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Phylogenetic Diversity and Composition of Plant Communities in the Semi-Arid Area of District Karak, KP, Pakistan

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ABSTRACT

Phylogenetic information has been used to determine the co-occurrence and evolutionary relation among the plant species in the plant communities. Phylogenetic studies provide an important tool to assign conservation value to the plant species. Keeping in view the importance of vegetation especially in semi-arid areas, we assessed the phylogenetic structure of plant communities for the conservation of plant communities of District Karak. We surveyed three different plant communities in Southeastern part of District Karak in Pakistan. We used phylogenetic information to compute phylogenetic diversity (PD) of all the plant species in local communities. We computed the standardized effect size of phylogenetic diversity to measure the species diversity among the different communities. Our study revealed positive values of the standardized effect size in the first and second communities indicated the tendency of higher species diversity in the communities while negative values in the third community indicated that there is tendency of less species diversity. We also observed linear correlation between species richness and phylogenetic diversity. We came to the conclusion that high phylogenetic diversity among the studied communities is the result of weak competitive exclusion due to stochastic factors such as recruitment limitations, dispersal limitations and environmental heterogeneity.

Keywords: Phylogeny; Over dispersion; Clustering; Seeds; Germination

INTRODUCTION

Ecologists are increasingly using the information of phylogeny of species to understand the ecological patterns. Phylogenetic information and tools are helpful to study the conservation value of individual species [1-4] and the assemblages of communities [5-8]. The phylogenetic relationships among species are used for understanding the mechanisms driving patterns of co-occurrence [9-12]. Phylogenetic study helps in determining whether species interactions and the environmental factors are the key factors of community pattern or phylogenetic scales sorting and exclusion are strongest [11]. Recently phylogenetic information has been used to determine that ecological processes alter as a result of evolutionary relationship among the members of community [13].

Phylogenetic and taxonomic information reveals the presence of genes, traits and evolutionary lineages in the community. A rich history of research has shown that communities have distinctive variations of species, resulting in different proportion of traits and genes in communities [14-16]. The variations in traits and genes are the result of evolution from a common species. Therefore, to know these differences among species the elucidations of phylogenetic relationships are reliable for the ecologists. However, despite the importance of phylogenetic tools [17-19] and role of history in community ecology [20,21], integration of evolutionary biology and community ecology remains indescribable. The reason for such discrepancies lies, that environmental niches and species interactions have decisive role in community structure.

The aim of phylogeny-based methods is to describe the community assembly through the phylogenetic relationships of the co-occurring species in the communities. Phylogenetic analysis helps to understand the variation in the mechanisms of plants community assembly [22]. For this purpose community structure is studied for exploring the phylogenetic clustering (The co-occurrence of closely related species) and over-dispersion (The co-occurrence of distinct species). Therefore, our general goal was to investigate the plant phylogenetic community structure of semi-arid area, considering the availability of phylogenetic information and tools used to assess the phylogenetic structure of community.

No study has assessed the phylogenetic structure of semi-arid area in Pakistan; we tried to answer the following questions (1). How is the phylogenetic structure of community in the semi-arid area? (2) Are the plant species phylogenetically closely related to one another? (3) Are the plant species phylogenetically distinct from one another? (4) How species are distributed among samples in a community with respect to phylogeny?

MATERIALS AND METHODS

Study site

A field work was conducted for one year during 2014-2015. The present project was based on the study of phylogenetic diversity of District Karak. We surveyed Tarkhun koi, Tangori chowk (Hereafter Community1), Dabli Lawagher, Sarachkhel (Hereafter Community 2), Amberi kala, Zarkhan Kala (Hereafter Community 3) in Southeastern part of District Karak (Figure 1). We used QGIS software to construct the map of the studied sites in District Karak. District karak is located in the south of Kohat and on the west side of District Bannu and Laki Marwat. Karak is located at 32.47°-33.28° latitude towards North and 70.30°-71.30° longitude towards East and spreads over an area of 3,372 km^2 with a population of approximately 536000. Mean air temperature (39.5°C) and wind speed (5.5 km/h) is generally high in June, relative humidity is usually high (77.21%) in month of September. Mean annual precipitation (121.6 mm) and soil temperature is about (26.77°C) in month of July, which indicate dry condition in area. Therefore, the plants of the areas are spiny, scrubby, dwarf type of vegetation. We placed randomly 12 plots of 100 m × 100 m, in five different areas of Karak. We sampled species with DBH (diameter of bresat height) ≥ 1 cm.

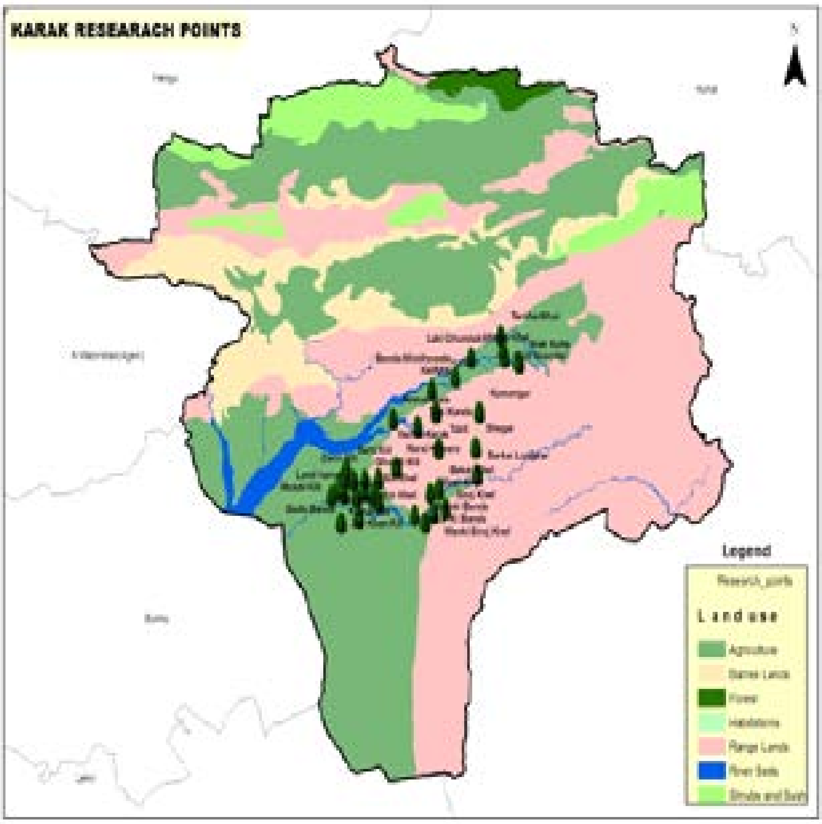

Figure 1: Map of district Karak and the studied sites represented as trees

Phylogenetic data

Considering all the species sampled in the sites, we constructed phylogenetic trees for all species (Figure 2). We used phylogenetic toolkit which is PHYLOMATIC software for the construction of phylogenetic trees [10]. This phylogenetic tree is derived from PHYLOMATIC reference tree (R20080417; Megatree), which is constructed using information from several published phylogenies [10]. PHYLOMATIC takes as input a list of taxa with family and genus information based on modern APG III (Angiosperm Phylogeny Group 2009) classification, matches the taxa to the most resolved position possible in any of a set of master trees in the database (the ‘Megatrees’), and returns the phylogeny [10]. Polytomies in family nodes were resolved by evenly spacing the genus node above the family node following several published molecular phylogenies. We used the BLADJ (branch length adjustment) averaging algorithm of the PHYLOCOM software package to assign the branch lengths of the phylogenetic trees [23]. BLADJ fixes the root node at a specified age and sets the length of all other branches by evenly spacing the undated nodes among the dated nodes and between dated nodes and terminal nodes [23]. The branch length was based on the minimum ages of nodes for orders, genera and families considering fossil data [24].

Phylogenetic diversity measures

We computed phylogenetic diversity (PD) which is the total branch length spanned by the tree including all species in a local community. In addition, we computed the standardized effect sizes of each diversity measure in order to

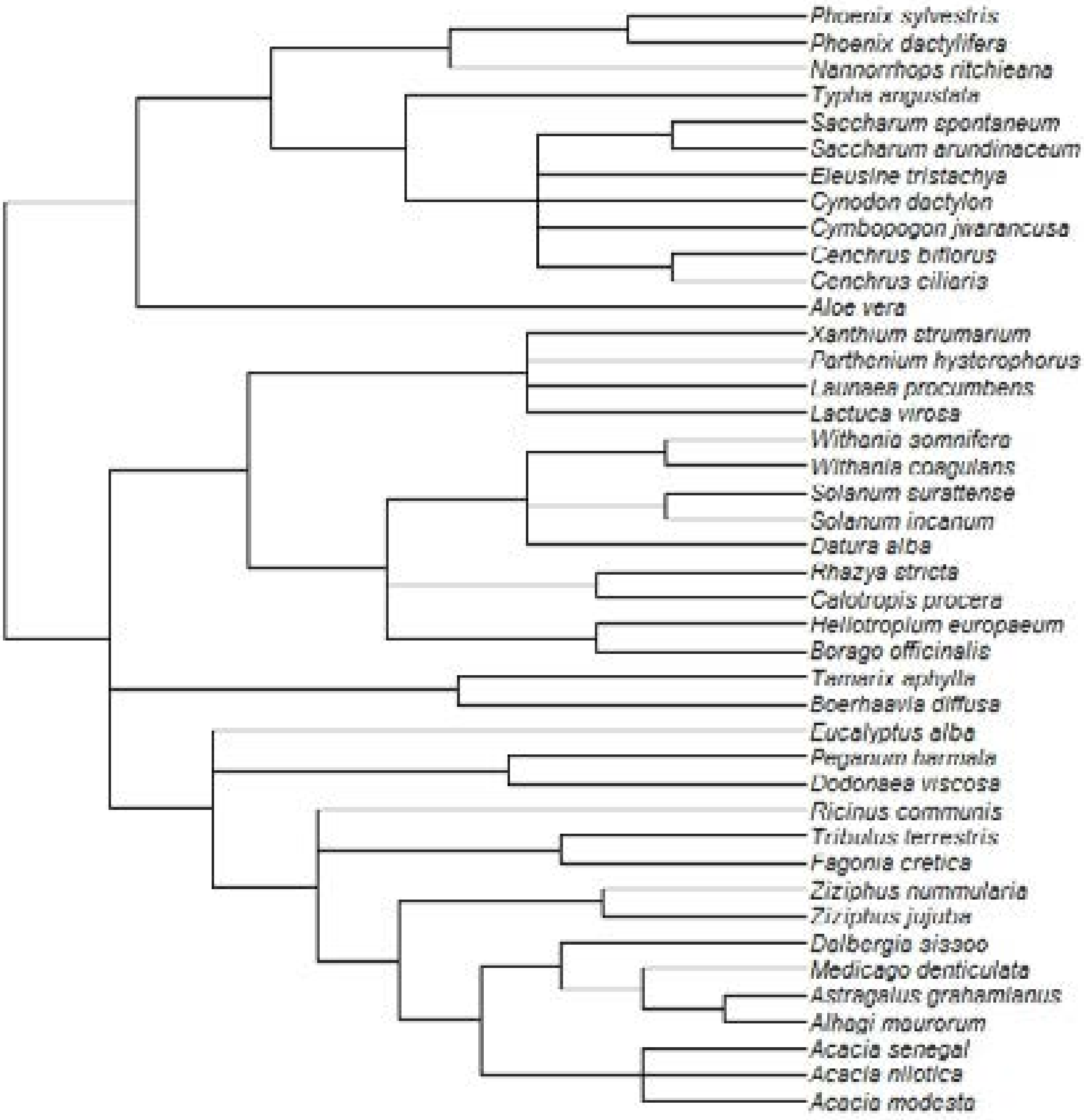

Figure 2: Phylogenetic tree of the sampled species in the three communities of southeastern Karak

compare values among different communities. Standardized effect sizes (Hereafter Z values) describe the difference between phylogenetic distances in the observed community versus null community generated by randomization. We computed the Z values of PD (SESPD) as:

Z values=(obs.value–rnd.value)/sd.rnd.value,

Where obs.value is the observed value of the metric under analysis, rnd.value is the mean metric value of null communities, and sd.rnd.value is the standard deviation of the 1,000 random values of the measure. We generated random values by reshuffling taxa labels across the tips of the phylogenetic tree of all the tree species sampled in studied sites. Positive Z values indicate that the site has a diversity value higher than expected by chance, i.e., a phylogenetic over dispersion of the local tree community, whereas negative Z values indicate that the site has a diversity value lower than expected by chance, i.e., a phylogenetic clustering [9,25]. We calculated all the metrics with the 'picante' package [26] for R environment [27].

RESULTS

We observed 23 species in community 1, 20 species in community 2 and 29 species in the third community (Table 1). Poaceae, Fabaceae and Solanaceae were the dominant families having 8, 7 and 5 species respectively. Our results indicate diversity in the species of all the communities (Table 2). We did not find any significant result in the species composition among all the three communities. However we observed negative Z value in the third community which indicate that there is tendency of less species diversity and the positive Z values in the first and second communities indicate the tendency of higher species diversity in the communities (Table 3). We also observed linear correlation between species richness and phylogenetic diversity (Figure 3).

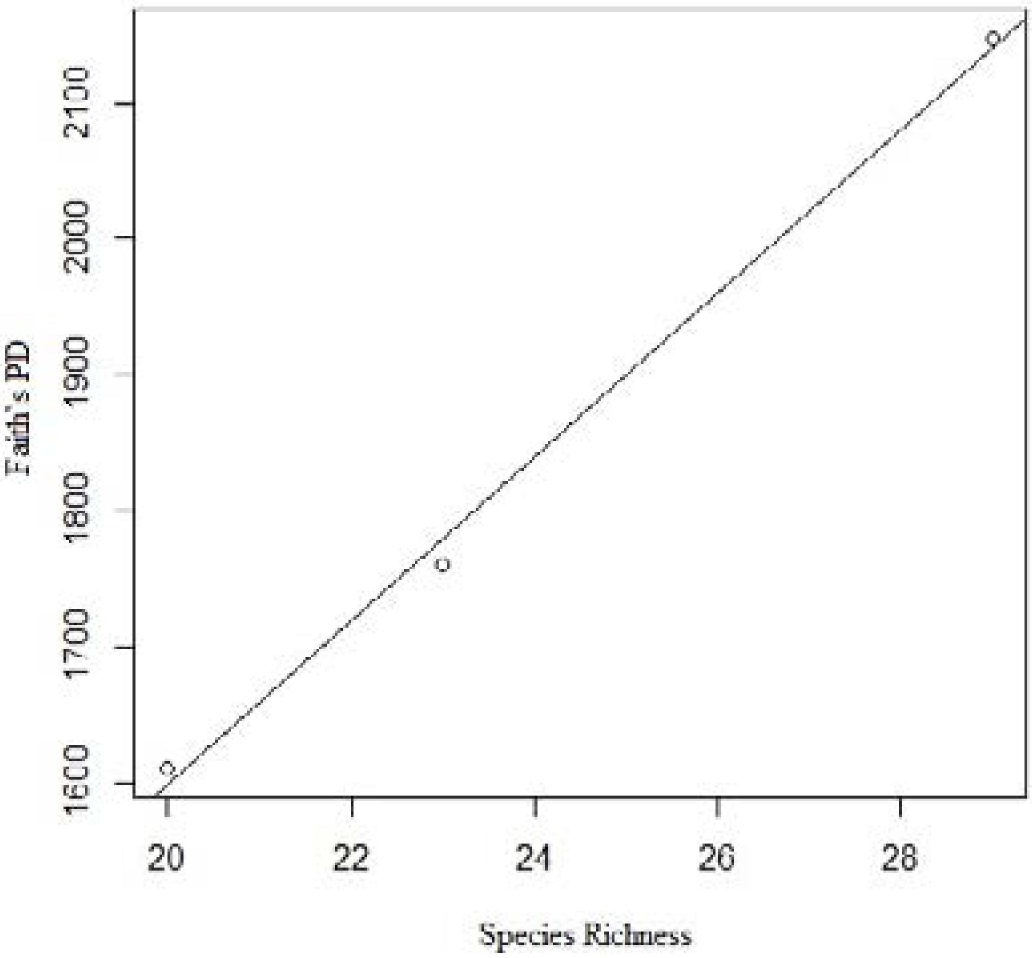

Figure 3: Correlation between species richness and phylogenetic diversity among the three communities of southeastern Karak Faith`s PD: Phylogenetic Diversity

Table 1: Distribution of plant species in the three communities

Species	Community 1	Community 2	Community 3
Acacia modesta (Wall.) P.J. Hurter	1	1	1
Acacia nilotica (L.) P.J. Hurter & Mabb	1	1	1
Acacia senegal (L.) Willd			1
Alhagi maurorum Medik.	1		1
Astragalus grahamianus Royle ex Benth.		1	
Medicago denticulata Willd.	1	1	1
Dalbergia sissoo Roxb.	1	1	1
Ziziphus jujuba Mill.	1	1	1
Ziziphus nummularia (Burm.f.) Wight&Arn	1	1	1
Fagonia cretica L.	1	1	
Tribulus terrestris L.			1
Ricinus communis Linn.		1	1
Dodonaea viscosa L.		1	1
Peganum harmala L.	1		
Eucalyptus alba Reinw. ex Blume		1	1
Boerhaavia diffusa L.		1	1
Tamarix aphylla (L.) Karst.	1		
Borago officinalis L.	1		
Heliotropium europaeum L.			
Calotropis procera (Aiton) W.T. Aiton	1	1	1
Rhazya stricta Decne.		1	1
Datura alba L.	1		
Solanum incanum L.	1		1
Solanum surattense Burm.f.		1	1
Withania coagulans (Stocks) Dunals.			1
Withania somnifera (L) Dunal.	1		
Lactuca virosa L.	1		
Launaea procumbens Roxburgh			1
Parthenium hysterophorus L.	1		
Xanthium strumarium L.	1		
Aloe vera (L.) Burm.f.	1		
Cenchrus biflorus Roxb.		1	1
Cenchrus spinifex Cav.		1	
Cymbopogon jwarancusa (Jones) Schult.	1	1	1
Cynodon dactylon (L.) Pers.	1	1	1
Eleusine tristachya (Lam.) Lam.			1
Phragmites Adans.		1	
Saccharum arundinaceae Hook.	1		1
Saccharum spontaneum L.			1
Typha angustata (Bory & Chaub.)			1
Nannorrhops ritchieana Griff.	1		
Phoenix dactylifera L.		1	1
Phoenix sylvestris (L.) Roxb			1

Table 2: Phylogenetic diversity among the three communities of the southeastern Karak

Communities	Phylogenetic diversity	Species Richness
Community 1	1760.5	23
Community 2	1611.167	20
Community 3	2147.444	29

Table 3: Phylogenetic structure of all the communities of southeastern Karak

Communities	PD Observed Z Value	P Value
Community 1	0.16620931	0.6039604
Community 2	0.01085925	0.5346535
Community 3	-0.0259269	0.4059406

PD: Phylogenetic Diversity; Z: Standardized Effect; P: Probability Value

DISCUSSION

Our results showed high phylogenetic diversity in all the three communities. However, we did not find significant phylogenetic conservation and convergence in all the communities. Non-significant distribution may be due to stochastic factors such as, dispersal limitations, which may causes random distribution of the plant species in all the studied communities. Therefore we argue that high phylogenetic diversity among the three communities is the result of weak competitive exclusion and stochastic factors such as recruitment limitations, dispersal limitations and environmental heterogeneity.

We observed random distribution of species phylogeny in the local communities. Random distribution may be due to stochastic factors prevailing in the communities such as dispersal and recruitment limitation. Dispersal limitations restrict the germination of new individuals near to the parental plants and recruitment limitations are the failure of species to establish itself in all sites [28]. Dispersal and recruitment limitations are generally strong to prevent competitive exclusion among species which exhibit the same or very similar adaptations for the most common environments [29]. Since all the plants were from the semi-arid area and most of the species in the three communities belonged to family poaceae, which generally propagate vegetative through layering and cutting. Vegetative propagation is associated with dispersal and recruitment limitations of plant species due to the absence of pollen and seed production [28,30]. Similarly the seeds of most of the plants from family Fabaceae were also dropped near the parent trees through animal dung. Animals from this area are usually domesticated and are restricted to churn and graze near the parent trees. Therefore these plants have more chance of germination near to one another. Germination near to the parental plant species reduce the chance of won for superior competitor and increases by default the chance of inferior species [28]. When there is limited dispersal the competitive species has less chance to reach the site [30]. In limited dispersal and recruitment, competitive exclusion is delay and slow due to very slow rate of introduction of new species (i.e., speciation) [16].

Random distribution may also be due to heterogeneity in the biotic and abiotic components of the environment. Heterogeneous environment represent variations in the abiotic environment such as topography, temperature, precipitation, substrate and biotic variables such as evapotranspiration. Heterogenic biotic and abiotic environment provides equal opportunity to every species for the growth and development. More heterogeneous environments can support more diversity than less heterogeneous ones [31-35]. For example, in South Africa [36] showed that topographic heterogeneity could improve plant richness both by increasing the number of niches in space and by keeping the number of niches relatively stable in time. Spatial heterogeneity can influence diversity both by increasing the number of habitats types and by affecting ecological processes such as dispersal and competition [35] through the spatial configuration of habitats.

CONCLUSION

It was the first phylogenetic analysis of the studied area and represented random occurrence of the plant species. We argued that random occurrence in the area is the result of environmental and stochastic factors.

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REFERENCES

[1] Vane-Wright RI, Humphries CJ, Williams PH. What to protect - systematics and the agony of choice. *Biol Conserv*, **1991**, 55: 235-254.

[2] Pavoine S, Ollier S, Dufour AB. Is the originality of a species measurable? *Ecol Lett*, **2005**, 8: 579-586.

[3] Redding DW, Mooers AO. Incorporating evolutionary measures into conservation prioritization. *Conserv Biol*, **2006**, 20: 1670-1678.

[4] Isaac NJB, Turvey ST, Collen B, Waterman C, Baillie JEM. Mammals on the EDGE: Conservation priorities based on threat and phylogeny. *PLOS ONE*, **2007**, 2: 296.

[5] Faith DP. Conservation evaluation and phylogenetic diversity. *Biol Conserv*, **1992**, 61: 1-10.

[6] Crozier RH. Preserving the information content of species: Genetic diversity, phylogeny and conservation worth. *Annu Rev Ecol Syst*, **1997**, 28: 243-268.

[7] Crozier RH, Dunnett LJ, Agapow PM. Phylogenetic biodiversity assessment based on systematic nomenclature. *Evol Bioinform Online*, **2005**, 1: 11-36.

[8] Davies TJ, Fritz SA, Grenyer R, Orme CDL, Bielby J. Phylogenetic trees and the future of mammalian biodiversity. *PNAS*, **2008**, 105: 11556-11563.

[9] Webb CO, Ackerly DD, McPeek MA, Donoghue MJ. Phylogenies and community ecology. *Ann Rev Ecol Syst*, **2002**, 33: 475-505.

[10] Webb CO, Donoghue MJ. Phylomatic: tree assembly for applied phylogenetics. *Mol Ecol*, **2005**, 5: 181-183.

[11] Cavender BJ, Wilczek A. Integrating micro- and macro-evolutionary processes in community ecology. *Ecology*, **2003**, 84: 592-597.

[12] Silvertown J, McConway K, Gowing D, Dodd M, Fay MF, et al. Absence of phylogenetic signal in the niche structure of meadow plant communities. *Proc Biol Sci*, **2006**, 273: 39-44.

[13] Cadotte MW, Cardinale BJ, Oakley TH. Evolutionary history and the effect of biodiversity on plant productivity. *PNAS*, **2008**, 105: 17012-17017.

[14] Preston FW. The commonness and rarity of species. *Ecology*, **1948**, 29: 254-283.

[15] Mac Arthur R. On the relative abundance of bird species. *Proc Natl Acad Sci*, **1957**, 43: 293-295.

[16] Hubbell SP. The unified neutral theory of biodiversity and biogeography. Monographs in population biology. Princeton University Press, Princeton, **2001**.

[17] Brooks DR, McLennan DA. Phylogeny, ecology and behavior: A research program in comparative biology. Chicago (IL): University of Chicago Press, **1991**.

[18] Losos JB. Phylogenies and comparative biology, Stage II: Testing causal hypotheses derived from phylogenies with data from extant taxa. *Syst Biol*, **1996**, 45: 259-260.

[19] Thompson JN, Reichman OJ, Morin PJ. Frontiers of ecology. *BioScience*, **2001**, 51: 15-24.

[20] Ricklefs RE. Community diversity: Relative roles of local and regional processes. *Science*, **1987**, 235: 167-171.

[21] Ricklefs RE, Schluter D. Species diversity in ecological communities: Historical and geographical perspectives. University of Chicago Press, **1993**, 414.

[22] Chang XY, Zhou T, Peng SL. Change in community phylogenetic structure of tropical forest along the southern coast of China during restoration. *Ecosphere*. **2015**, 6: 1-3.

[23] Webb CO, Ackerly DD, Kembel SW. Phylocom: Software for the analysis of phylogenetic community structure and character evolution. *Bioinformatics*. **2008**, 24: 2098-2100.

[24] Wikström N, Savolainen V, Chase MW. Evolution of the angiosperms: Calibrating the family tree. *Proc Biol Sci*, **2001**, 268: 2211-2220.

[25] Pavoine S, Bonsall M. Measuring biodiversity to explain community assembly, a unified approach. *Biol Rev*, **2011**, 86: 792-812.

[26] Kembel SW, Cowan PD, Helmus MR, Cornwell WK, Morlon H, et al. Picante: R tools for integrating phylogenies and ecology. *Bioinformatics*, **2010**, 26: 1463-1464.

[27] http://www.r-project.org/

[28] Hurtt GC, Pacala SW. The consequences of recruitment limitation. Reconciling chance, history and competitive differences between plants. *J Theor Biol*, **1995**, 176: 1-12.

[29] Hubbell SP. Neutral theory in community ecology and the hypothesis of functional equivalence. *Funct Ecol*, **2005**, 19: 166-172.

[30] Marin VM, Dorken EM Barrett CHS. The ecological and evolutionary consequences of clonality for plant mating. *Annu Rev Ecol Evol Syst*, **2010**, 41: 193-213.

[31] Rosenzweig ML. Species diversity in space and time. Cambridge University Press, **1995**.

[32] Lundholm JT, Larson DW. Relationships between spatial environmental heterogeneity and plant species diversity on a limestone pavement. *Ecography*, **2003**, 26: 715-722.

[33] Pausas JG, Carreras J, Ferre A, Font X. Coarse-scale plant species richness in relation to environmental heterogeneity. *J Veg Sci*, **2003**, 14: 661-668.

[34] Leigh JR, Davidar RP, Dick CW, Puyravaud JP, Terborgh J, et al. Why do some tropical forests have so many species of trees? *Biotropica*, **2004**, 36: 447-473.

[35] Dufour A, Gadallah F, Wagner HH, Guisan A, Buttler A. Plant species richness and environmental heterogeneity in a mountain landscape: Effects of variability and spatial configuration. *Ecography*, **2006**, 29: 573-584.

[36] Thuiller W, Midgley GF, Rouget M, Cowling RM. Predicting patterns of plant species richness in mega diverse South Africa. *Ecography*, **2006**, 29: 733-744.