DOI : <http://doi.org/10.22438/jeb/38/6/MRN-282>

JEB™

ISSN: 0254-8704 (Print)
ISSN: 2394-0379 (Online)
CODEN: JEBIDP

Studies on taxonomic diversity of plant communities and modeling its potential distribution in Yazılı Canyon Nature Park, Turkey

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Key words

Diversity indices
Modeling
Plant community
Regression tree technique
Taxonomic diversity

Publication Info

Paper received : 02.03.2016
Revised received : 30.08.2016
Re-revised received : 22.12.2016
Accepted : 10.05.2017

Abstract

Aim : The objective of the present study was to generate taxonomic diversity of plant communities and modeling its potential distribution in Yazılı Canyon Nature Park (Turkey).**Methodology :** In the present study, taxonomic plant diversity were measured from the data obtained from 107 sampling plots and then modeled to visualize its' potential distribution by using regression tree technique (RTT) across the Yazılı Canyon Nature Park situated in the Mediterranean region, Turkey.**Results :** Taxonomic diversity values were between 3.427 and 4.459. The variables made up the regression tree model were slope (%), distance to stream, solar illumination, altitude and aspect. The explained variances of tree models were unexpectedly found low with the values of 31.05% and 24.21% for training and testing data.**Interpretation :** Even though tree model does not have high explanation ability, it was visualized to see the potential distribution of the taxonomic diversity in the study area. The distribution map illustrated that the places immediate environment to Yazılı stream and highly very steep places of the canyon has more taxonomic diversity values than its' other parts. This result was found meaningful since those places are more humid and include the plant species having more taxonomic distances from each other compared to its' other parts.

Introduction

Various indices have been used in defining biodiversity in conservation biology and community ecology (Gülsoy and Özkan, 2008; Özdemir and Karnieli, 2011). Those indices are divided mainly into two groups, which are traditional diversity indices and character based diversity indices. Among traditional diversity indices, the most popular ones are Shannon-Wiener entropy, Simpson dominance, Margalef index and Brillion index (Chiarucci *et al.*, 2011; Svensson *et al.*, 2012; Bandeira *et al.*, 2013; Magurran, 2013). Character based diversity indices are known functional diversity and taxonomic diversity indices. Measuring functional diversity of living communities requires data about functional traits of the species. However, knowing the places in taxonomic hierarchy of the species is sufficient for measuring taxonomic diversity. In addition to this, taxonomic diversity is highly related to functional diversity, as well as species diversity of living communities (Özkan, 2012).

The explanations dealing with calculating taxonomic diversity for living communities were given by Warwick and Clarke (1995, 1998) and Clarke and Warwick (1998, 1999, 2001). These studies have attracted attention and, several researchers like Desrochers and Anand (2004), da Silva and Batalha (2006), You-Hua and Zhi-Bo (2009), Koperski (2010) and Gwali *et al.* (2010) have preferred taxonomic diversity index for calculating biodiversity in their studies.

Even though advantages of taxonomic diversity has been well-explained by Warwick and Clarke (1995, 1998). Traditional diversity indices are still being used often in determining biodiversity than taxonomic diversity index. The reasons are probably due to fact that calculating taxonomic diversity is more complex than calculating biodiversity by using traditional diversity indices, preparing data for measuring taxonomic diversity is a long time consuming process, all species considered should be identified at species level to measure taxonomic diversity and the number of statistical package programs including measuring taxonomic diversity is insufficient. Due to these probable reasons, a study about modeling and mapping of taxonomic diversity has not been generated in forest ecosystems so far. On view of the above, the present study was carried out to generate taxonomic diversity of plant communities and modeling its potential distribution in Yazılı Canyon Nature Park, Turkey.

Materials and Methods

Study area : The data was obtained from Yazılı Canyon Nature Park, situated in the Mediterranean region of Turkey (Fig.1). The study area has a typical Mediterranean climate (dry-hot summers/rainy winters). arth average annual precipitation if 950 mm. The most arid and hottest months are July and August (with an annual average temperature of 13.1° C, and 54 % average relative humidity). Heavy rains occur in November, December, January and February, while water deficit extends from June to mid-October (DMI, 2006). The canyon is a short (~6 km) deep

limestone valley with a height varying between 100 m and 400 m. Topography is irregular. Major soil types are brown forest soil, reddish-brown Mediterranean soil and reddish Mediterranean soil. Brutian pine (*Pinus brutia* Ten.) and Oak species (*Quercus* spp.) are dominant species in the forest. The nature park is rich in endemic species with twenty four endemic plant taxa (Özkan and Süel, 2008).

One hundred seven sample plots were surveyed in the Park (Fig. 1) and total of one hundred eighty two plant taxa were identified. The coverage of vascular plant taxa was documented according to Braun Blanquet method and transformed according to Whittaker (1973). All the datas were arranged and stored in Excel files for statistical analysis.

Response data : Taxonomic diversity index (Δ^*) is empirical relationship with Shannon–Wiener diversity but it has an added component of taxonomic separation. This index, as defined in Equation 1 was firstly employed by Warwick and Clarke (1995).

$$\Delta^* = \frac{\sum_{i,j} w_{ij} x_i x_j}{\sum_{i,j} x_i x_j + \sum_i x_i (x_i - 1) / 2}$$

where, x_i and x_j refers to numerical statement of the species abundances (e.g. number of individuals) and w_{ij} refers to 'distinctness weight' given to the path length linking species i and j in the hierarchical classification.

Taxonomic diversity values of sample plots were calculated by Paleontological Statistics (PAST) software version 1.89 (Hammer *et al.*, 2001).

Environmental data : All environmental variables were provided from digital elevation model belonging to study area. In this context, Digital elevation model (ELEVATION) was taken from General Directory of Forestry (OGM). Slope % (SLOPE) and aspect (ASPECT) were created from the elevation built function provided using ArcGIS. Topographic position index (TPI) and landform category (LFC) maps were made from the elevation map by placing "tpi_jen.avx" file into the Arcview extensions directory (Weiss, 2001). Solar illumination index (SOLAR) map was derived using elevation map by Topography tools extension in ArcGIS 10.2. (Lyatsky *et al.*, 2001). Distance to stream index (STREAMDS) map was obtained by calculating the distance from the points in the sampling design to nearest stream line in ArcGIS. Thereafter, these maps were resampled with a resolution of 20 m by 20 m grids using nearest neighbour interpolation as simplest technique for assigning pixel values to the new grid.

Radiation index (RI), used in the present study as an explanatory variable, was calculated for each pixel by the following equation (McCune and Keon, 2002) :

$$RI = \frac{[1 - \cos((\pi / 180)(Q - 30))]}{2}$$

where, θ is an azimuth value measured from true north. This assigns a value of zero to land oriented in the north-north

east direction (typically the coolest and wettest orientation) and a value of one on the hotter, drier south-south westerly slopes (Moisen and Frescino, 2002).

Modeling technique : Various modeling techniques are used in ecological researches. One of the most popular of them is regression tree technique (RTT) model. RTT is a non-parametric and nonlinear approach that is to partition the dataset into homogeneous subgroups with respect to same classes (Drapeau *et al.*, 2000; Özkan *et al.*, 2013; Özkan *et al.*, 2015).

In regression trees, the response vector (Y) represents the response values for each observation of the variable matrix X. Regarding impurity criterion, splits of a regression tree are performed in accordance with squared residuals minimization algorithm which implies that expected sum of variances for two resulting nodes should be minimized.

At each node, the regression tree solves the following minimization problem :

$$\arg \min_{x_j \leq x_j^R, j=1, \dots, M} [P_l \text{Var}(Y_l) + P_r \text{Var}(Y_r)]$$

where, P_l and P_r are probabilities of left and right nodes. M is the number of variables in learning sampling. x_j is variable j . x_j^R denotes best splitting value of variable x_j . $\text{Var}(Y_l)$, $\text{Var}(Y_r)$ are response vectors for corresponding left and right child nodes. $x_j \leq x_j^R, j=1, \dots, M$ means optimal splitting question which satisfies the condition.

Squared residuals minimization algorithm and Gini splitting rule are the same. When assigning to objects of class k the value 1, and value 0 to objects of other classes, sample variance of those values would be equal to $p(k|t)[1-p(k|t)]$. Summarizing by number of classes K , impurity measure $i(t)$ is found the following way.

$$i(t) = 1 - \sum_{k=1}^K P^2(k|t)$$

where, $p(k|t)$ - conditional properties of class k provided in node t ; K - number of classes; k - index of class and, t - index of node.

Before applying the RTT, 30% of the data was separated for testing. Remaining data was used for modeling. The initial tree was pruned by testing set, where error rates were calculated for full tree in addition to smaller subtrees. Subtree with smallest error rate was then chosen as optimal tree for response variable, the coefficient of determination (R^2) was used as a criterion to evaluate the model performances.

RTT were run by using DTEG (Sherrod, 2014). After running RTT, if-then rules were written for each path of tree graphs in Excel file to calculate the predicted values of response variable (Özkan and Berger, 2014).

The estimated values obtained from tree model were calculated at each grid (20x20 m). All grids were digitalized to form a niche based distribution map of taxonomic diversity.

Results and Discussion

One hundred eighty two species recognized in the sample plots were represented by 152 genus, 59 family, 41 order, 3 class and 2 phylum in taxonomic hierarchy. The numerical values transformed according to Westhoff and van der Maarel (1973) of the species varied between 9 and 48 per plot (mean=29). The most highly speciose family was Asteraceae (23 species). Of the 182 species encountered, *Daphne*, *Salvia*, *Sideritis*, *Trifolium* and *Verbascum* were dominant.

Taxonomic diversity values varied between 3.427 and 4.459. RTT was applied for modeling the distribution of taxonomic diversity (response variable) by means of environmental factors (explanatory variables). The optimal regression tree of taxonomic diversity produced a tree with 6 terminal nodes and 4 splits (Fig. 2). The explained variances of tree model were 31% and 24% for training and testing data. Özkan and Berger (2014) studied the Yukarıgökdere forest district in the mountain zone of the Mediterranean region. To build a distribution model of species diversity, the researchers used RTT, and reported the explained variance of the distribution model as 63%. Dogan and Dogan (2006) modeled plant species richness using by Simpson D diversity index with multiple regression analysis in The Nallıhan district of Turkey. As a result of the study, a distribution model with an explanation rate of 59% was obtained. When comparing the results of the studies done by Özkan and Berger (2014) and Dogan and Dogan (2006), the explained variance value of the distribution model obtained from the present study seems to be remained insufficient. One of the reasons of insufficiency of the distribution model we obtained is probably related to scale of the study area. Because Yukarıgökdere Forest district and Nallıhan district are correspond to middle scale-area and large scale area, respectively. However Yazılı Canyon Nature Park is a small-scale area.

The second reason of the weakness of the model is probably related to considerable potential contribution of topographical heterogeneity to the distribution model. As explained by several researchers (MacArthur and MacArthur, 1961; Tilman, 1982; Palmer, 1992; Huston, 1994; Vivian-Smith, 1997; Crawley and Haral, 2001; Willis and Whittaker, 2002; Steiner and Köhler, 2003; Dufour *et al.*, 2006), increasing biodiversity is often associated with greater environmental or topographical heterogeneity. In this regard, we may postulate that the variation of taxonomic diversity is not very sensitive in the variations of environmental variables among the sample plots level but environmental heterogeneity within sample plot. Unfortunately we did not measure the data belonging to micro habitat heterogeneity even though the study area has a high topographical variability due to its' irregular, karstic structure. That

Fig. 1 Location of Yazılı Canyon Nature Park in the Mediterranean Region, Turkey

Fig. 2 : Fitted regression tree and estimated values of taxonomic diversity

is why we do not know how much micro habitat (topographical) heterogeneity within sample plot is significant to explain the variations of taxonomic diversity.

As Warwick and Clarke (1998), Heino *et al.* (2007) and Gwali *et al.* (2010) pointed out, taxonomic diversity index is appropriate to demonstrate the effect of anthropogenic disturbance and degradation of biotic communities. In this sense, it might be thought that insufficiently explanation variance of the distribution model is related to degradation. However, Yazılı Canyon Nature Park is a well-managed protected area, not subjected to anthropogenic disturbance for a long time.

On the context of the explanations above, to better explain the interrelationships between environmental factors and taxonomic diversity, further studies of taxonomic diversity-environmental relations are clearly needed.

The tree model was created by slope %, distance to stream, solar illumination, aspect and altitude. The highest Δ^* value occurred on plots with more than 81.825 of slope % and solar illumination greater than 108.5. Regarding the least Δ^* value, the environmental variables played roles were slope

% (less than 81.825), distance to stream (less than 15.255) and aspect (less than 20.56). Model based map of taxonomic diversity is shown in Fig. 2. As seen in the distribution map, the places immediate environment to middle and upper areas and very steep places of the canyon showed richer in taxonomic diversity values than other parts. According to a study carried out on endemic plant species in the Yazılı Canyon Nature Park (Özkan and Süel, 2008), estimating species diversity obtained from Simpson Reciprocal Index was found higher in the lower part, in particular, valley bottom of the Yazılı Canyon. As compared to the results of Özkan and Süel (2008) to the result of the present study, a negative correlation between species diversity and taxonomic diversity was noted. It is well-known that taxonomic diversity is calculated by using taxonomical distances (Desrochers and Anand, 2004; Da Silva and Batalha, 2006; You-Hua and Zhi-Bo, 2009; Koperski, 2010; Gwali *et al.*, 2010) among the species, whereas species diversity is calculated by considering the number of species and their relative values when Shannon-Wiener index (Shannon, 1948) or Simpson reciprocal index (Simpson, 1949) are used. Such a negative relationship between taxonomic diversity and species diversity was not new, since woody and herbaceous species shows approximately uniform distribution (well-balanced

Fig. 3 : Spatial distribution modeling of Δ^* in the Yazılı Canyon Nature Park

distribution) in the upper part of the Canyon whereas majority of the species composed of herbaceous species in lower part of valley bottom of the study area.

Turkey resigned biodiversity convention in 1996 (Glowka *et al.*, 1996). After signing this convention, the studies dealing with measuring biodiversity, examining biodiversity-environment relationships, and modeling and mapping of biodiversity using remote sensing data and GIS gained much more importance (Maddock and du Plessis, 1999; Özdemir and Donoghue, 2013; Özdemir, 2014). As mentioned before, diversity has been studied in different ways (Clarke and Warwick, 2001; Shimatani, 2001; Petchey *et al.*, 2004; Ozkan, 2012; Negiz *et al.*, 2015). Unlike the traditional diversity indices, taxonomic diversity is calculated considering the places in taxonomic hierarchy of the species. That is why taxonomic diversity is not related only to species diversity but also to functional diversity and genetic diversity

among the species and structural diversity of vegetation communities (Özkan, 2012).

As a conclusion, taxonomic diversity index is a more suited equation to explain biodiversity than traditional diversity indices (Vane-Wright *et al.*, 1991; Izsák and Papp, 1995; Somerfield *et al.*, 1997). The distribution maps of taxonomic diversity are, therefore, one of the most essential information layers intended for preparing and implementations of conservation and management plans to enable sustainability of the ecosystems.

Acknowledgments

We thank Prof. Serkan Gülsoy, Prof. Mehmet Güvenç Negiz and Prof. Halil Süel for their valuable contribution during our study.

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