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The geography of high-value biodiversity areas for terrestrial vertebrates in Western Europe and their coverage by protected area networks

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Abstract. We identified high-value biodiversity areas (HVBAs) of terrestrial vertebrates according to a combined index of biodiversity (CBI) for each major taxon and a standardized biodiversity index (SBI) for all taxa in 2195 cells of 50×50 km in Western Europe to evaluate whether these areas are included in the current protected area networks. The World Database on Protected Areas (WDPA) and NATURA 2000 protected area network were used to assess the protected area cover in HVBAs. WDPA and NATURA 2000 were geographically quite complementary as WDPA is more densely represented in Central and Northern Europe and NATURA 2000 in the Mediterranean basin. A total of 729 cells were identified as HVBAs. From the total of these HVBA areas, NATURA 2000 network was present in more cells (660) than the WDPA network (584 cells). The sum of protected land percentages across all the HVBA cells was 28.8 %. The identified HVBA cells according to the SBI included 603 or 78.2 % of all vertebrate species in the study region, whereas the identified HVBA cells according to the SBI for individual taxa included 47 (90.4 %) species of amphibians, 79 (74.5 %) of reptiles, 417 (88.5 %) of birds, and 130 (91.5 %) of mammals. However, neither network was present in 7 or 3 % of the identified HVBA cells. Thus, we recommend expanding protected areas in Europe to fill this gap and improve coverage of vertebrate species to strengthen biodiversity conservation.

1 Introduction

There is strong evidence that biodiversity is declining and the pressures on biodiversity are rising (e.g. Butchart et al., 2010, 2012; Hoffman et al., 2010). Similarly, responses for protecting biodiversity are increasing as well (Butchart et al., 2010), and conservation actions have been shown to be useful to improve the conservation status of endangered species (Hoffman et al., 2010). In this context, identifying high-value biodiversity areas at the regional scale and assessing if such areas are included in protected area networks is a primary goal for biological conservation (Jennings, 2000; Cayuela et al., 2006; Rey Benayas et al., 2006; Pressey et al., 2007; Branquart et al., 2008).

Protected area networks are important to preserve species and ecosystems, specifically those that are located in inten-

sively human-disturbed areas (Hanski and Walsh, 2004). In addition, including information on species conservation status at the regional scale has become a primary approach to generate effective conservation policies (Díaz Páez and Ortiz, 2003; Rey Benayas and de la Montaña, 2003). In the last decade, several studies have proposed different methods for species and ecosystems conservation planning by analysing species distribution patterns of different taxonomic groups and at different grain size (Morrone, 2000a). However, a number of studies have shown that protected area networks do not necessarily ensure the conservation of biodiversity (Margules and Pressey, 2000; Branquart et al., 2008; Wiersma and Nudds, 2009; Butchart et al., 2012). This is mostly a consequence of the traditional "political" approach to selecting protected areas that is primarily determined by

economic and cultural aspects rather than by biological factors (Margules and Sarkar, 2007).

Global biological diversity studies indicate that at least 12 % of vertebrate species are not included in any protected area network, and half of the important sites for biodiversity conservation remain unprotected. Therefore, established protected areas have to be complemented with new reserves incorporating the objectives of representativeness and persistence (Rodrigues et al., 2004; Butchart et al., 2012), along with the key concepts of complementarity, irreplaceability and vulnerability, in order to prevent the loss of unique biodiversity (Rodrigues et al., 2004; Sarkar et al., 2006). To accomplish this, it is fundamental to identify how well biodiversity is represented by current protected area networks (Margules and Pressey, 2000; Maxted et al., 2008), the so-called gap analysis. The concept of gap analysis was first described by Burley (1988) as "gaps of conservation" by identifying and classifying various elements of biological diversity (e.g. major ecosystems or species) and determining which elements are poorly represented in the current network of protected areas.

There are several gap analysis studies supporting that different taxa are underrepresented in protected area networks at the global (Rodrigues et al., 2004; Jenkins and Joppa, 2009) and continental or country scales (Rey Benayas and de la Montaña, 2003; Rey Benayas et al., 2006; Araújo et al., 2007; Maiorano et al., 2007; Wiersma and Nudds, 2009). Here we explore how well vertebrate taxa (amphibians, reptiles, birds, and mammals) are represented in the protected areas of Western Europe. Our goals are two-fold: firstly, to investigate the distribution of high-value biodiversity areas (HVBAs) for the four vertebrate taxa in Europe; and secondly, to analyse to what extent the current protected area network represents the HVBAs of this region.

2   Methods

2.1   Data

Distribution maps for reptile, amphibian, breeding bird, and mammal species were obtained from Gasc et al. (1997), Hagemeijer and Blair (1997) and Mitchell-Jones et al. (1999). The presence of 52 amphibian, 106 reptile, 471 bird, and 142 mammal species was recorded in each cell of an UTM grid comprising 2195 cells of 50×50 km, and the species richness of each vertebrate group was obtained for each cell. Marine species as well as all cells with less than 50 % inland cover and all islands except Great Britain were excluded from the analysis.

We used maps resulting from the World Database on Protected Areas (WDPA) and the NATURA 2000 network to represent the percentage of protected area within each UTM cell. The WDPA database (version 2010) is the most comprehensive global spatial dataset on marine and terrestrial protected areas available and includes all nationally desig-

nated (e.g. national parks) and internationally recognized protected areas (WDPA, IUCN and UNEP-WCMC, 2010) except, unfortunately, those of Great Britain, which is part of our study region. The NATURA 2000 is an ecological network of protected areas that aims to protect biodiversity in Europe and is composed of sites designated under the Birds Directive (Special Protection Areas, SPA) and the Habitats Directive (Sites of Community Importance, SCIs, and Special Areas of Conservation, SACs) of the European Union. The European database on NATURA 2000 sites was obtained from the European Environmental Agency (EEA, 2009) (available at http://www.eea.europa.eu/data-and-maps/data/natura-2000).

We used Kernel density plots to investigate the percentage of UTM cells included in the WDPA, NATURA 2000, and the combined protected area networks. The Kernel density plot is considered a smoother version of a histogram and estimates the probability density rather than breaking the counts into discrete categories (Scott, 1992; Faraway, 2006).

2.2   Criteria for identifying high-value biodiversity areas

Areas of high-value biodiversity (HVBAs) for each taxon (j) were identified by using the combined biodiversity index (CBI) proposed by Rey Benayas and de la Montaña (2003). This index integrates species richness, rarity and vulnerability, and corresponds to the following formula:

$$\text{CBI} = \sum_{i=1}^{sj} (1/n_i) v_i.$$

In this index, species richness is implicit in $\sum_{i=1}^{sj}$, where sj defines the number of species in taxa j; rarity for a particular species is calculated as the inverse of the number of cells where the species is present ($1/ni$), and vulnerability (vi) is computed on the basis of standard vulnerability categories of species present in the cell. Specifically, for this we used the International Union for Conservation of Nature Red List of Threatened species Version 2010.4 (IUCN, 2010), which defines the following vulnerability categories: least concerned (595 species; $vi = 1$), data deficient (two species; $vi = 2$), near threatened (53 species; $vi = 3$), vulnerable (110 species; $vi = 4$), endangered (nine species; $vi = 5$), critically endangered (two species; $vi = 5$). Assunção-Albuquerque et al. (2012) provides maps showing the geographical pattern of species richness, rarity, vulnerability, and combined biodiversity index for the four taxonomic groups in the study area based on the grid cells used in this study.

We also computed the standardized biodiversity index (SBI, Rey Benayas and de la Montaña, 2003) by dividing the combined index of biodiversity of each vertebrate group in every cell by its mean across all cells (m_j). The SBI formula is
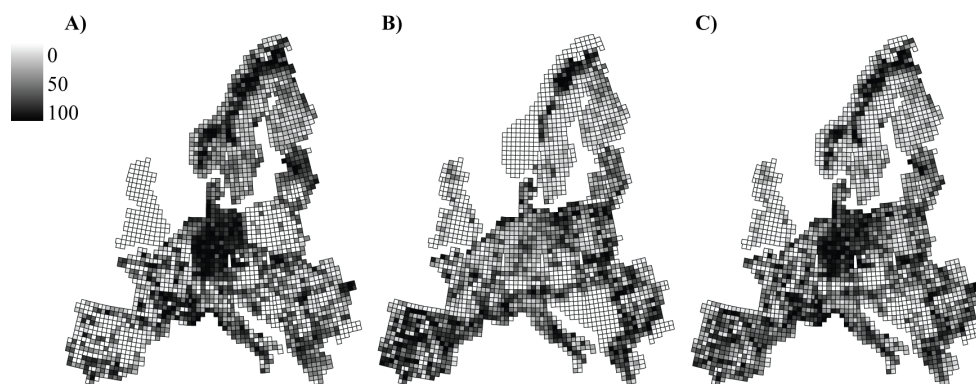
Figure 1. Proportions of protected areas included in the World Database on Protected Areas **(A)**, the NATURA 2000 network **(B)** and both networks combined **(C)** in 50×50 km UTM grid cells covering continental Western Europe and Great Britain. The grey scale indicates the percentage of protected area in each cell.

$$SBI = \sum_{j=1}^{4} CBI_j / m_j .$$

Once every cell was assigned a CBI value for each taxon, we used ArcGIS 9.3 to compute the $G*$ spatial statistics (Getis and Ord, 1992) and thus identify CBI-based HVBAs for each taxon. This technique allows the identification of cells with higher CBI value than randomly expected by comparing the value for a given observation with locations in the neighbourhood, thus providing an explicit consideration of space (Getis and Ord, 1992; Nelson and Boots, 2008). We also applied this technique to SBI values and thus calculate HVBAs for all taxa together.

2.3 Gap analysis

To investigate how well current protected areas represent high-value diversity areas for the four vertebrate groups across Europe, the maps of HVBAs and the maps of protected area networks (WDPA, NATURA 2000 and the combined networks) were overlapped. Then, the percentage of protected area networks in each grid cell was calculated. Those cells containing HVBAs but not protected areas were considered full gaps.

3 Results

### 3.1 Spatial distribution of protected areas

WDPA and NATURA 2000 protected areas occurred in 1758 and 1889 cells, respectively, which represent 80.1 % and 86.1 % of the cells included in the study region (Fig. 1). A total of 1541 cells contained both networks, whereas only 89 cells did not include any protected area. The correlation between the percentage cover of protected areas according to WDPA and NATURA 2000 was highly significant but weak

($r = 0.37$, $p < 0.0001$), and the networks showed contrasted distributions of cells with high cover of protected areas. In the case of the WDPA, these cells were found mainly in Central Europe (Germany), west Fennoscandia and in the Alps (Fig. 1a), whereas for the NATURA 2000 network they occurred more frequently in Sweden, northern Poland and especially across the Mediterranean basin (Fig. 1b). These results indicate that both networks complement each other to some extent, so that regions with low coverage of protected areas in one network are sometimes well represented in the other (e.g. while the Iberian Peninsula is poorly covered by the WDPA, it shows a dense representation of NATURA 2000 areas), as indicated in the combined map shown in Fig. 1c.

Considering all cells, Kernel density plots of the percentage protected area within cells covered by the WDPA and NATURA 2000 networks indicated that most cells included a small proportion of protected areas. For instance, 1800 (81.9 %) and 1805 (82.2 %) cells had less than 20 % of their area included in such networks, respectively (Fig. 2a, b), including 407 and 307 cells with no coverage at all of such networks, respectively. The percentage of cells with less than 20 % of their area included in the combined network was 64 % or 1484 cells (Fig. 2c). Similarly, most of HVBA cells included a small proportion of protected areas: 442 (82.3 %) and 357 (68.1 %) of them included less than 20 % of WDPA and NATURA 2000 cover, respectively (Fig. 2d, e), whereas 305 (58.2 %) has less than 20 % of combined network cover (Fig. 2f). The summing of protected land percentages across all the HVBA cells was 28.8 %.

3.2 Geographical distribution of high-value biodiversity areas and gap analysis

A total of 729 cells were identified as HVBAs according to the combined index of biodiversity. These cells included between 74.5 % of reptiles – the least favoured species – and 91.5 % of mammals – the most favoured group. Of
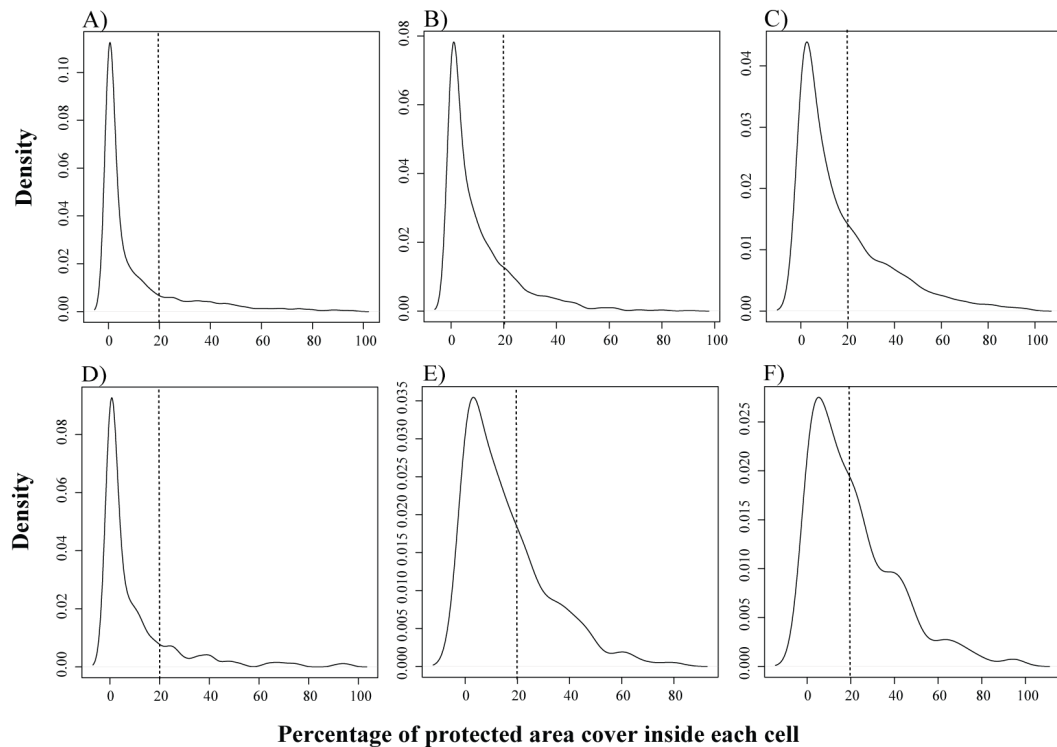
Figure 2. Kernel density plots showing the relative frequency of 50×50 km UTM grid cells that include a particular percentage of protected area for all cells in the study area **(A, B, C)** and those cells identified as high-value biodiversity areas only **(D, E, F)** according to the World Database on Protected Areas network **(A, D)**, the NATURA 2000 network **(B, E)**, and the combined map comprising both networks **(C, F)**.

all not included species, one (*Pelodytes caucasicus*), four (*Phyllodactylus europaeus, Lacerta bonnali, Lacerta derjugini, Vipera kaznakovi*), four (*Polysticta stelleri, Tetrao mlokosiewiczi, Colinus virginianus, Sitta krueperi*), and one (*Bison bonasus*) were near-threatened or threatened amphibian, reptile, bird, and mammal species, respectively. The distribution of these HVBA cells (Fig. 3a–d) indicated that most of them were located in the Mediterranean region, especially in Iberia and the Balkans. Secondary clusters of HVBA cells were also observed in the Alps for mammals, and at various more or less isolated spots for the rest of the groups.

NATURA 2000 network included a higher number of HVBA cells for the four taxonomic groups (660 cells, 90.5 %) than the WDPA network (584 cells, 80.1 %). The 660 NATURA 2000 cells included 93.1 % of amphibian, 86.7 % of reptile, 92.8 % of bird, and 89.1 % of mammal species, whereas the 584 WDPA cells included 79.3 % of amphibian, 86.7 % of reptile, 78.8 % of bird, and 78.4 % of mammal species. Across all four vertebrate groups, 145 gap cells (19.9 %) according to the WDPA network, 69 gap cells (9.5 %) according to the NATURA 2000 network, and 7 gap cells (3 %) according to the combined network were identified. These full gaps mainly occurred in areas of the Mediterranean basin (particularly in Iberia and the Balkans regions), although for birds they were also present in localized areas of southern England and Scotland (Fig. 3a–d). The lowest num-

ber of gap cells was observed for reptiles in the WDPA network (16 cells, 13.3 %), amphibians in the NATURA 2000 network (12 cells, 6.9 %), and amphibians in the combined network (one cell, 0.6 %); on the other side, the highest number of gap cells was observed for mammals in the WDPA network (55 cells, 21.6 %), reptiles in the NATURA 2000 network (16 cells, 13.3 %), and mammals in the combined network (16 cells, 6.3 %) (Table 1).

The standardized biodiversity index that integrated all taxa simultaneously produced a total of 226 HVBA cells (Table 1), which included 83 % of amphibian, 75 % of reptile, 88 % of bird, and 91 % of mammal species. Of the not included species, 9 (17 %), 26 (24 %), 54 (11 %) and 12 (8 %) were threatened amphibian, reptile, bird, and mammal species, respectively. Most of these HVBA cells were located in the Mediterranean region (Fig. 3e). From these, a total of 7 cells (3 %) did not include any protected area and were thus considered full gaps (Table 1).

4   Discussion

This study identified the geographic location of high-value biodiversity areas for amphibians, reptiles, birds and mammals across Western Europe using different biodiversity criteria (richness, rarity, vulnerability), and pursued to assess
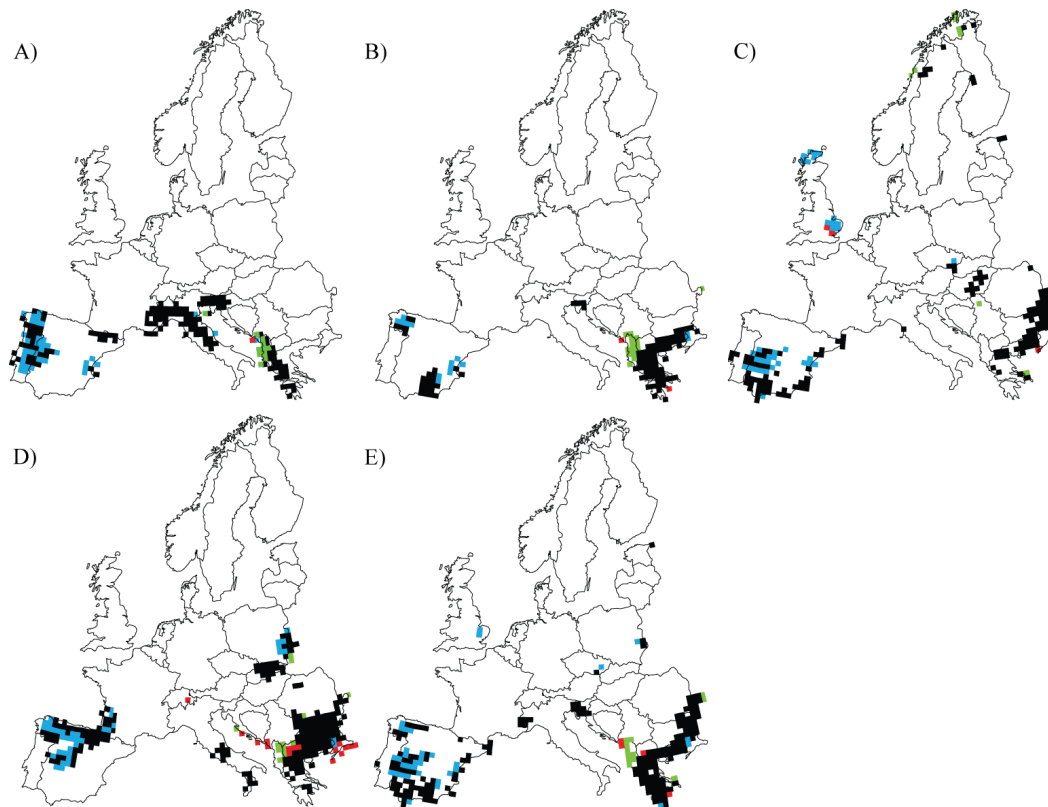
Figure 3. Distribution of cells representing high-value biodiversity areas for amphibians **(A)**, reptiles **(B)**, birds **(C)**, mammals **(D)**, and all taxa together **(E)** across continental Western Europe and Great Britain. Colors differentiate between high-value biodiversity area cells that contain protected areas included in both the World Database on Protected Areas and the NATURA 2000 network (black) from those cells that represent full gaps with respect to either the World Database on Protected Areas (blue), the NATURA 2000 network (green), or both networks combined (red).

Table 1. Summary of results on the amounts of (1) cells comprising HVBAs for the species of four vertebrate groups (based on combined biodiversity index values obtained for each group; see Methods) and for all species (based on standardized biodiversity index values); (2) species occurring in HVBA cells; and (3) HVBA cells not included in the WDPA, NATURA 2000 and combined protected area networks (i.e. gap cells).

Species group (and biodiversity index)	HVBA cells	Species in HVBA cells	HVBA cells excluded from protected area networks		
			WDPA	NATURA 2000	Combined
Amphibians (CBI)	174	47 (90.4 %)	36 (20.7 %)	12 (6.9 %)	1 (0.6 %)
Reptiles (CBI)	120	79 (74.5 %)	16 (13.3 %)	16 (13.3 %)	2 (1.7 %)
Birds (CBI)	180	417 (88.5 %)	38 (21.1 %)	13 (7.2 %)	3 (1.7 %)
Mammals (CBI)	255	130 (91.5 %)	55 (21.6 %)	28 (10.9 %)	16 (6.3 %)
All species (SBI)	226	603 (78.2 %)	39 (17.3 %)	16 (7.1 %)	7 (3.0 %)

how well these HVBAs are covered by two major networks of protected areas, namely WDPA and NATURA 2000.

We found that HVBA cells for the four vertebrate groups were mostly distributed across the Mediterranean basin, which agrees with previous results that support the Mediterranean area as being one of the most biodiverse European regions (Araújo et al., 2007) and a relevant biodiver-

sity hotspot at global scale (Myers et al., 2000; Shi et al., 2005; Blondel et al., 2010; Eklund et al., 2011). In agreement with our findings, Araújo and Pearson (2005) identified several relevant priority areas for amphibian and reptile species in the Mediterranean basin, and Rey Benayas and de la Montaña (2003) and Nogués-Bravo and Martínez Rica (2004) did the same for amphibian and mammal species

in Spain. In contrast with this key importance of the Mediterranean basin for biodiversity conservation, this region has been reported as being highly disturbed and with ongoing strong biodiversity losses (Myers et al., 2000; Maiorano et al., 2006). Moreover, previous evaluations of the effectiveness of the protected area networks in the Mediterranean basin have been limited to only some taxonomic groups and areas such as the Iberian (Martín-Piera, 2001; Carrascal and Lobo, 2003; Lobo and Araújo, 2003; Rey Benayas and de la Montaña, 2003; Araújo, 2004; Martínez et al., 2006; Araújo et al., 2007) and the Italian (Maiorano et al., 2006) peninsulas. Thus, the present study is a valuable effort to evaluate how well the terrestrial vertebrate diversity of this region, as well as Western Europe as a whole, is covered by protected area networks. Previously, Araújo et al. (2011) performed an assessment at the European scale under climate change conditions.

There is some overlap in the coverage of both WDPA and NATURA 2000 networks (Fig. 1); however, we found that WDPA is more densely represented in Central and Northern Europe and NATURA 2000 in the Mediterranean basin. So, both networks are complementary to some extent in protecting Western European biodiversity, which makes conservation efforts easier. Although WDPA intends to be the most comprehensive global spatial dataset on marine and terrestrial protected areas available, it does not cover Great Britain, and, additionally, our results showed gaps of $\geq 13.3\%$ of the HVBA cells for the various taxonomic groups (see Table 1). These figures are consistent with the results of Rodrigues et al. (2004), who concluded that WDPA is far from accomplishing its conservation goals. Also, Chape et al. (2003), Catullo et al. (2008) and Gallo et al. (2009) support that WDPA is not adequate for biological conservation purposes. NATURA 2000 includes a higher number of HVBA cells for all taxa than WDPA because it spreads over more cells, and therefore this result is expected by chance (Table 1). This agrees with previous studies that found that this network best represented vertebrate species across various European areas (Rey Benayas et al., 2006; Martínez et al., 2006; Araújo et al., 2007; Gaston et al., 2008). However, coverage by natural protected areas does not completely guaranty the enhancement of the conservation status of particular species at particular sites (Rey Benayas and de la Montaña, 2003). Further, although NATURA 2000 has a greater coverage than WDPA, the degree of protection of NATURA 2000 may be actually lower than other types of protected areas as a wide range of human activities are allowed in the former.

Our results also highlighted that the highest number of absolute cell gaps of HVBAs was observed for mammal species (16 of cells in the combined network of protected areas). Many mammal species are facing population declines and are, or will be soon, under the risk of extinction (Cardillo et al., 2004; Rondinini et al., 2011; Visconti et al., 2011). Moreover, one fourth of mammal species are globally threatened or extinct (Vié et al., 2009), and the representation of

mammals in protected areas is far from being complete, as reported by Rodrigues et al. (2004) for the Globe, Catullo et al. (2008) for Southeast Asia, and Albuquerque et al. (2011) for the Brazilian Atlantic Forest Biosphere Reserve. Thus, extra efforts are required to ensure mammal species conservation, especially for those not included in protected areas.

More than a debate on how to tackle conservation strategies, there is agreement that more land should be protected quickly, and that this protection should be expanded off reserve (Mawdsley et al., 2009; Heller and Zavaleta, 2009). On one hand, other strategies outside protected areas such as land stewardship or voluntary programs targeting native species and habitats on private, working landscapes or private land conservation could act as a framework for safeguarding biodiversity (Cox and Underwood, 2011). On the other hand, to assess future conservation strategies, it should be considered that biodiversity values are not static in time and that climate change represents a crucial potential threat for the future protected areas' effectiveness (Hannah et al., 2007). Since climate change may cause shifts in species distribution range, rigorously defined networks of protected areas may play a key role in mitigating the negative impacts of climate change on biodiversity (Hole et al., 2009).

We conclude that existing networks of protected areas in Western Europe include most but not all areas that were identified as highly valuable for vertebrate diversity, and that more efforts are necessary to complete the current natural protected networks, particularly for the Mediterranean basin and mammal species. Identifying gaps in the inclusion of high-value biodiversity areas and species representation in protected areas is a critical issue to assess so that future conservation strategies assure species preservation.

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