



Amphibian biodiversity congruence and conservation priorities in China: Integrating species richness, endemism, and threat patterns



Zhenhua Luo, Shichao Wei, Wei Zhang, Mian Zhao, Hua Wu*

Institute of Evolution and Ecology, International Research Centre of Ecology and Environment, School of Life Sciences, Central China Normal University, Wuhan 430079, Hubei, China

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ABSTRACT

Species richness, endemism, and threat status represent different biodiversity attributes important in identifying biodiversity hotspots and conservation priorities. Global distributions of areas with the most species overall, most endemic species, and most threatened species are often not coincident. Previous studies have only considered single patterns or have considered patterns separately, such that an integrated biodiversity index is needed for biodiversity assessment and conservation planning. Based on a comprehensive database of amphibian distributions in China, we analyzed the congruence of species richness (SR), endemic species richness (EMSR), IUCN threatened species richness (THSR), proportion of endemic species (%EM), and proportion of IUCN threatened species (%TH). To identify conservation priorities and protection gaps for Chinese amphibians, we explored an integrated indicator that simultaneously considered the five biodiversity patterns using principal component analyses. Although we found significant nonlinearities among SR, EMSR, and THSR patterns, their relationships to %EM and %TH were weak, and overlaps in hotspots of the five biodiversity types were limited. Our results showed that amphibian biodiversity hotspots are focused in southern, southwestern, and central China, and that the national protected area network is not effective in representing amphibian species distributions and addressing amphibian conservation priorities in China. The network is particularly ineffective in the south, which has the highest biodiversity in China, but small and insufficient protected areas. Policy, governance, and the protected area system must be revised and improved. We provide an integrated biodiversity indicator that can provide a reference for conservation priority setting for different taxa in other areas.

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1. Introduction

Understanding spatial patterns of biodiversity is essential to conservation strategies (Gaston, 2000; Hillebrand, 2004; Lamoreux et al., 2006). Under limited conservation resources, efforts, and investment, identifying regions of high conservation value, that is, biodiversity hotspots or conservation priorities, has a prominent role in biodiversity protection, and is the foremost step for conservation planning (Loyola et al., 2007; Orme et al., 2005).

Species richness, endemism, and threat status are often used as general indices of biodiversity pattern and are instrumented in setting conservation priorities, because they are critical attributes reflecting the complexity, uniqueness, and endangerment of biodiversity (Bonn et al., 2002; Caldecott et al., 1996; Kremen et al., 2008; Margules et al., 1988; Myers et al., 2000). Based on the Convention on Biological Diversity (United Nations, 1992), biodiversity conservation should focus on areas with high species richness, to maximize numbers of species

covered, and an area with large numbers of species found nowhere else or under high risk of extinction (Ceballos and Ehrlich, 2006; Lamoreux et al., 2006; Myers et al., 2000). Although species richness, endemism, and threat status are positively correlated in some areas (e.g., Hobohm, 2003; Orme et al., 2005), many previous studies found different geographic patterns of the three indices of biodiversity globally and at national scales (Bonn et al., 2002; Ceballos and Ehrlich, 2006; Crain and Tremblay, 2014; Grenyer et al., 2006; Lamoreux et al., 2006; Stohlgren et al., 2005; Xu et al., 2008). Hence, relationships among these biodiversity attributes need to be explored in more taxa to assess congruence among their patterns at global, continental, and especially national scales (Myers et al., 2000; Orme et al., 2005).

Effective *in situ* conservation requires networks of protected areas that address high conservation values in biodiversity. As limited resources and time prohibit detailed inventories for all taxa, some indicator groups can be assessed, and their overall species richness, endemic species richness, and IUCN threatened species (critically endangered, endangered, or vulnerable species in the IUCN Red List) richness (IUCN, 2001, 2014) are frequently cited as criteria for setting priorities and designating protected areas (Bonn et al., 2002; Prendergast et al., 1993). However, little is known about the extent to which protected area systems succeed in meeting these major goals: protecting areas

* Corresponding author at: Institute of Evolution and Ecology, School of Life Sciences, Central China Normal University, 152 Luoyulu, Hongshan District, Wuhan 430079, Hubei, China.

E-mail address: wuhua@mail.ccnu.edu.cn (H. Wu).

with the highest numbers of species, endemic species, and threatened species (Ceballos and Ehrlich, 2006; Kremen et al., 2008; Lamoreux et al., 2006; Rodrigues et al., 2004a,b; Wei et al., 2012).

Furthermore, protected area systems based in response to a single indicator may overlook other aspects of biodiversity attributes (Loyola et al., 2007; Myers et al., 2000; Xu et al., 2008). Some research has shown that effective biodiversity hotspot identification and conservation priority assessment can be based on patterns in surrogate taxa: Lamoreux et al. (2006) used terrestrial vertebrates as surrogates for overall species diversity globally, Loyola et al. (2007) used terrestrial vertebrates as surrogates for overall species diversity across Brazil, and de Pous et al. (2011) analyzed conservation priorities and representativeness of conservation area networks across Morocco using amphibians and reptiles as surrogates. However, those surrogates are quite region- or taxon-dependent (Gaston, 1996). Studies of distributions and hotspot patterns of British birds (Williams et al., 1996); South African birds (Bonn et al., 2002); Australian amphibians (Slatyer et al., 2007); and global patterns for vascular plants, amphibians, reptiles, birds, and mammals (Lamoreux et al., 2006; Myers et al., 2000; Orme et al., 2005) have indicated few overlaps among different biodiversity indicators. Protected area selection based on any single indicator may thus lead to inefficient conservation planning (Kremen et al., 2008); a comprehensive method and an effective indicator by which to integrate these patterns are urgently needed for biodiversity hotspot identification and conservation priority setting.

Gap analysis is a geographic planning approach for setting land management priorities, establishing new protected areas, and changing management practices of the existing protected areas (Scott et al., 1993). By assessing the comprehensiveness of the existing protected area networks and identifying failures in coverage of biodiversity, gap analysis can provide focus, direction, and accountability for future conservation efforts (Rodrigues et al., 2004b; Scott et al., 1993). Gap analysis can also provide a valuable reference for conservation strategies, especially at the national or regional scales.

China ranks among the top mega-biodiversity countries (SEPA, 1998) with >30,000 higher plant species and nearly 6500 vertebrates (Xu et al., 2008), including large numbers of endemic and threatened species (Jiang and Luo, 2012). Although biodiversity surveys and related studies that provide distributional data have been conducted nationwide in China over recent decades, little is known about spatial patterns and congruence between different biodiversity indices. Because many conservation programs have been established, the number of protected areas has been increasing rapidly, improving the protected area network in the country over the past 60 years (MEP, 2011). 2588 protected areas (14.9% of the total area of the country) were established by the end of 2010 (MEP, 2011). However, many of these protected areas are unable to meet biological conservation goals because social–economic and esthetic criteria usually dominate in area selection (Iojă et al., 2010; Oldfield et al., 2004). The efficiency of biodiversity conservation of the protected area system in China has rarely been tested, such that evaluations of biodiversity hotspots and conservation priorities and a detailed gap analysis are urgently needed.

With limited dispersal ability, specialized habitat requirements, unique life histories, and relatively small geographic distributions, amphibians usually have higher proportions of endemism and are at greater risk of extinction compared to other taxa (Slatyer et al., 2007). Although 298 amphibian species occur in China, of which 70% are endemic species and >35% are threatened (critically endangered, endangered, and vulnerable; IUCN, 2001; Jiang and Luo, 2012), protected area selection has been based on higher plants, birds, or mammals (Xu et al., 2008). Hence, detailed tests of congruence among biodiversity patterns are required in China, especially for amphibians. A conservation priority assessment (biodiversity hotspot identification) and a gap analysis would provide a valuable reference for conservation planning of Chinese amphibians, and a useful framework for conservation of other taxa in other countries.

In this study, we compiled distributions of amphibian species and a spatial dataset of protected areas in China. Using correlation analysis, a principal component analysis (PCA)-based integration procedure, and a gap analysis, our aims were: (1) to understand patterns of species richness, endemism, and threat of Chinese amphibians, and test congruence among these indices of biodiversity pattern and hotspots; (2) to produce a comprehensive indicator of amphibian diversity, which simultaneously considers species richness, endemism, and threat patterns, and test its efficiency for assessing conservation value and identifying biodiversity priorities at national scales; and (3) to detect gaps between Chinese protected area networks and amphibian biodiversity priority patterns, and to offer recommendations on conservation strategies and future protection actions.

2. Materials and methods

2.1. Study area

This study was conducted across the mainland and the two main islands (Taiwan and Hainan) of the People's Republic of China, across latitudes ranging 18–54°N and longitudes ranging 73–135°E.

2.2. Data collection and organization

We obtained distribution maps of Chinese amphibians from the IUCN database at <http://www.iucnredlist.org> (IUCN, 2014), and we also digitized the amphibian distribution maps from Fei et al. (2012) and Fei (1999). An exhaustive spatial dataset of the distributions of 298 Chinese amphibian species was thus compiled. We then updated the distribution dataset according to comprehensive literature and faunistic atlases, and we removed species with taxonomic disputes or with insufficient distribution information (some species only have one or two suspected observation records from informal publications) from the overall dataset, leaving 273 species in our analyses. All the polygon maps of species distributions were converted to rasters within a 10 km × 10 km equal-area grid system. We used five biodiversity indexes in our studies: overall species richness (SR), the number of species occurring in a grid cell; endemic species richness [EMSR; endemism followed Fei et al. (2012)], the number of endemic species occurring in a grid cell; threatened species richness [THSR; included species defined as a critically endangered, endangered, or vulnerable species as listed by the IUCN Red List (IUCN, 2001, 2014)], the number of threatened species occurring in a grid cell; proportion of endemic species (%EM = EMSR / SR); and proportion of threatened species (%TH = THSR / SR). Thus, we regrouped our species distribution dataset into subsets of endemic amphibians (204 species) and threatened amphibians (107 species: 12 critically endangered, 20 endangered, and 75 vulnerable species). To show patterns of species richness, endemism, and threat, we mapped SR, EMSR, THSR, %EM, and %TH.

Based on the World Database on Protected Areas (WDPA; UNEP-WCMC, 2011), Wu et al. (2011), and MEP (2011), we compiled a spatial database of protected areas across China. As protected areas are generally classified into national, provincial, municipal, and prefectural levels, and management efforts of the last three are usually unreliable, with some of them regarded as “paper protected areas” only (Maiorano et al., 2008), we included only national protected areas (319 national protected areas with a total area of 92.68×10^4 km²) in the analyses. Furthermore, to show the pattern of conservation efforts at the national scale, we defined conservation intensity as the percent of the area covered by national protected areas (% protected area) and calculated conservation intensity in a 100 km × 100 km grid cell system across the country.

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