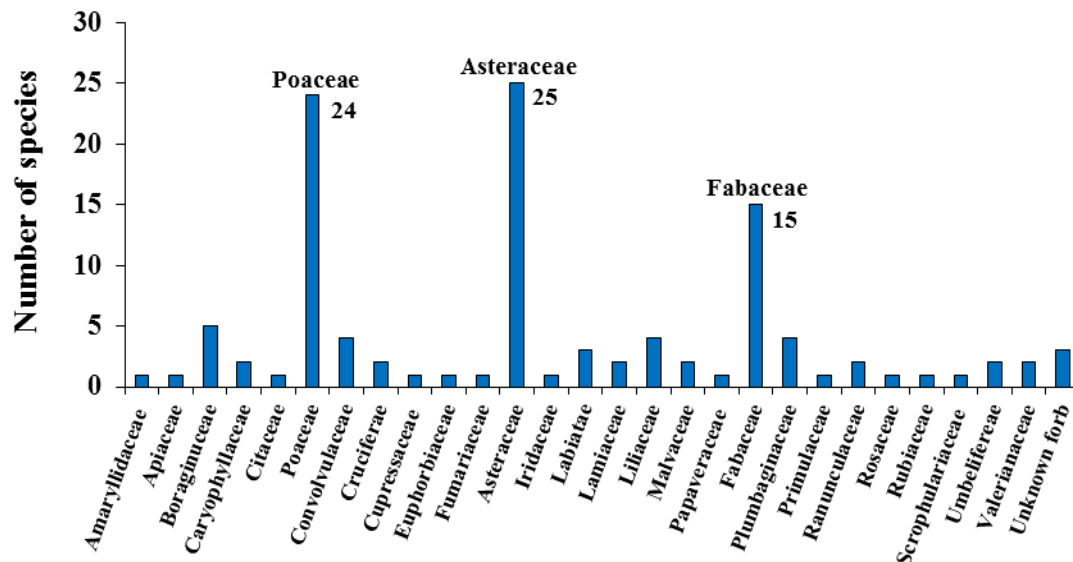

Fig. 2. Number of species for each family in the study area.

Species richness in the regions
In Rika region, the observed number of species was 89, represented 87.76% of the mean estimated species richness (101.4 species) which estimated from different species richness estimators. In Dalab, 76 species was observed, representing 84.85% of the mean estimated (89.6 species). In addition, the total observed species richness (114) was very close to the mean of species richness estimators (118.6) (Table 1). Paired t-test of the nine estimators of

ACE, ICE, Chao1, Chao2, Jack1, Jack2, Bootstrap, MRuns, and MMMens) showed that species richness in Rika was significantly higher than in Dalab (t = 9.50, df = 8, *p*-value < 0.0001).

Table 1. Species richness estimators for both Rika and Dalab.

Abbreviation	Estimator	Rika	Dalab	Total
ACE	Abundance-based coverage estimator of species Richness	93.45	80.73	117.92
ICE	Incidence-based coverage estimator of species Richness	104.77	87.58	118
Chao1	Abundance-based estimator of species richness	92.11	88	118.67
Chao2	Incidence-based estimator of species richness	99.9	89.56	117.95
Jack1	First-order Jackknife richness estimator	108.5	93.55	121.9
Jack2	Second-order Jackknife richness estimator	112.69	101.39	123.92
Bootsreap	Bootstrap richness estimator	98.94	84.28	118.14
MMRuns	Transformation of Michaelis-Menten hyperbole by Raaijmakers. Estimate curves averaged over randomizations (runs)	101.31	90.66	115.57
MMMens	Transformation of Michaelis-Menten hyperbole by Raaijmakers. Estimate curve computed once for mean species	101	90.29	115.58
Mean	The mean of the all estimators	101.4	89.4	118.6
Real	Real observed richness	89	76	114

Diversity pattern in each region

The results of diversity partitioning methods for whole data revealed that diversity among plots (β_1) had the highest contribution to the total diversity for species richness ($\beta_1 = 3.85$) and β-Shannon ($\beta_1 = 3.19$). However, diversity among regions (β_3) exhibited the highest possible value for both species richness and Shannon index [1.39 and 1.38 from 2 (highest possible value)]. In addition, diversity within plots was greater than that within sites. However, diversity among plots was smaller than that among regions (Table 2).

Similarly, hierarchical diversity partitioning in Rika and Dalab indicated that the highest β-species richness and β-Shannon occurred among plots. Species richness and Shannon diversities within plots were also lower than expected values in both Rika and Dalab regions, whereas diversity among plots and sites (β_1 and β_2) were always significantly greater than expected values (Table 2).

Table 2. Partitioning plant species diversity components against expected values according to the randomization model in the different spatial scales.

Diversity	Scale	Species richness			Shannon–Wiener Index		
		Observed	HP†	P*	Observed	HP†	P*
Whole regions							
α_1	Within plots	12.82	80	1.00	9.84	80	1.00
β_1	Among plots	3.85	10	0.00	3.19	10	0.00
β_2	Among sites	1.67	4	0.00	1.36	4	0.00
β_3	Among regions	1.39	2	0.00	1.38	2	0.00
γ		114.6			58.9		
Dalab region							
α_1	Within plots	10.89	40	1.00	8.38	40	1.00
β_1	Among plots	4.35	10	0.00	3.59	10	0.00
β_2	Among sites	1.61	4	0.00	1.35	4	0.00
		76.2			40.6		
Rika region							
α_1	Within plots	14.9	40	1.00	11.69	40	1.00
β_1	Among plots	3.46	10	0.00	2.82	10	0.00
β_2	Among sites	1.72	4	0.00	1.38	4	0.00
		88.7			45.5		

† The highest possible value
*p = 0.00 indicates that the observed diversity value is significantly larger than the randomized datasets produced. P = 1.00 indicates that diversity value of the randomized datasets produced is significantly larger than that observed.

Hierarchical cluster analysis between studied regions

Cluster analysis identified two main clusters at the first step in which the clusters were accordance with whole data coming from both regions. The first cluster included Dalab. while the second contained Rika. However, the cluster analysis failed to separate sites (in each region) and plots (in each site) (Fig. 3).
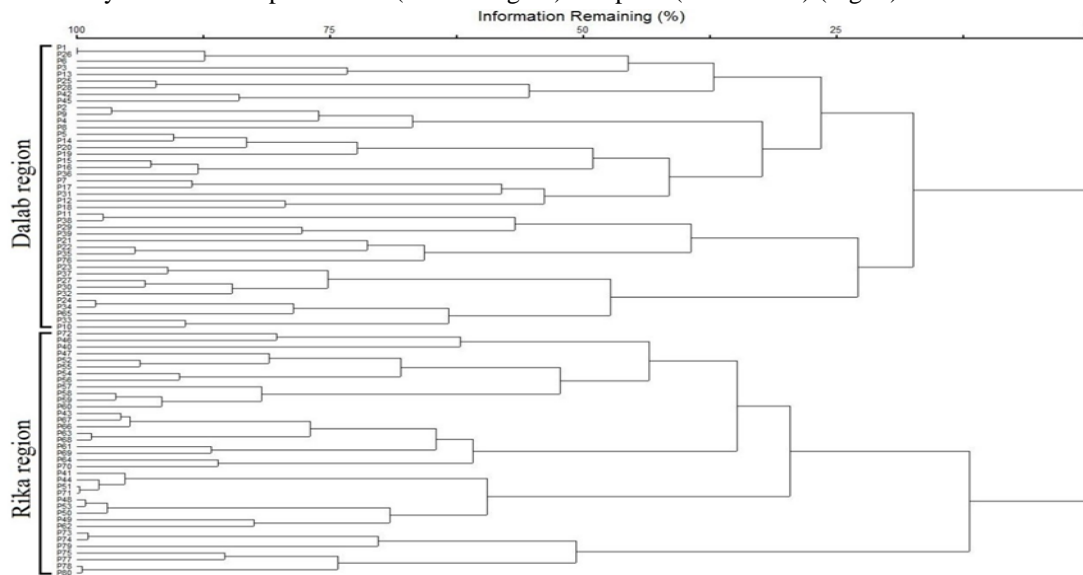

Fig. 3. Hierarchical cluster analysis for 80 plots between two regions (Rika and Dalab) in west of Iran. The Bray–Curtis similarity coefficient was used as a measure for species turnover among the plots.

DISCUSSION

We used randomization test for revealing the plant diversity patterns. The results indicated that all β-diversity components were significantly higher than the expected values. These results were similar to previous studies, i.e., Chandy *et al.* (2006) in the forest communities, Paknia & Pfeiffer (2011) in the ant communities, Rodríguez & Ojeda (2011) in the small mammal's communities and Erfanzadeh *et al.* (2015) in the rangeland communities. This significant deviation of most diversity components from their expected values revealed that plant species were distributed non-randomly among scales. This result points out to the importance of biotic or abiotic factors at the local and spatial scales for determining community composition and richness. In addition, the results exhibited that the local α-diversity component (α_1) was consistently lower than the expected values in both Rika and Dalab regions for both diversity indices (species richness and Shannon). Such scale-dependent deviations of the observed diversity from the expected can be generally explained by species aggregation at a relatively small scale and, accordingly, spatial differentiation of diversity at a large scale (He & Legendre 2002; Crist *et al.* 2003; Summerville *et al.* 2003; Weiher & Howe 2003). These aggregations of species could be a result of animal grazing in both regions. Another key result found in the current study was that species richness in Rika (with arid condition: lower precipitation) was higher than in Dalab (with semi-arid condition: higher precipitation). We think that the shrubby species in Rika play an important role in facilitating growth conditions for other plant species (nurse role: Flores & Jurado 2003). On the one hand, arid regions are characterized by limited and variable rainfall (Chesson *et al.* 2004), and on the other hand, there are few plant species (i.e. thermal-tolerant) which tolerate this harsh condition. Therefore, non-thermal-tolerant species had to migrate into shrubby nurse species (e.g. *Astragalus microcephalus* Willd.). In this regard, nitrogen fixing (Jankju 2013), better condition in the moisture (Gomez-Aparicio 2009) and better soil properties (Piroozi *et al.* 2018) under shrubby species such *Astragalus* sp. resulted in facilitated growth condition for other plant forms (e.g. herbal grass and forb). Moreover, in arid regions, fewer competition for capturing resources (i.e. light and nutrient) might increase plant diversity (Tahmasebi *et al.* 2017). However, more precipitation in Dalab resulted in increased cover percentage of plant species in comparison with Rika (unpublished data). In addition, better environmental condition in the semi-arid region of Dalab (i.e. higher precipitation) may increase competition for resource capture led to dominance of some competitor species and decrease species diversity. Over the last century shifts in climatic trends (global temperature gains) and shifting precipitation patterns have been documented with several studies reporting associations between recent climatic patterns and temporal change in the vegetation (e.g. Parolo & Rossi 2008;

Gottfried *et al.* 2012). Therefore, we supposed that global warming could shift the climatic condition of Dalab (semi-arid) into the climatic condition of Rika (arid), leading to a higher richness in Dalab region in the future. We found that diversity in the local scales (plot and sites) had the highest contribution to the total diversity in each region, whereas diversity components in the largest scale (region) were provided fewer contributions to the total diversity. In addition, diversity among regions (β3) had the highest possible value (1.39 and 1.38 of 2 for species richness and Shannon index, respectively). These results are similar to those obtained by Sasaki & Yoshihara (2013) who found that local-scales had little influence on regional plant richness in a Mongolian grassland, because the diversity among landscape units contributed the most to the total diversity. However, Chandy *et al.* (2006) reported that in forest ecosystem, small and intermediate scales contained the largest proportion of total diversity of tree and understory species in the forest ecosystems. It is well known that β-diversity of plant communities may be decreased by dispersal between spatial units which acts as a homogenizing force (Loreau 2000). Dispersal processes operate at different spatial scales, at the micro-scale by seed rain, while at the mesoscale operate by cultivation and machinery, animals and wind (Gabriel *et al.* 2007). Nevertheless, in macro-scales (e.g. the regions in our study), dispersal agents might play a minor role in seed dispersal, remaining heterogeneity between regions. We conclude that vegetation composition and diversity in the entire area are derived from climatic condition (deterministic factors) rather than animal grazing and seed dispersal (stochastic factors). Based on the cluster analysis, Dalab and Rika regions exhibited different and separate plant species compositions. Since, highest possible amount of β-diversity was occurred between the regions (1.39 and 1.38 from 2 for species richness and Shannon index, respectively) compared to β-diversity in plots and sites, it can be concluded that the role of seed dispersal (mostly by epizoochory and exochory) might be more prominent in the smaller scales (plots and sites) compared to regional scale. However, relatively higher distance between the two regions could lead to limitation in species entrance from each region into the other. Movements between spatial units, such as dispersal or migration, can lead to an elevated α-diversity and a decreased β-diversity, due to a homogenizing effect (Loreau 2000) and restricted dispersal among sites can cause an increased vegetation heterogeneity (Willson 1993).

CONCLUSION

We found that nursing role of shrubby species in a short extent of climate condition might increase plant species diversity. In fact, elevated temperature and decreased precipitation (alteration in climate from semi-arid into arid) can lead to migration of herbal species into the beneath of shrubby species which facilitate the growth condition of herbals. As a result, climate change increases plant species diversity through species migration in our study area, but this migration leads to increased community patchiness, followed by loss of community function (i.e. soil production). In addition, our results suggested that plant diversity in largest-scale (region) had the highest value, so decision-makers should focus on this scale for conservation of plant diversity.

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تأثیر شرایط اقلیمی بر مؤلفه‌های تنوع گیاهی در علفزارهای غرب ایران با استفاده از روش تقسیم‌بندی افزایشی

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چکیده

هدف تحقیق حاضر بررسی تأثیر شرایط اقلیمی مختلف (خشک و نیمه خشک) بر الگوی تنوع و غنای گیاهی و همچنین، بر ترکیب گیاهی در دو منطقه تحت چرای شدید بود. دو منطقه‌ی مورد مطالعه در غرب ایران و در فاصله نزدیکی از هم قرار داشتند. بر اساس روش طبقه‌بندی اقلیمی دومارتن، مناطق ریکا ($I = 9.94$) و دالاب ($I = 18.54$) به ترتیب دارای اقلیم خشک و نیمه خشک تفکیک شدند. در هر منطقه نمونه‌برداری با استفاده از طرح نمونه‌برداری تودرتو (آشیانه‌ای) در دو مقیاس محلی (۸۰ پلات) و منطقه‌ای (۱۶ سایت) انجام شد. تجزیه و تحلیل الگوی پراکنش گیاهان، غنای گونه‌ای و شباهت ترکیب گیاهی به ترتیب با استفاده از روش‌های تقسیم‌بندی ضربی تنوع، تخمین‌گرهای غنای گونه‌ای و آنالیز خوشه‌ای انجام شد. نتایج نشان داد که مقدار مؤلفه‌های تنوع گونه‌ای در همه مقیاس‌های مورد مطالعه دارای اختلاف معنی‌داری ($P < 0.000$) با مقدار مورد انتظار آن بود که نشان‌دهنده پراکنش غیرتصادفی گونه‌های گیاهی در درون و بین مقیاس‌های مورد مطالعه است. همچنین غنای گونه‌ای در منطقه ریکا (۸۹ گونه) بیش از منطقه دالاب (۷۶ گونه) بود. نتایج حاصل از آنالیز خوشه‌ای مشخص کرد که دو منطقه مورد مطالعه دارای ترکیب گیاهی متفاوت هستند. بر اساس این تحقیق می‌توان اظهارد کرد که نقش عواملی از قبیل پخش بذر (کاهش دهنده تنوع بتا) ممکن است در مقیاس‌های محلی (پلات و سایت) مهم‌تر از مقیاس‌های منطقه‌ای باشد، زیرا بیشترین مقدار ممکن تنوع بتا مربوط به مقیاس بین مناطق بود. همچنین نتایج نشان داد که بیشترین مقدار تنوع گونه‌ای در بزرگترین مقیاس (منطقه‌ای) وجود دارد. بنابراین، مرتعداران باید برای حفاظت از تنوع گونه‌ای، در برنامه‌های حفاظتی به مقیاس مذکور توجه داشته باشند.

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