



## Towards biodiversity hotspots effective for conserving mammals with small geographic ranges



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### ARTICLE INFO

#### Article history:

Received 23 June 2016

Received in revised form

12 October 2016

Accepted 15 November 2016

Available online 8 December 2016

#### Keywords:

Biodiversity conservation

Efficiency

Endemism

Global priorities

Range-size rarity

Threat

### ABSTRACT

The main goal of using global biodiversity hotspots for conservation purposes is to protect taxa with small geographic ranges because these are highly vulnerable to extinction. However, the extent to what different hotspots types are effective for meeting this goal remains controversial because hotspots have been previously defined as either the richest or most threatened and richest sites in terms of total, endemic or threatened species. In this regard, the use of species richness to set conservation priorities is widely discussed because strategies focused on this diversity measure tend to miss many of the taxa with small geographic ranges. Here we use data on global terrestrial mammal distributions to show that, hotspots of total species, endemism and threat defined in terms of species richness are effective in including 27%, 29% and 11% respectively, of the taxa with small geographic ranges. Whilst, the same hotspot types defined in terms of a simple diversity index, which is a function of species richness and range-size rarity, include 68%, 44% and 90% respectively, of these taxa. In addition, we demonstrate that index hotspot types are highly efficient because they conserve 79% of mammal species (21% more species than richness hotspot types), with 59% of species shared by three hotspot types (31% more than richness hotspot types). These results suggest that selection of different diversity measures to define hotspots may strongly affect the achievement of conservation goals.

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### 1. Introduction

The identification of biodiversity hotspots at multiple scales have become one of the most used strategies to prioritize areas for conservation worldwide (Myers et al., 2000; Mittermeier et al., 2004). From its genesis, the main goal of using global biodiversity hotspots for conservation purposes was to protect taxa with small geographic ranges because these are highly vulnerable to extinction (Myers, 2003). However, the extent to what hotspots are effective for meeting this goal remains controversial because hotspots were defined as either the richest or most threatened and richest sites in terms of total, endemic or threatened species (Ceballos and Ehrlich, 2006). In this regard, the use of species richness to set conservation priorities is widely discussed (Brooks et al., 2006) because taxa with large geographic ranges contribute more to the spatial patterning in species richness than taxa with small geographic ranges (Brooks et al., 2006). Under this evidence,

we expect that hotspots of total species, endemism and threat defined in terms of species richness be biased to protect a high proportion of taxa with large than small geographic ranges. To increase the protection of taxa with small geographic ranges, we propose that hotspots should be defined in terms of diversity measures that promote the representativeness of these taxa. In this work, we assess how the effectiveness to include mammals with small geographic ranges change in hotspots of total species, endemism and threat defined from measures of (a) species richness and (b) a diversity index which is function of species richness and range sizes rarity (Kier and Barthlott, 2001).

To increase the protection of taxa with small geographic ranges, we propose that hotspots should be defined in terms of diversity measures that promote the representativeness of these taxa while maximizing the total number of species to be conserved (Myers et al., 2000; Myers, 2003). We consider that a measure that can accomplish with this requirement is an index that is function of species richness and range sizes rarity (Kier and Barthlott, 2001). Conceptually, the calculation of this index will give higher weights to species with small ranges, and progressively lower weights to

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those species with larger ranges (i.e., this index is proportional to the inverse of species distributional range size) (Laffan and Crisp, 2003). For example, when the totality of a species' range falls into a mapping unit (such a biogeographic region, or a grid cell), its entire value (i.e., 1 range equivalent) is attributed to this area, but if a species is distributed in two mapping units, the half of its value (i.e., 0.5 range equivalent), are attributed to each mapping unit and so on (Kier et al., 2009). Then, the index is calculated by summing the fractions of the inverse of species range size by mapping unit. Although we are conscious that other diversity measures, such as dispersion fields (Graves and Rahbek, 2005), can be tested for its ability to identify hotspots that include a high number of small ranged taxa, this measure has lower correlation with species richness. Therefore, for this contribution, we prefer the diversity index presented herein because it better reflects both range size rarity and species richness (Kier and Barthlott, 2001). This decision is based on the spirit of biodiversity hotspots thesis which is to protect the greatest number of species with small range sizes per dollar invested (Myers et al., 2000; Myers, 2003).

In this work, we assess how the effectiveness to include mammals with small geographic ranges change in hotspots of total species, endemism and threat defined from measures of (a) species richness and (b) the diversity index.

## 2. Materials and methods

### 2.1. Data source and diversity measures

To estimate measures of mammal diversity, we utilized digital maps of the geographic ranges of 5285 terrestrial species (IUCN, 2013). Diversity measures were obtained by dividing the world (except Antarctica) into 18,571 equally-distanced cells of  $1^\circ \times 1^\circ$ , with geographic projection and coordinate system measured in decimal degrees of latitude/longitude. We used this scale because the use of range map data at finer scales increases the probability of false occupancies, whereas using coarser scales reduces such probability (Hurlbert and Jetz, 2007). We calculated species richness by counting the number of overlapping range maps that fall within each of 18,571 cells. Conversely, the diversity index was calculated as follows: first, counting the number of cells in which each species is distributed; second, calculating its inverse value (i.e., dividing one by the number of cells in which each species is distributed); and third, summing the inverse value of all species that fall within each of 18,571 cells (Kerr, 1997; Kier and Barthlott, 2001). Using this index, cells with equal species richness, but with a high proportion of taxa with small geographic ranges, will have higher scores than cells containing taxa with large geographic ranges (Kerr, 1997). Species richness and diversity index were calculated for three nested categories of mammal distributions: total species ( $n = 5258$ ); endemic species ( $n = 2236$ ), and threatened species ( $n = 1096$ ). We considered as endemic those taxa with geographic ranges smaller than or equal to 25 cells (Ceballos and Ehrlich, 2006), and as threatened those taxa deemed susceptible to extinction by the IUCN (i.e., critically endangered [CR], endangered [EN], vulnerable [VU]; Ceballos and Ehrlich, 2006; IUCN, 2014). Hotspots were defined as 2.5% of cells with the highest scores (Ceballos and Ehrlich, 2006; Lennon et al., 2004) for each diversity measure in the three categories of mammal distributions. Thus, we identified six types of hotspots: three based on measures of species richness (RH), considering total (RHS), endemic (RHE) and threatened species (RHT); and three based on measures of diversity index (IH), considering total (IHS), endemic (IHE) and threatened species (IHT). For a precise evaluation about the effectiveness of these six hotspot types for conserving taxa with small but also with larger geographic ranges, we partitioned the data on

total, endemic, and threatened species into geographic range-size quartiles (Rahbek et al., 2007): from those with small ranges (1st quartile), to those with large ranges (4th quartile).

### 2.2. Mapping and hotspots

To build the grids at different scales and rasterize the range maps shapefiles of terrestrial mammal species, we used the freely available SAM software (Rangel et al., 2010). As in Orme et al. (2005), hotspot definitions were based on the percentage of terrestrial cells covered; thus, where quantile scores fell within a diversity class, we used the number of cells for that class. Particularly, with this methodology we found a higher number of grid cells as richness hotspot types (because species counts are a discrete variable) than as index hotspot types (where index scores are a continuous variable). In order to assess whether the effectiveness of IH for including more taxa with small geographic ranges, compared to RH, depends on the threshold and scale used in our study, we performed the same analyses at different thresholds (5%, 10%, 25%, 50% and 75%) and scales ( $2^\circ \times 2^\circ$ ,  $4^\circ \times 4^\circ$  and  $8^\circ \times 8^\circ$ ). When we analysed the number of endemic species falling within both RHE and IHE at scales of  $4^\circ \times 4^\circ$  (approximately 160,000 km<sup>2</sup>), we divided species range-sizes into two groups (based on the median value): taxa with small and with large geographic ranges. At scales of  $8^\circ \times 8^\circ$ , there was a only one range-size group, because geographic ranges of endemic species were smaller than grid cells sizes.

### 2.3. Statistical analyses

To recognize the ability of diversity measures to capture richness patterns of species with different geographic ranges, we used the SAM software (Rangel et al., 2010) to perform Spearman rank correlations (with Bonferroni correction) between diversity measures (richness and diversity indices) and richness patterns of total, endemic and threatened species belonging to range-size quartiles. In addition, we also performed Spearman rank correlations to assess spatial correspondence among richness patterns of total species, endemism and threat and among index patterns of total species, endemism and threat. Spatial structure of species composition between RH and IH was analysed with Mantel tests. To this end, we calculated a Jaccard similarity matrix based on the species composition found in each hotspot type, and a matrix of Euclidean geographic distances according to hotspot locations (we used latitude and longitude considering the centroid of grid cells). Based on these analyses, we were able to evaluate the similarity in composition of closely located cells. We performed Mantel tests with the package ade4 (Dray and Dufour, 2007) in R (R Core Team, 2012), correlation scores were based on Spearman rank, using 99,999 randomizations.

## 3. Results and discussion

Global geographic distributions of grid cells identified as being RH were similar to those described elsewhere (Ceballos and Ehrlich, 2006) (Fig. 1a–c); instead, in cells identified as being IH there were some overlapped with their respective RH and others were idiosyncratic, the latter recognized here as potential new hotspots (Fig. 1d–f). The percentages of spatial overlap between IH and RH were very variable: 23% between RHS and IHS, 62% between RHE and IHE, and 12% between RHT and IHT. Overlapping hotspots were roughly located, IHS, IHE and IHT in the north of South America, Central Africa and south east of Asia, IHS and IHE in the south of Central America, and IHE in the south of North America and Central South America. Instead, potential new

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