

ORIGINAL PAPER

Conservation priority of endemic Chinese flora at family and genus levels

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Received: 1 June 2015/Revised: 19 October 2015/Accepted: 13 November 2015/ Published online: 20 November 2015 © Springer Science+Business Media Dordrecht 2015

Abstract Endemism is an important concept in biogeography and biodiversity conservation, and much attention has been given to methods that operationally identify centers or hotspots of endemic species diversity to effectively protect biodiversity. China is one of the richest countries in terms of plant biodiversity and has very high levels of plant endemism. In this study, conservation priorities for endemic seed flora in China based on a distribution database that includes both specimen records and published references. In China, a total of 12,824 endemic species belong to 194 families and 1598 genera. Biogeographically weighted endemic evolutionary distinctiveness indices were constructed to identify endemic flora conservation priorities at family and genus levels. All of the grids ranked within the top 5 % for the constructed indices were designated as hotspots and conservation priority areas. Distributions of Chinese endemic flora varied at the family and genus levels. At the family level, 14 centers of biodiversity were identified as priority areas for conservation of Chinese endemic flora. All centers were distributed in subtropical evergreen broad-leaved forest, tropical monsoon/rainforest, or mountainous areas of south

Communicated by P. Ponel.

Electronic supplementary material The online version of this article (doi:10.1007/s10531-015-1027-0) contains supplementary material, which is available to authorized users.

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Qinghai. At the genus level, 15 centers were identified as conservation priority areas, and most were distributed within the Qinling Mountains and further south or the Hengduan Mountains and to the east. Among the 15 centers, 11 overlapped with conservation priority areas for endemic flora families. Our analysis indicates that different groups have different diversity centers, and different taxa ranks have similar, but not identical, diversity distribution patterns.

Keywords Biodiversity conservation · Endemism · Evolutionary distinctiveness · Priority areas · Priority taxa

Introduction

Previous studies have shown that both taxa and areas are important for biodiversity conservation. Initially, biological conservation efforts focused on single species (Ladle and Whittaker 2011); however, limitations of available conservation resources rendered protection of single species ineffective. Identifying higher taxon-level biodiversity conservation priorities is an extremely effective approach, because different species within higher taxa possess different evolutionary information and importance, but often overlapping spatial distributions. Many researchers have focused on identifying conservation priority areas based on taxon richness. Biodiversity hotspots are popular conservation priority areas. The criteria for identifying global biodiversity hotspots are: 1. the endemic plant species comprise at least 0.5 % of all plant species worldwide, and 2. at least 70 % of the primary vegetation has been lost (Myers et al. 2000).

In past decades, researchers have paid much attention to species diversity, which includes species richness and number of endemic, rare, or threatened species, as the most prominent and readily recognizable form of biodiversity (Reid 1998; Brummitt and Lughadha 2003; Orme et al. 2005). However, in recent decades, a substantial amount of research has focused on evolutionary diversity and processes to set conservation priorities (Vane-Wright et al. 1991; Faith 1992; Sechrest et al. 2002; Redding and Mooers 2006; Forest et al. 2007; Isaac et al. 2007). Phylogenetic trees have become increasingly important for identifying biodiversity hotspots (Spathelf and Waite 2007; Rosauer et al. 2009; Cadotte et al. 2010a, b), because they show relationships of extant species and provide more information about evolution along broad time scales (Omland et al. 2008).

A number of diversity measurements that combine phylogenetic data and geological distributions of taxa have been proposed. Some of these measurements focus on phylogenetic diversity (Faith 1992; Forest et al. 2007) or taxonomic distinctiveness (Vane-Wright et al. 1991; Redding and Mooers 2006). Phylogenetic endemism (Rosauer et al. 2009) and biogeographically weighted evolutionary distinctiveness (Cadotte et al. 2010a) are two metrics used to identify hotspots based on measurements that combine phylogenetic features and weighted endemism (Isaac et al. 2007; Rosauer et al. 2009; Cadotte et al. 2010a). When conservation resources are limited, phylogenetic endemism and biogeographically weighted evolutionary distinctiveness are useful tools for understanding biogeographic patterns and subsequently setting biodiversity conservation priorities (Rosauer et al. 2009; Cadotte et al. 2010a).

China is one of the world's mega-biodiversity countries, and one of the richest countries in terms of plant biodiversity (Wu and Wang 1983; McNeely et al. 1990; Fu et al. 1993;

Mittermeier et al. 1997). The total recognized number of vascular plant species in China is 31,142 (Editorial Committee of Flora Reipublicae Popularis Sinicae 2004). Chinese flora is highly endemic (Wu and Wang 1983; Fu et al. 1993), and endemic species account for 52.1 % of total seed plant species (Huang et al. 2011). Furthermore, China has a large number of threatened species (Jenkins et al. 2003). Of the World Wildlife Fund's Global 200 Most Critical and Endangered Ecoregions, 17 are located in China (Olson and Dinerstein 2002). Moreover, of the 34 global biodiversity hotspots identified by Conservation International (Mittermeier et al. 2005), four are at least partly within China.

Although a couple of studies on endemism of Chinese flora have been conducted (Ying and Zhang 1994; Lopez-Pujol et al. 2011), insufficient data exists to provide systematic guidance for biodiversity conservation in China, especially if family- and genus-level biodiversity is considered. Family-level biodiversity within China has been largely ignored, because there are few endemic flora families in China. However, there are several publications on genus-level biodiversity. China has four endemic families (Wu and Wang 1983; Wang 1992), 243 endemic genera, and three centers of endemism (Ying and Zhang 1994). In China, 52.1 % (ca. 15,000 species) of seed plant species are endemic (Huang et al. 2011), and there are 20 biodiversity hotspots for Chinese endemic woody seed plant species (Huang et al. 2012). Although individual studies identified genus- or species-level conservation priorities, we are unaware of any studies that combined family, genus, and species biodiversity to identify conservation priority areas. Consequently, to aid in local biodiversity conservation efforts, we established a new method to identify conservation priority regions by integrating family and genus biodiversity.

Methods

Data sources

Based on a published checklist of Chinese endemic seed plants (Huang et al. 2011), we compiled a database of endemic species in China. In this study, endemic refers to taxa that naturally occur in China and nowhere else worldwide; this designation is completely based on political boundaries. Species distribution information was collated by consulting references and checking herbarium specimens. The references included over 1000 volumes of national, provincial, and local flora and checklists; nature reserve reports; and numerous journal articles and monographs relevant to Chinese flora. Specimen data were collected from 37 herbaria, which included the main botanical institutes throughout China. The total number of species that belong to each genus and family were collected based on a relevant monograph (Wu et al. 2006).

A total of 12,824 Chinese endemic seed plant species were identified that belong to 1598 genera and 194 families. Grids $(100 \times 100 \text{ km})$ were sampled as spatially operational geographic units (OGUs). This grid size was chosen to reduce effects of sampling artifacts, such as artificially empty quadrats and mapping errors (Linder 2001). Distribution records from references and floral point records were an political unit of county level. Across China, there are 2377 counties, which range in size from 22.4 to 208,134.0 km², with 162 (accounting for 6.8 % of all counties) counties over 10,000 km². Because of the county size distribution, a grid size of 100×100 km was optimal.

Data analysis

Genus- and family-level endemism in China

From the perspective of protection of special groups, a genus or family to contain more endemic species in a region, so this area can be treated as genera of the corresponding key protection area. Based on the above protection concepts, for the conservation importance of genera or families was ranked by proportion of endemic species. However, to date, no relevant literature has been published on this topic. Therefore, we established indices of endemic rates of genera and families to quantify the degree of endemism for genera and families within China. For a given area, the endemic rate of a genus was calculated as the ratio of the number of species within the genus endemic to the area to the total number of species within this genus worldwide; similarly, the endemic rate of a family was calculated as the ratio of the number of species within the family endemic to the area to the total number of species within the family worldwide, as shown in Eq. (1),

$$F_{er}(G_{er}) = N_e/N_s \tag{1}$$

where F_{er} (or G_{er}) is the degree of endemism of a family (or genus), e is the number of species endemic to the area within the genus or family, and s is the total number of species within the genus or family worldwide.

Phylogenetic tree construction

A phylogenetic supertree was constructed by inputting the endemic seed plant data into the plant phylogeny database Phylomatic (Webb and Donoghue 2005). Phylomatic uses the latest Angiosperm Phylogeny Group classification (Bremer et al. 2009) as the backbone of a supertree. Branch lengths of our phylogenetic tree were adjusted using the BLADJ algorithm (Webb et al. 2008) with "known" molecular and fossil dates (Wikstrom et al. 2001). The "known" molecular and fossil dates used to calibrate the supertree are estimates, but they improve the robustness of phylogenetic analyses of endemism compared with nodal distances, which are the alternative (Webb 2000).

Endemic evolutionary distinctiveness index construction

An index, species evolutionary distinctiveness, between taxa was determined using information from the nodes and branches of the terminal taxa of the phylogenetic tree (Isaac et al. 2007). This index is often used to denote the amount of specific genetic information within a taxon. Here, family or genera were the terminal taxa of the phylogenetic tree, and were considered for calculating taxa evolutionary distinctiveness (TED). The indices for evolutionary distinctiveness of families and genera were calculated using Eq. (2),

$$TED_i = \sum_{i=1}^n \frac{L_i}{N_i} \tag{2}$$

where L_i is length of branch *i*, N_i is the number of terminal groups derived from branch *i*, and *n* is the number of terminal taxa. Here, the endemic evolutionary distinctiveness (EED) index was calculated to fully determine taxa with the highest degrees of endemism and evolutionary distinctiveness. The EED index is based on the premise both endemism and

evolution are equally important. To date, no studies have shown that one is more important than the other. However, we expect get a synthesis evaluation based on two aspects. The formulae used to calculate the indices are shown in Eqs. (3) and (4),

$$EED_f = \frac{F_{er}/F_{ermax} + TED_f/TED_{fmax}}{2}$$
(3)

$$EED_g = \frac{G_{er}/G_{ermax} + TED_g/TED_{gmax}}{2}$$
(4)

where F_{ermax} (or G_{ermax}) denotes the maximum degree of endemism of a family (or genus), and TED_{fmax} (or TED_{gmax}) represents the maximum degree of evolution of a family (or genus). These equations indicate maximum value of evolutionary distinctiveness of a family (or genus) across the phylogenetic tree with families (or genera) as terminal taxa for each grid.

Because limited resources are available for conservation, identifying priority areas is an effective approach to protect more taxa within a minimal spatial range. We combined the distribution range of taxa with an index derived by Cadotte et al. (2010b) to calculate a biogeographically weighted endemic evolutionary distinctiveness (BEED) index for higher taxa of Chinese endemic flora using Eq. (5),

$$BEED = \sum_{i=1}^{n} \frac{EED_i}{R_i}$$
(5)

where R_i is the distribution range of family (or genus) *i* of Chinese endemic flora. R_i was determined by the number of grid cells where a family (or genus) of Chinese endemic flora is present. *EED_i* is the EED of taxon *i*.

The regions with the top 5 % of BEED index values were identified as taxon-based conservation priority areas for Chinese endemic flora. All calculations were carried out in R 3.2.2 (R Core Team 2015). TED was calculated using the evol.distinct function in the R package picante. All geographic distribution patterns of Chinese endemic flora were mapped using ArcGIS 9.0 (ESRI 2004).

Results

Analyses of family- and genus-level endemic rates

Family-level endemic rates

There were 10 families with endemic rates greater than or equal to 50 %, which included Ginkgoaceae, Eucommiaceae, Adoxaceae, Elaeagnaceae, Aceraceae, Stachyuraceae, Theligonaceae, Aucubaceae, Acoraceae, and Torricelliaceae. Of these families, seven were monotypic and three were oligotypic. The endemic rate of Ginkgoaceae was 100 %, which is typical of monotypic families and genera. Both Elaeagnaceae and Aceraceae are made up of large numbers of species. With the exception of Aucubaceae, which had 14 species, the remaining families had fewer than 10 species. There were 60 families with endemic rates greater than or equal to 10 % but less than 50 %. The remaining 124 families, which accounted for 63 % of all Chinese flora families, had endemic rates less than 10 %.

Genus-level endemic rates

There were 203 genera with endemic rates of 100 %, which accounts for approximately 12.7 % of the total number of Chinese endemic flora genera. This result differs from the findings of Wang and Zhang (1994) and Ying and Zhang (1994), most likely because of the implementation of different criteria to determine endemism. There were 179 genera with endemic rates greater than or equal to 50 % but less than 100 %. Endemic rates of 640 genera were greater than or equal to 10 % but less than 50 %. The remaining 470 genera had endemic rates less than 10 %, which accounts for about 30 % of Chinese endemic flora genera.

The 203 genera identified as 100 % endemic belonged to 68 families. Among them, four families contained more than 10 genera, including Gesneriaceae (29 genera), Asteraceae (18 genera), Poaceae (13 genera), and Lamiaceae (10 genera). These four families included a cumulative 476 endemic species. Monotypic genera were more common than oligotypic genera within the 203 endemic genera. Oligotypic and monotypic genera accounted for 92.6 % of all endemic genera. The 15 polytypic genera made up the remaining 7.4 % of the Chinese endemic genera, but contained 38.9 % of all endemic species.

Family- and genus-level EED analyses

The Chinese endemic flora families in order of protection priority are listed in Appendix S1. Conservation priority greatly differed among families. The 10 families with the highest endemic rates and EED included Ginkgoaceae, Eucommiaceae, Adoxaceae, and Elaeagnaceae.

The top 200 Chinese endemic flora genera in order of protection priority are listed in Appendix S2. When ranked based on endemic rate, 157 of the top 200 ranked genera were common to the top 200 ranked for protection priority.

Conservation priority areas for Chinese endemic flora families and genera

Priority spatial areas for Chinese endemic flora family conservation include 14 centers of diversity (Table 1; Fig. 1), with seven major centers; major centers included at least three connected grid cells. The other seven centers were minor, with only one or two grids. All centers excerpt for the mountainous areas of south Qinghai were distributed in the sub-tropical evergreen broad-leaved forest and tropical monsoon/rainforest regions.

Fifteen priority conservation areas were identified based on Chinese endemic flora genera (Table 1; Fig. 2). Among the 15 priority areas, six were major (Table 1), and 11 overlapped with family-level priority areas.

Priority areas for Chinese endemic flora conservation were not consistent between family and genus levels. Ten of the 14 family-level priority areas overlapped with 11 of the 15 genus-level priority areas, because priority conservation area size differed between genus and family levels. For example, at the genus level, the mountainous areas of north Zhejiang and south Zhejiang are two centers, but at the family level are one center (Table 1; Figs. 1, 2). Additionally, at the family level, the junction of Shaanxi–Chongq-ing–Hubei, mountainous areas of southwest Hubei, and mountainous areas of northwest Hubei are three priority areas, whereas they are one center at the genus level (Table 1; Figs. 1, 2).

Code	Priority areas	Family-level endemic evolutionary distinctiveness	Genus-level endemic evolutionary distinctiveness	Centers of endemism (Lopez- Pujol et al. 2011)
1	Hengduan Mountains	++	++	++
2	Mountainous areas of east Yunnan and west Guangxi	++	++	++
3	Mountainous areas of central Sichuan	++	++	++
4	Mountainous areas of north Zhejiang	++	+	+
5	Mountainous areas of south Zhejiang		+	+
6	Hainan Island	++	++	+
7	Mountainous areas of central Guangdong	++	+	++
8	North Yunnan	++	+	++
9	Mountainous areas of south Qinghai	+	/	/
10	Mountainous areas of southeast Shaanxi, northeast Chongqing and west Hubei	+	++	++
11	Mountainous areas of southwest Hubei	+		
12	Mountainous areas of northwest Hunan	+		
13	Mountainous areas of central Guangxi	+	++	++
14	Mountainous areas of southwest Chongqing	+	+	+
15	Mountainous areas of southeast Jiangxi and northwest Fujian	+	/	/
16	Mountainous areas of southwest Hunan	/	+	+
17	Mountainous areas of south Taiwan	/	+	/
18	Mountainous areas of southwest Yunnan	/	+	/
19	Mountainous areas of southeast Tibet	/	+	/

Table 1 Priority areas for Chinese endemic flora from this study and from another study (Lopez-Pujol et al.2011)

++: major center; +: minor center; /: no center

Discussion

Priority Chinese endemic flora taxa for protection

Endemic rates of Chinese flora differ at the family and genus levels. Endemic rates of most families were less than 10 %. Most families and genera with high endemic rates were



Fig. 1 Distribution of priority areas for conservation of Chinese endemic flora families with top biogeographically weighted endemic evolutionary distinctiveness at the 5 % level. There were 14 priority areas, designated as centers: 1 Hengduan Mountains; 2 Mountainous areas of east Yunnan and west Guangxi; 3 Mountainous areas of central Sichuan; 4 Mountainous areas of Zhejiang; 6 Hainan Island; 7 Mountainous areas of central Guangdong; 8 North Yunnan; 9 Mountainous areas of south Qinghai; 10 Mountainous areas of southeast Shaanxi, northeast Chongqing, and west Hubei; 11 Mountainous areas of southwest Chongqing; and 15 Mountainous areas of southeast Jiangxi and northwest Fujian. Albers projection. Priority area center codes are consistent with those listed in Table 1, except for center 4

monotypic and oligotypic, but some were polytypic. The monotypic and oligotypic families and genera with high endemic rates were ancient and isolated taxa which indicate that their current distribution areas form preservation centers or refuges (Raven and Axelrod 1974; Lu 1999). However, the current distribution areas of the polytypic families and genera with high endemic rates are likely their diversity or distinctiveness centers. For example, Elaeagnaceae is an oligotypic family, but *Elaeagnus* is polytypic genus, which contains ancestral and specialized species. Many the monotypic and oligotypic families and genera originated in the Tertiary or Quaternary periods and are ancient relic or remnant plants; they are also rare and endangered plants, with some, such as ginkgo (*Ginkgo biloba*), silver fir (*Cathaya argyrophylla*), dawn redwood (*Metasequoia glyptostroboides*), Taiwan fir (*Taiwaria cryptomerioides*), black chokeberry (*Dipteronia sinensis*), rubber bark tree (*Eucommia ulmoides*), and handerkerchief tree (*Davidia involucrata*), listed as

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Fig. 2 Distribution of priority areas for conservation of Chinese endemic flora genera with top biogeographically weighted endemic evolutionary distinctiveness at the 5 % level. There were 15 priority areas, designated as centers: 1 Hengduan Mountains; 2 Mountainous areas of east Yunnan and west Guangxi; 3 Mountainous areas of central Sichuan; 4 Mountainous areas of north Zhejiang; 5 Mountainous areas of south Zhejiang; 6 Hainan Island; 7 Mountainous areas of central Guangdong; 8 North Yunnan; 10 Mountainous areas of southeast Chongqing, west Hubei, and northwest Hunan; 13 Mountainous areas of central Guangxi; 14 Mountainous areas of southwest Chongqing; 16 Mountainous areas of southwest Hunan; 17 Mountainous areas of south Taiwan; 18 Mountainous areas of southwest Yunnan; and 19 Mountainous areas of southeast Tibet. Albers projection. Priority area center codes are consistent with those listed in Table 1, except for center 10

national key protected plants. Therefore, the Chinese biodiversity centers for these genera are also most likely their diversification or origin centers (Lu 1999).

Ginkgo, which is monotypic, was distributed throughout the northern and southern hemispheres in the Triassic, Jurassic, and Cretaceous periods, but the distribution range narrowed during the Tertiary period (Ying and Chen 2011). Today, it is only naturally found in the mountainous areas of Zhejiang, China. Furthermore, a typical relict plant, the rubber bark tree, was distributed widely throughout Eurasia and America in the Tertiary period, but became restricted to China after the Quaternary glacial period (Wu 2003). Schisandraceae, an old ancient tropical Tertiary period relic (Wu 2003), differentiated and spread during the Paleogene age. Sabiaceae has only one genus, *Sabia*, which is characteristic of East Asia, because it originated, differentiated, and spread in East Asia. Lardizabalaceae was promoted to an independent order because of its unique phylogenetic position; its distribution is centered in East Asia, where the family differentiated at the

genus and species levels. Lardizabalaceae contains Cretaceous period to Paleogene age relics native to tropical and subtropical mountains. The cycad is the oldest seed plant group on Earth, which, according to existing fossil data, some experts claim originated in northwest Gansu Province, China (Ying and Chen 2011). Adoxaceae is widely spread from north temperate regions to the subarctic, with a small branch centralized in western China. The majority of Elaeagnaceae is located in East Asia. The Buxaceae distribution shows its antiquity (Wu 2003). Consequently, because of China's complicated geographical features and history, large inland and coastal habitats, and diverse climates, many important floral taxa have originated, survived, and differentiated in China (Wu and Wang 1983; Axelrod et al. 1996; Ying 2001; Wu et al. 2007).

Conservation resources are typically limited; therefore, it is most important to protect typical taxa from the phylogeny, because organisms have basic hierarchical organizational structures and complexity. Moreover, it is worth considering endemic rate to identify priority taxa for conservation.

Since the Origin of Species was published, Darwin's theory of evolution has widely penetrated into all areas of the natural sciences. Nowadays, it is well known that evolution is a prominent process that shapes life. The composition and distribution of extant plant species result from the interactions between historic influences, modern environmental factors, and species-specific development and evolution. To protect plant diversity, we should consider the current patterns and take into account evolutionary potential. Therefore, in this study, we applied an evolutionary distinctiveness index to determine priority Chinese endemic flora taxa for conservation. These conservation priority taxa are representative of Chinese flora composition and development. Many of these taxa are typical relict taxa, which indicate that the quantified indices emphasized the importance of unique Chinese endemic flora.

Priority spatial areas for Chinese endemic flora conservation

The largest center for endemic families and genera included the mountainous areas of east Yunnan and west Guangxi. This center is larger than the Hengduan Mountain center. The east Yunnan and West Guangxi center appears to possess older flora than the Hengduan Mountain center. This result was supported by the findings of previous researchers, who found that there are more neoendemic taxa throughout the Hengduan Mountain center and more palaeoendemic taxa throughout the mountainous areas of east Yunnan and West Guangxi (Lopez-Pujol et al. 2011).

In the mountainous areas of Zhejiang, family-level centers were bigger than genus-level centers. It is possible that the mountainous areas of Zhejiang form another important preservation center of Chinese endemic flora. Indeed, the oldest "living fossil plant," ginkgo, is extant in this center. Moreover, an old relict plant, *Abies beshanzuensis*, was recently discovered in the mountainous areas of Zhejiang. Consequently, this region is important to Chinese endemic flora development and evolution.

China is one of the richest countries in terms of plant biodiversity (Wang et al. 1993; Chen 1998; Tang et al. 2006), and Chinese flora is highly endemic. Species distribution and diversity patterns depend on current environmental and long-term evolutionary processes acting on individual species. Although biodiversity distribution patterns across China have attracted some researchers, species composition and evolutionary characteristics in biodiversity hotspots have not been a research focus.

Twelve out of 14 centers of Chinese endemic flora families identified here corresponded with Chinese endemic centers identified by Lopez-Pujol et al. (2011). Five out of seven major Chinese endemic flora family centers overlapped with evolutionary distinctiveness centers. Two Chinese endemic flora family centers identified here, the Hengduan Mountains and northern Yunnan, were identified as one center by Lopez-Pujol et al. (2011). Furthermore, the Chinese endemic flora family center in eastern Yunnan and western Guangxi in our study was identified as two centers by Lopez-Pujol et al. (2011). Finally, the center within the mountainous areas in Zhejiang Province identified in this study was identified as two separate centers by Lopez-Pujol et al. (2011). At the genus-level, 12 out of 15 distribution centers of Chinese endemic flora were consistent with those identified by Lopez-Pujol et al. (2011). These findings show that the endemism centers and conservation priority areas were relatively consistent between our study and that of Lopez-Pujol et al. (2011).

Conservation strategy implications

Our analysis supports that different plant groups have different diversity centers, and that different taxa ranks have similar, but not identical, diversity distribution patterns. Consequently, we think higher taxa (family or genus) should be used to identify hotspots for biodiversity conservation at the global level, whereas species should be used to identify hotspots for biodiversity conservation at the regional or national level. Therefore, research on regional- or national-level biodiversity hotspots should emphasize species with narrow distributions. Moreover, further consideration and research is required for designating hotspots with higher taxa. Hierarchical targeted analysis of existing data at temporal and spatial scales may provide practical scientific guidance for biodiversity conservation in China.

Acknowledgments We would like to thank Christine Verhille at the University of British Columbia for her assistance with English language and grammatical editing of the manuscript. We are particularly grateful to the associate editor and anonymous reviewers for their valuable comments on the manuscript. This research was supported by the National Natural Science Foundation of China (41471048), National Non-profit Institute Research Grant of the Chinese Academy of Forestry (CAFYBB2014MA005), and National Nonprofit Institute Research Grant of the Institute of Forest Ecology, Environmental and Protection, Chinese Academy of Forestry (CAFIFEEP2015B02).

References

- Axelrod DI, Al-Shehbaz I, Raven PH (1996) History of the modern flora of China. In: Zhang AL, Wu SG (eds) Floristic characteristics and diversity of east Asian plants. China Higher Education Press, Beijing, pp 43–55
- Bremer B, Bremer K, Chase MW, Fay MF, Reveal JL, Soltis DE, Soltis PS, Stevens PF, Anderberg AA, Moore MJ, Olmstead RG, Rudall PJ, Sytsma KJ, Tank DC, Wurdack K, Xiang JQY, Zmarzty S, Grp AP (2009) An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III. Bot J Linn Soc 161:105–121
- Brummitt N, Lughadha EN (2003) Biodiversity: where's hot and where's not. Conserv Biol 17:1442-1448
- Cadotte MW, Borer ET, Seabloom EW, Cavender-Bares J, Harpole WS, Cleland E, Davies KF (2010a) Phylogenetic patterns differ for native and exotic plant communities across a richness gradient in Northern California. Divers Distrib 16:892–901
- Cadotte MW, Jonathan Davies T, Regetz J, Kembel SW, Cleland E, Oakley TH (2010b) Phylogenetic diversity metrics for ecological communities: integrating species richness, abundance and evolutionary history. Ecol Lett 13:96–105

Chen C (1998) Biodiversity of China: a country study. China Environmental Science Press, Beijing

Editorial Committee of Flora Reipublicae Popularis Sinicae (2004) Flora Reipublicae Popularis Sinicae, vol 1. Science Press, Beijing

ESRI (2004) ArcGIS 9.0. ESRI Press, New York

- Faith DP (1992) Conservation evaluation and phylogenetic diversity. Biol Conserv 61:1–10
- Forest F, Grenyer R, Rouget M, Davies TJ, Cowling RM, Faith DP, Balmford A, Manning JC, Proches S, van der Bank M, Reeves G, Hedderson TAJ, Savolainen V (2007) Preserving the evolutionary potential of floras in biodiversity hotspots. Nature 445:757–760
- Fu L, Feng Z, Zhuang J, Ying J (1993) Species Diversity. In: Chen LZ, Wang XP, Wang S (eds) Biodiversity in China: status and conservation strategy. Science Press, Beijing, pp 31–99
- Huang J, Chen J, Ying J, Ma K (2011) Features and distribution patterns of Chinese endemic seed plant species. J Syst Evol 49:81–94
- Huang J, Chen B, Liu C, Lai J, Zhang J, Ma K (2012) Identifying hotspots of endemic woody seed plant diversity in China. Divers Distrib 18:673–688
- Isaac NJB, Turvey ST, Collen B, Waterman C, Baillie JEM (2007) Mammals on the EDGE: conservation priorities based on threat and phylogeny. PLoS ONE 2:1–7
- Jenkins M, Green RE, Madden J (2003) The challenge of measuring global change in wild nature: are things getting better or worse? Conserv Biol 17:20–23
- Ladle RJ, Whittaker RJ (2011) Conservation biogeography. John Wiley & Sons Ltd, Chichester
- Linder HP (2001) Plant diversity and endemism in sub-Saharan tropical Africa. J Biogeogr 28:169–182
- Lopez-Pujol J, Zhang FM, Sun HQ, Ying TS, Ge S (2011) Centres of plant endemism in China: places for survival or for speciation? J Biogeogr 38:1267–1280
- Lu A (1999) Geography of family and genera about seed plant. Science Press, Beijing
- McNeely JA, Miller KR, Reid WV, Mittermeier RA, Werner TB (1990) Conserving the world's biological diversity. IUCN, WRI, WWF, World Bank, Washington
- Mittermeier RA, Gil PR, Mittermeier CG (1997) Megadiversity Earth's Biologically Wealthiest Nations. Conservation International (CI), Washington, DC
- Mittermeier RA, Gil PR, Hoffman M, Pilgrim J, Brooks T, Mittermeier CG, Lamoreux J, Fonseca GABd (2005) Hotspots revisited. The University of Chicago Press, Chicag
- Myers N, Mittermeier RA, Mittermeier CG, da Fonseca GAB, Kent J (2000) Biodiversity hotspots for conservation priorities. Nature 403:853–858
- Olson DM, Dinerstein E (2002) The Global 200: priority Ecoregions for global conservation. Ann Mo Bot Gard 89:199–224
- Omland KE, Cook LG, Crisp MD (2008) Tree thinking for all biology: the problem with reading phylogenies as ladders of progress. BioEssays 30:854–867
- Orme CDL, Davies RG, Burgess M, Eigenbrod F, Pickup N, Olson VA, Webster AJ, Ding TS, Rasmussen PC, Ridgely RS, Stattersfield AJ, Bennett PM, Blackburn TM, Gaston KJ, Owens IPF (2005) Global hotspots of species richness are not congruent with endemism or threat. Nature 436:1016–1019
- R Core Team (2015) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org/
- Raven PH, Axelrod DI (1974) Angiosperm biogeography and past continental movements. Ann Mo Bot Gard 61:539–673
- Redding DW, Mooers AO (2006) Incorporating evolutionary measures into conservation prioritization. Conserv Biol 20:1670–1678
- Reid WV (1998) Biodiversity hotspots. Trends Ecol Evol 13:275-280
- Rosauer D, Laffan SW, Crisp MD, Donnellan SC, Cook LG (2009) Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. Mol Ecol 18:4061–4072
- Sechrest W, Brooks TM, da Fonseca GAB, Konstant WR, Mittermeier RA, Purvis A, Rylands AB, Gittleman JL (2002) Hotspots and the conservation of evolutionary history. PNAS 99:2067–2071
- Spathelf M, Waite TA (2007) Will hotspots conserve extra primate and carnivore evolutionary history? Divers Distrib 13:746–751
- Tang Z, Wang Z, Zheng C, Fang J (2006) Biodiversity in China's mountains. Front Ecol Environ 4:347-352

Vane-Wright RI, Humphries CJ, Williams PH (1991) What to protect? Systematics and the agony of choice. Biol Conserv 55:235–254

- Wang H (1992) Floristic plant geography. Science Press, Beijing
- Wang H, Zhang Y (1994) The biodiversity and characters of spermatophytic genera endemic to China. Acta Bot Yun 16:209–220
- Wang X, Feng Z, Fu L, Wu P, Xing G (1993) Key taxa and biodiversity areas in China. In: Chen L, Wang X, Wang S (eds) Biodiversity in China: status and conservation strategy. Science Press, Beijing, pp 164–205

- Webb CO, Donoghue MJ (2005) Phylomatic: tree assembly for applied phylogenetics. Mol Ecol Notes 5:181–183
- Webb CO, Ackerly DD, Kembel SW (2008) Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Bioinformatics 24:2098–2100
- Wikstrom N, Savolainen V, Chase MW (2001) Evolution of the angiosperms: calibrating the family tree. Proc Biol Sci 268:2211–2220
- Wu Z (2003) The families and genera of angiosperms in China, a comprehensive analysis. Science Press, Beijing
- Wu Z, Wang H (1983) Physical Geography of China: phytogeography (I). Science Press, Beijing
- Wu Z, Zhou Z, Sun H, Li D, Peng H (2006) Areal-types of seed plants and their origin and differentiation. Yunnan Science and Technology Press, Kunming
- Wu Z, Sun H, Zhou Z, Peng H, Li D (2007) Origin and differentiation of endemism in the flora of China. Front Biol China 2:125–143
- Ying J (2001) Species diversity and distribution pattern of seed plants in China. Biodivers Sci 9:393-398

Ying J, Chen M (2011) Plant geography of China. Shanghai Scientific & Technical Publishers, Shanghai

Ying J, Zhang Y (1994) The endemic genera of seed plants of China. Science Press, Beijing