

Identifying areas of high-value vertebrate diversity for strengthening conservation

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Abstract

Identifying areas with relevant features of biodiversity is useful to rank priorities for strengthening the design of well-sited natural protected areas and to optimize resource investment in conservation. This study provides decision makers critical tools for highlighting pieces of land worthy of conservation in Spain. We studied four taxa—amphibians, reptiles, nesting birds and mammals—in a 50 × 50 km grid ($n = 259$ cells). We used five criteria for identifying areas of high-value diversity: species richness, rarity, vulnerability, a combined index of biodiversity, and a Standardized Biodiversity Index that measured all four taxa together. As far as we know, the combined index of biodiversity and the Standardized Biodiversity Index are original. Areas of high-value diversity were defined as those cells within the 15% top segment of ranked values for the different criteria. Congruence of areas of high-value diversity for taxa pairs was moderate to low, and averaged 38.5% for areas of high-value diversity based on the combined index of biodiversity. The performance based on the average proportion of threatened species excluded from areas of high-value diversity followed the rank combined index of biodiversity = rarity (0.3%) > vulnerability (9.9%) > species richness (13.8%). The areas of high-value diversity identified according to the Standardized Biodiversity Index included all amphibian and mammal species, all but one reptile species (categorized as rare) and all but six bird species (three of which were categorized as threatened). About 70% of the areas of high-value diversity identified based on the Standardized Biodiversity Index included natural protected areas. However, they average only 274.6 km², thus occupying a small fraction of the areas of high-value diversity, and there is no guarantee that the species found in an area of high-value diversity site will be present in its protected fraction. Consequently, we urge managers of natural protected areas to conduct diversity surveys. We also urge that additional natural protected areas be established to include the gap of 30% of areas of high-value diversity not currently protected. We took an step for biodiversity conservation planning in the studied region, and discuss the usefulness of maps of areas of high-value diversity for conservation, ecological restoration, and environmental impact assessment and mitigation.

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1. Introduction

The scientific community has witnessed a considerable debate about biodiversity conservation during the last decade. The debate has been fuelled by studies of the increasing rates of biodiversity loss (Heywood, 1995; Costanza et al., 1997; Pimentel et al., 1997; Ricketts et al., 1999; Terborgh, 1999; Tilman, 1999; Bininda-Emonds et al., 2000; Cincotta et al., 2000; Myers et al., 2000; Pimm and Raven, 2000). Biodiversity conservation

usually requires decision making that needs input by both conservation biologists and ecologists. Reserves alone are not adequate for nature conservation but they are the cornerstone on which regional strategies can be built (Margules and Pressey, 2000), and it is necessary to set prior targets (Ceballos et al., 1998; Myers et al., 2000). We address this problem of setting prior targets by identifying areas of high-value diversity of vertebrate species in Spain, evaluating the effectiveness of various criteria used to define them, and examining their geographical coincidence with the existing network of natural protected areas. Thus, we hope to provide decision makers with critical tools for identifying tracts of land particularly worthy of conservation.

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Detecting areas of high-value diversity is useful, in our view, as a tool for four major tasks related to nature conservation. These are (1) creating networks of natural protected areas, (2) conservation out from natural protected areas favored by a wise natural resource management, (3) ecological restoration as an action to preserve threatened species and communities, and 4) environmental impact assessment and mitigation. This paper focuses on the first topic. Establishing natural protected areas is one of the most useful tools for preserving large pools of biodiversity. Unfortunately, throughout most of the world there are neither the resources nor the time to carry out detailed inventories for most taxa before designating protected areas (Groombridge, 1992; Raven and Wilson, 1992; Prendergast et al., 1993). Besides, this is often expensive because land needs to be purchased and managed for species conservation (Mittermeier et al., 1998; James et al., 1999). Therefore, it is important to rank priorities of sites with relevant features of biodiversity to optimize resource investment in conservation. These relevant features of biodiversity are most frequently based on criteria such as species richness, rarity (particularly endemic taxa), taxonomic uniqueness, threatened species and indicator taxa (Usher, 1986; Williams et al., 1991; Prendergast et al., 1993; Faith and Walker, 1996; Castro et al., 1997; Reid, 1998; Rey Benayas et al., 1999; Virolainen et al., 2001).

To accomplish our objectives it is necessary, first, to identify what areas are relevant for their biodiversity features. We used four taxa of vertebrate species: amphibians, reptiles, breeding birds and mammals. These are well studied taxa because they are conspicuous. Birds are also “popular”, whereas amphibians and reptiles figure less prominently in site selection. Many of these species have been used as bioindicators. Particularly, mammals such as *Ursus arctos*, *Lutra lutra* and *Lynx pardina* are outstanding indicators of habitat quality in the study area. We used five criteria for identifying areas of high-value diversity: species richness, rarity, vulnerability, a combined index of the three former, and a Standardized Biodiversity Index that measured all four taxa together. Our analyses are illustrative, not exhaustive. A similar approach can be taken to identify areas of high-value diversity elsewhere, using either different species groups or criteria.

Site selection would be easier if there was overlap of areas of high-value diversity of different taxa and areas of high-value diversity identified according to different criteria. We evaluated the effectiveness of the various criteria used to identify areas of high-value diversity by looking at the species lists that were included and excluded. Finally, we overlaid the produced maps of areas of high-value diversity with the existing network of natural protected areas to examine coincidences and highlight gaps. Our intention is to provide useful information for

diversity conservation to decision makers (politicians, technicians, land managers, managers of natural protected areas, etc.).

1.1. The study area and its existing network of natural protected areas

The Iberian Peninsula and the Balearic Islands include a variety of biomes, relief, climates, and soil types despite their relatively small area (585,644 km² in total). Two major climatic zones, Mediterranean and Atlantic, impinge on Iberia (Font Tullot, 1983). The Mediterranean climate is characteristic of most of Iberia and the Balearic Islands, whereas the Atlantic climate is found in a band ca. 100 km wide along the western and northern coasts, and it also influences the Pyrenean Mountains. The current driest and warmest areas served as a *refugium* during Pleistocene glaciations. In contrast, the northern transition zone is substantially younger, having emerged only after the glacial retreat.

Spain is one of the most diverse countries in the European Union. The Canary Islands will not be considered in this study because they represent Macaronesic biotas completely different to the rest of the country. The Spanish network of natural protected areas currently comprises 33,304 km². About 86.2% of this land (28,721 km²) belongs to 12 National Parks, 91 Natural Parks—including 1 Biosphere Reserve—and 11 Regional Parks (Fig. 1 and Appendix A) (Gómez-Limón et al., 2000). Their mean area in continental Spain and the Balearic Islands is 274.6 ± 419.1 km², and range between 0.45 and 2143.4 km². Four National Parks and 11 Natural parks are located in the Canary Islands. By law, national, natural and regional parks must implement a management plan of natural resources, and hence are the most robust figs. of natural protected areas.

2. Methods

2.1. Analytical units and data sources

Our analyses used cells defined by Universal Transverse Mercator (UTM) coordinates as analytical units (Fig. 1). The modal cell size was 2500 km². This is the smallest size common to all taxa considered in this study. The cells adjacent to borders between different UTM coordinate zones are slightly different in size. We examined the presence and absence of amphibian, reptile, breeding bird, and mammal species in a total of 259 cells. The cell-by-species matrices were built using species distribution atlases (Gasc et al., 1997; Hagemeyer and Blair, 1997; Mitchell-Jones et al., 1999). We counted 27, 42, 269, and 89 amphibian, reptile, breeding bird, and mammal species, respectively. Information on

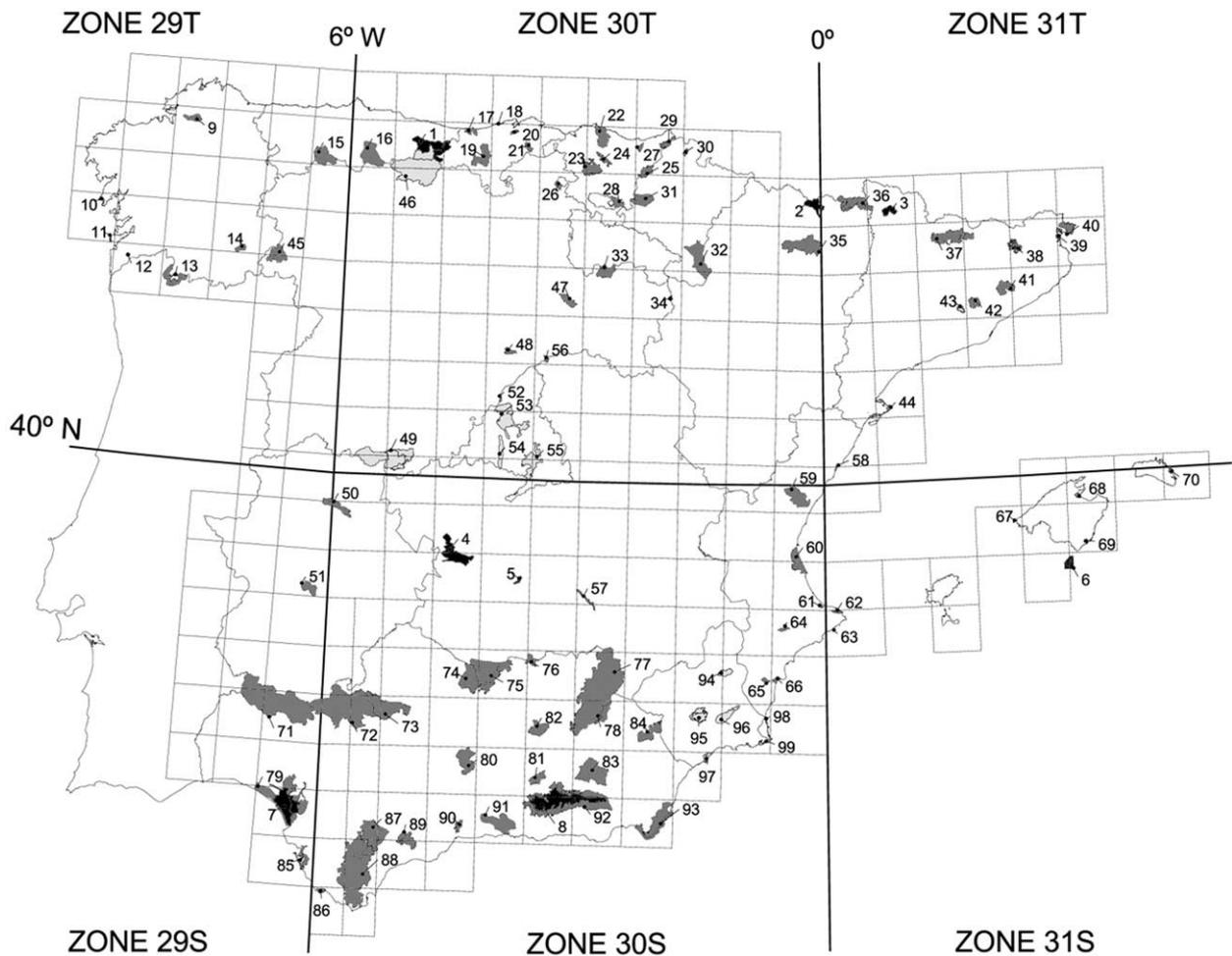


Fig. 1. Map of continental Spain and the Balearic Islands (area is 497,508 km²). It illustrates the grid used for the analysis of areas of high-value diversity—based on UTM coordinates—, the political distribution of the territory (autonomous regions), and the location of national, natural and regional parks (black, dark grey, and light grey spots, respectively; spot no. 22 is a Biosphere Reserve). Source of the location of the natural protected areas was Gómez-Limón et al. (2000). A complete list of the natural protected areas considered in this study can be found in Appendix A.

species presence for breeding birds and mammals was not available for two and six cells, respectively.

2.2. Criteria for identifying areas of high-value diversity

We used four criteria to identify areas of high-value diversity for a single taxa: species richness, rarity, vulnerability, and a combined index of biodiversity. There are many forms of rarity, that respond to different combinations of geographical range, local abundance, habitat specificity and habitat occupancy (Rabinowitz, 1981; Rey Benayas et al., 1999). In this study, rarity of species i was defined by its geographical range measured as the inverse of the number of cells where it was present ($1/n_i$). Currently, there are not official criteria in Spain classifying species into rarity categories according to their geographical ranges (Perring and Farrel, 1983; Cameron, 1998). For a cell r , the rarity index was $\sum_{i=1}^S (1/n_{ri})/s_r$, where s_r was the number of species found in the cell.

Vulnerability of a species was quantified using the categories of the *Red Book of Spanish Vertebrates* (Blanco and González, 1992). The species categories that were considered are the following: endangered, vulnerable, rare, undetermined, insufficiently known, introduced, and non-threatened. These categories were previously defined by the International Union for Nature Conservation (IUCN, 1988). A complete list of the species studied here and their vulnerability category and number of cells where they were found are available from the authors upon request. Currently, these categories are being revised, but no publications have been released yet. We assigned to every category a score related to its degree of vulnerability, ranging from 5 for endangered species to 1 for non-threatened and introduced species. The intermediate categories were assigned 4 (vulnerable and undetermined), 3 (rare) and 2 (insufficiently known). Since the undetermined species are those that are known to belong to the endangered, vulnerable, or rare categories, we decided to assign them

the score=4 because it is the average score of these categories. We acknowledge the subjectivity of these scores; they just represent a rank and have a relative value, and any other choice would have been subjective as well. For a cell, the vulnerability index was $\sum_{i=1}^S V_{ri}/s_r$, where V_{ri} was the vulnerability score of the species present in the cell. As vulnerability is actually a surrogate concept of rarity plus rates of habitat loss and other threats, we expect a positive correlation between these two indices. For every cell and taxonomic group, we defined a combined index of species richness, rarity, and vulnerability: $\sum_{i=1}^S (1/n_{ri}) V_{ri}$. In this index, species richness is implicit in $\sum_{i=1}^S$. As far as we know, this index is original. Since the combined index of biodiversity is a function of three other indices, we expect in general a positive correlation between this combined index and richness, rarity, and vulnerability.

We also used a Standardized Biodiversity Index that measured species richness, rarity and vulnerability of all four taxa together in every cell. This index is original as well. We standardized by dividing the combined index of biodiversity of each taxonomic group in every cell by its mean across all cells, and then summed the four standardized combined indices. The Standardized Biodiversity Index formula is

$$\sum_{j=1}^4 1/m_j \sum_{i=1}^{jS} (1/n_{ji}) V_{ji},$$

where m_j refers to the mean combined index of biodiversity of the taxonomic group j across cells. Next, all indices for the various taxa and the Standardized Biodiversity Index were ranked. We considered areas of high-value diversity those cells within the upper 15% (39 cells) of ranked values for the various criteria. This percentage was chosen because it represents the target proportion of land preserved for nature conservation in the European Union (79/409/EEC Bird Directive and 92/43/EEC Habitat Directive) (European Commission, 1996). In spite of that, we acknowledge the arbitrariness of this threshold; any other choice would have been arbitrary as well. Statistics of all criteria used to identify areas of high-value diversity in the study area are reported in Table 1. Our identification of these areas is

not affected by the different species richness of the taxa analysed in this study because we ultimately used ranks.

2.3. Data analysis

We examined the relationships between the four criteria within taxa and across taxa by means of correlation analysis using Bonferroni corrections for multiple comparisons. These correlations will hint the macro-ecological trends of diversity in the area. The congruence between areas of high-value diversity for different taxa was examined by means of contingency tables. To evaluate the effectiveness of the various criteria used to identify areas of high-value diversity, we examined the proportions of species included in them and threatened species that were excluded from them. For our purposes, “threatened species” were considered to be those belonging to the endangered, vulnerable, rare, and undetermined categories of IUCN (1988). Finally, we looked at the coincidence between areas of high-value diversity and national, natural and regional parks using contingency tables to highlight possible gaps.

3. Results

3.1. Correlations between criteria used to identify areas of high-value diversity

Within taxa, after applying corrections for multiple comparisons, the pair-wise correlation coefficients between the different criteria used to identify areas of high-value diversity were usually significant at $P < 0.05$ (Table 2). The exceptions were species richness and vulnerability, which were not correlated for any taxonomic group, and species richness and rarity, which were not correlated for amphibian, reptile, and breeding bird species. That is, the richest communities did not necessarily include the rarest and most vulnerable species. As expected, rarity and vulnerability were significantly correlated, but the correlation for breeding birds and mammals were low (Table 2). The combined index of biodiversity was significantly correlated with the other three criteria except in the cases of species richness of amphibians and vulnerability of mammals. Thus, in

Table 1
Statistics of all criteria used to identify areas of high-value diversity in the study area

	Amphibians ($n=259$)			Reptiles ($n=259$)			Breeding birds ($n=257$)			Mammals ($n=253$)		
	Mean	S.D.	Range	Mean	S.D.	Range	Mean	S.D.	Range	Mean	S.D.	Range
Richness	8.91	3.79	0–16	14.69	5.16	2–25	112.26	32.85	13–175	28.12	13.77	1–65
Rarity	0.013	0.026	0–0.372	0.012	0.011	$4.7 \cdot 10^{-3}$ – $8.3 \cdot 10^{-2}$	$9.7 \cdot 10^{-3}$	$6.6 \cdot 10^{-3}$	$4.7 \cdot 10^{-3}$ – $5.7 \cdot 10^{-2}$	$1.1 \cdot 10^{-2}$	$3.7 \cdot 10^{-3}$	$5.8 \cdot 10^{-3}$ – $3.1 \cdot 10^{-2}$
Vulnerability	1.08	0.283	0–3	1.153	0.269	1–2.8	1.439	0.145	1.1–2	1.734	0.405	1–3.33
Combined index	0.153	0.363	0–5.337	0.282	0.359	$9.5 \cdot 10^{-3}$ –2.263	1.965	1.836	0.11–23.1	0.699	0.602	$5.8 \cdot 10^{-3}$ –4.19

For the Standardized Biodiversity Index of all taxa, statistics are the following: mean=4.04, S.D.=3.60, range=0.203–36.746 ($n=253$).

Table 2
Correlation coefficients between criteria used to identify areas of high-value diversity within taxa

	Amphibians (<i>n</i> = 259)			Reptiles (<i>n</i> = 259)			Nesting birds (<i>n</i> = 257)			Mammals (<i>n</i> = 253)		
	Richness	Rarity	Vulnerab.	Richness	Rarity	Vulnerab.	Richness	Rarity	Vulnerab.	Richness	Rarity	Vulnerab.
<i>Amphibians</i>												
Rarity	–0.106											
Vulnerability	–0.088	0.736										
Combined index	0.117	0.917	0.564									
<i>Reptiles</i>												
Rarity				–0.163								
Vulnerability				–0.052	0.778							
Combined index				0.227	0.744	0.718						
<i>Breeding birds</i>												
Rarity							–0.183					
Vulnerability							–0.037	0.296				
Combined index							0.367	0.615	0.324			
<i>Mammals</i>												
Rarity										0.639		
Vulnerability										–0.027	0.243	
Combined index										0.247	0.841	<u>0.197</u>

Coefficients in bold are significant at $P < 0.05$ after applying Bonferroni's corrections for multiple comparisons. Underlined correlation coefficients are significant at $P < 0.05$ if corrections for multiple comparisons were not applied.

general, cells with high values of the combined index of biodiversity also included rich communities with rare and vulnerable species. This indicates that a cell that has been identified as an area of high-value diversity based on one criterion (e.g. species richness), may not be an area of high-value diversity if based on a different criterion (e.g. rarity) (Fig. 2a–d).

Among taxa, the pair-wise correlations between the same criteria were very different (Table 3). After applying Bonferroni's correction, the species richnesses of taxa were always significantly correlated ($P < 0.05$). Four of six correlations between the combined indices of biodiversity were significant, as were three of six correlations between the rarity measures. The correlation between the vulnerability measures was significant ($P < 0.05$) only between amphibians and reptiles. Only amphibians and reptiles exhibited significant correlations for all criteria. The correlation coefficients were usually low.

The Standardized Biodiversity Index was highly correlated with the combined index of biodiversity of all taxa ($r = 0.80$ for amphibians, 0.64 for reptiles, 0.46 for nesting birds, and 0.51 for mammals, $P < 0.0001$ in all cases). Thus, it was deemed a good synthetic diversity measure of species richness, rarity, and vulnerability of the four taxonomic groups together.

3.2. Congruence of high-value diversity areas

To what extent do areas of high-value diversity for the four taxa overlap? Despite most pairs of taxa

exhibited non-random positive associations, congruence of areas of high-value diversity—cells within the 15% top segment of ranked values for the different criteria—among taxa was found to be moderate to low (Table 4, Fig. 2a–d). It was lowest for the pairs amphibians–birds, mammals–birds and mammals–reptiles based on species vulnerability (2.6% in all cases), and highest for the pair amphibians–reptiles based on species rarity (61.5%). Congruence averaged 40.5, 47.8, 16.2, and 38.5% for areas of high-value diversity based on species richness, rarity, vulnerability, and the combined index of biodiversity, respectively. Thus, vulnerability is the criterion that produced the highest areas of high-value diversity dispersion for the different taxa, whereas rarity produced the highest areas of high-value diversity aggregation. The inconsistency of areas of high-value diversity congruence based on these two significantly correlated indices is explained by the low correlation coefficients between them for breeding birds and mammals (Table 2).

3.3. Evaluation of areas of high-value diversity

A few species were not included in the areas of high value diversity, irrespective of the criteria used to identify them (Table 5, Appendix B). The performance based on the average proportion of species included in areas of high-value diversity for the different taxa were ranked: rarity (97.9%), combined index of biodiversity (97%), species richness (95.2%), and vulnerability (87.7%). The performance based on the average proportion of threatened

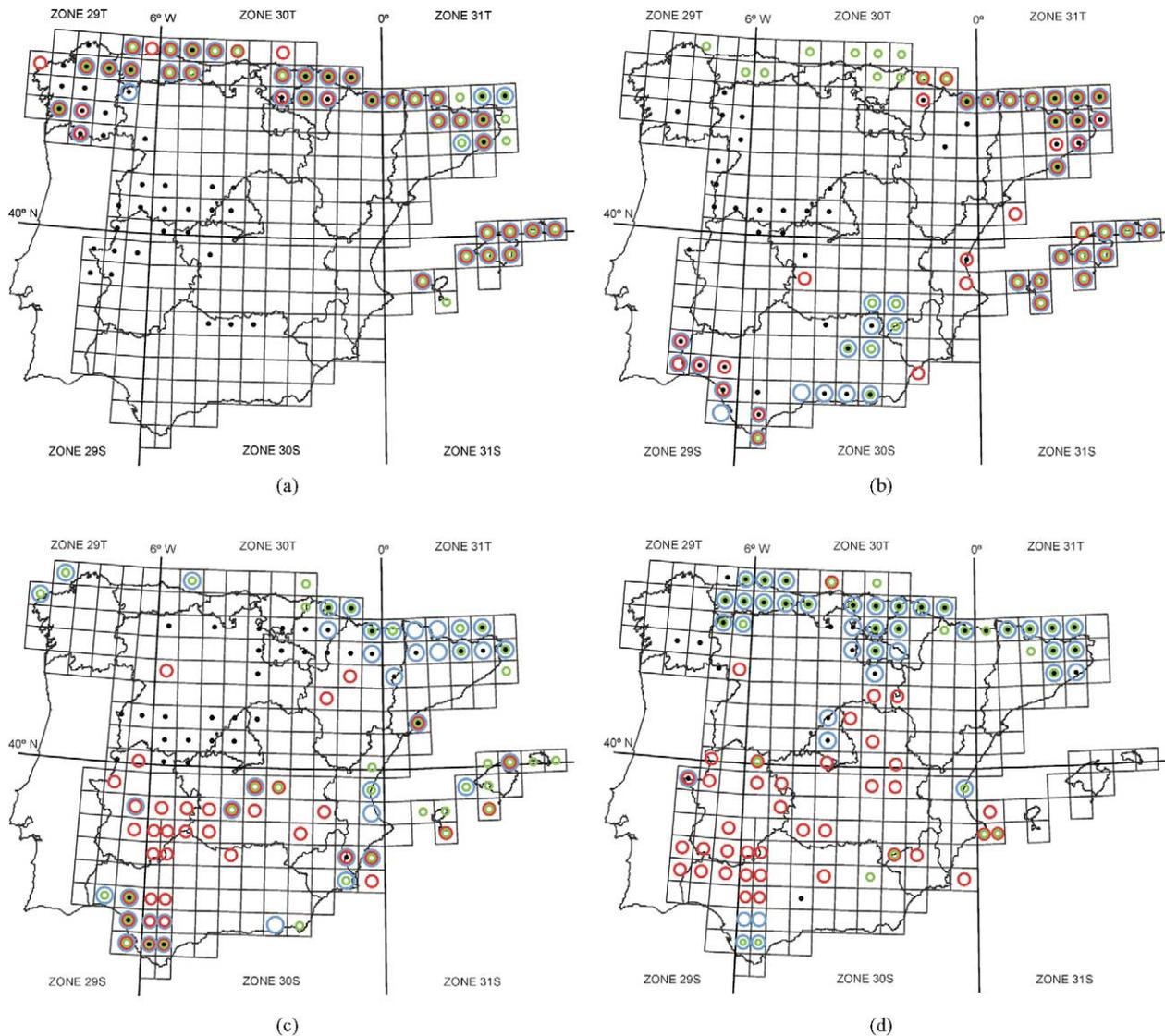


Fig. 2. Maps of areas of high-value diversity identified according to different criteria for (a) amphibians, (b) reptiles, (c) breeding birds, and (d) mammals. Symbols are the following: black solid dots are species richness AHVD, green rings are rarity AHVD, red rings are vulnerability AHVD, and blue rings are AHVD according to the combined index of biodiversity.

species excluded from areas of high-value diversity for the different taxa were ranked: combined index of biodiversity and rarity (0.3%), vulnerability (9.9%), and species richness (13.8%). The areas of high-value diversity identified according to the Standardized Biodiversity Index of all taxa together included all amphibian and mammal species, all but one reptile species (categorized as rare) and all but six bird species (one categorized as endangered, two categorized as rare, and the other three were non-threatened or introduced species) (Table 6, Appendix B).

3.4. Coincidence between areas of high-value diversity and natural protected areas

A total of 110 cells included at least a fraction of a national, natural or regional park. The coincidence

between areas of high-value diversity and cells including these natural protected areas was low (Table 7). Coincidences between areas of high-value diversity and natural protected areas were not statistically associated except for rarity of mammals and the combined index of bird diversity, which exhibited non-random positive associations. The coincidences between areas of high-value diversity based on the combined index of biodiversity and NPAs followed the rank amphibians < reptiles = mammals < birds. Thus, the existing network of natural protected areas provides a reasonable guarantee for conservation of bird diversity, whereas large pools of amphibian diversity are outside protected areas. Natural protected areas were included in 69.2% of areas of high-value diversity identified based on the Standardized Biodiversity Index of all taxa together ($\chi^2 = 13.46$, $P < 0.004$) (Fig. 3).

Table 3
Correlation coefficients for criteria used to identify areas of high-value diversity between taxa. Presentation as in Table 2

	Amphibians (n = 259)				Reptiles (n = 259)				Breeding birds (n = 257)			
	Richness	Rarity	Vulnerab.	Combined index	Richness	Rarity	Vulnerab.	Combined index	Richness	Rarity	Vulnerab.	Combined index
<i>Reptiles</i>												
Richness	0.686											
Rarity		0.429										
Vulnerability			0.398									
Combined index				0.229								
<i>Breeding birds</i>												
Richness	0.487				0.571							
Rarity		0.262				0.53						
Vulnerability			<u>-0.188</u>				<u>0.156</u>					
Combined index				0.067				0.261				
<i>Mammals (n = 253)</i>												
Richness	0.575				0.468				0.501			
Rarity		0.086				<u>0.191</u>				0.087		
Vulnerability			<u>-0.149</u>				<u>-0.196</u>				0.016	
Combined index				<u>0.173</u>				0.26				0.217

Table 4
Percentage congruence between areas of high-value diversity of pairs of taxa identified according to different criteria

	Amphibians				Reptiles				Breeding birds			
	Richness	Rarity	Vulnerab.	Combined index	Richness	Rarity	Vulnerab.	Combined index	Richness	Rarity	Vulnerab.	Combined index
<i>Reptiles</i>												
Richness	47.7****											
Rarity		61.5****										
Vulnerability			46.2****									
Combined index				41.0****								
<i>Breeding birds</i>												
Richness	43.9****				43.9****							
Rarity		48.7****				48.7 (1)****						
Vulnerability			2.6				17.9 (1)					
Combined index				35.9**				41.0****				
<i>Mammals</i>												
Richness	43.6 (1)****				30.7 (1)				33.3*			
Rarity		53.8 (1)****				43.6 (2)****				30.8 (2)*		
Vulnerability			2.6				2.6 (2)				25.6	
Combined index				51.3 (1)****				23.1 (2)				38.5 (1)**

The statistical significance of the associations according to χ^2 tests is indicated (* $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$). (1) and (2) are the number of cells that cannot overlap because of the lack of information for a taxonomic group.

Table 5
Numbers and percentages of species included and threatened species excluded from the areas of high-value diversity identified according to different criteria. Threatened species were defined according to Blanco and González (1992). Lists of species excluded are in Appendix B

	Amphibians		Reptiles		Nesting birds		Mammals	
	Species included	Threatened species excluded						
Richness	24 (88.8%)	2 (40%)	41 (97.6%)	1 (9%)	257 (95.5%)	5 (6.3%)	88 (98.9%)	0
Rarity	25 (92.6%)	0	42 (100%)	0	266 (98.9%)	1 (1.2%)	89 (100%)	0
Vulnerability	26 (96.3%)	0	39 (92.9%)	1 (9%)	223 (82.9%)	15 (19%)	70 (78.7%)	3 (11.5%)
Combined index	26 (96.3%)	0	39 (92.9%)	0	266 (98.9%)	1 (1.2%)	89 (100%)	0

Table 6

Numbers and percentages—over the total number of species considered in this study—of species included in the areas of high-value diversity identified according to the Standardized Biodiversity Index of all taxa

	Total number of species (427)	Number of endangered species (25)	Number of vulnerable species (34)	Number of rare species (45)	Number of undetermined species (17)	Number of insufficiently known species (28)
Amphibians	27(100%)	1 (100%)	1 (100%)	3 (100%)	0 (100%)	0 (100%)
Reptiles	41 (97.6%)	2 (100%)	4 (100%)	3 (75%)	1 (100%)	0 (100%)
Mammals	89 (100%)	6 (100%)	7 (100%)	5 (100%)	8 (100%)	9 (100%)
Breeding birds	263 (97.8%)	15 (93.8%)	22 (100%)	31 (94%)	8 (100%)	19 (100%)
All groups	420 (98.4%)	24 (96%)	34 (100%)	42 (93.3%)	17 (100%)	28 (100%)

Table 7

Coincidence in percentage between areas of high-value diversity and natural protected areas. The statistical significance of the associations have been tested by means of χ^2

	Species richness	Rarity	Vulnerability	Combined index
Amphibians	43.8%, $\chi^2 = 0.27$	53.9%, $\chi^2 = 2.39$	56.4%, $\chi^2 = 3.6$	53.8%, $\chi^2 = 2.43$
Reptiles	61.4%, $\chi^2 = 6.8$	56.4%, $\chi^2 = 2.49$	56.4%, $\chi^2 = 3.6$	61.5%, $\chi^2 = 6.83$
Breeding birds	56%, $\chi^2 = 2.4$	56.4%, $\chi^2 = 3.47$	46.2%, $\chi^2 = 0.01$	66.7%, $\chi^2 = 10.7^{**}$
Mammals	59%, $\chi^2 = 4.53$	66.7%, $\chi^2 = 10.1^*$	35.9%, $\chi^2 = 3.02$	61.5%, $\chi^2 = 6.12$

* $P < 0.05$. ** $P < 0.01$.

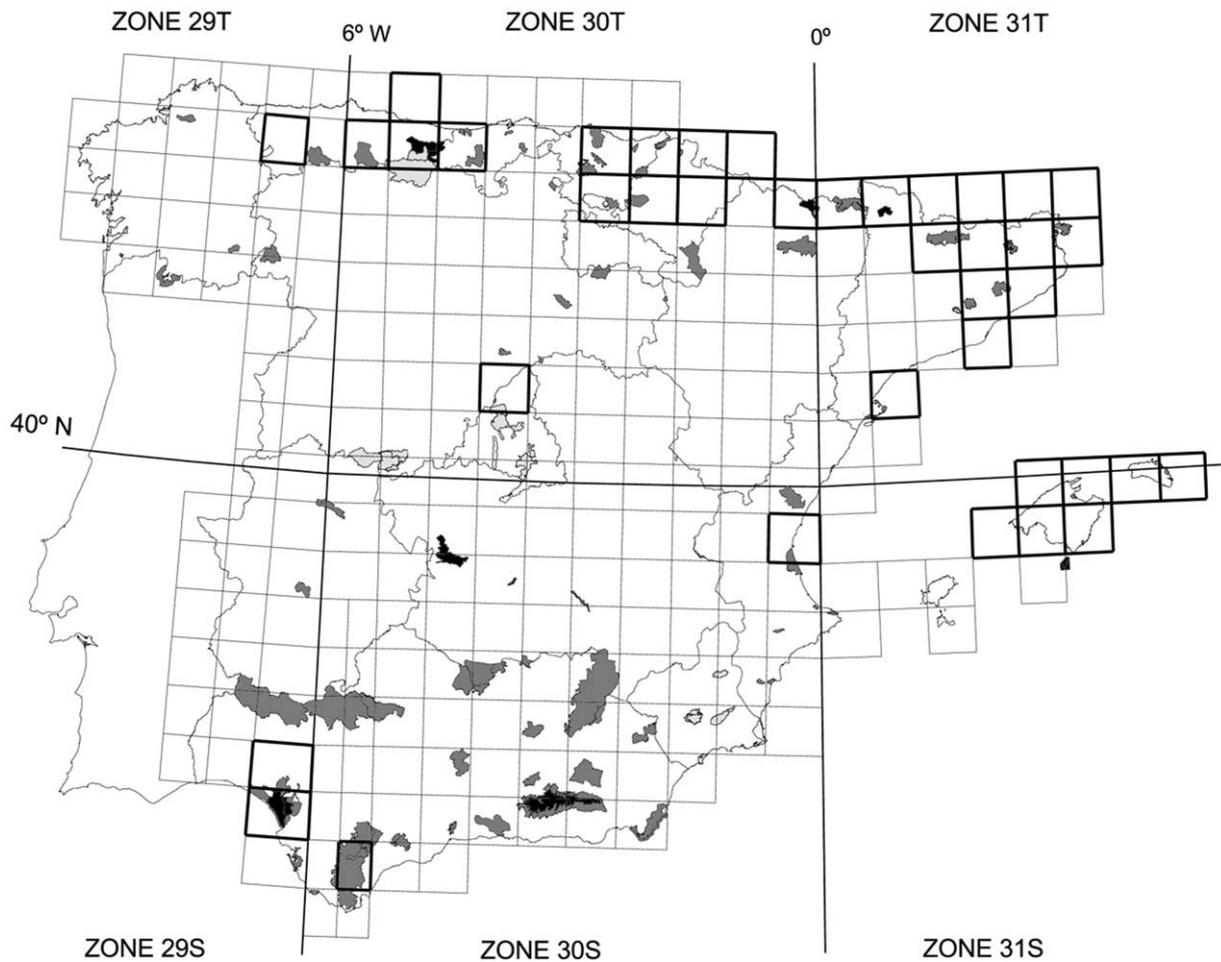


Fig. 3. Coincidence of areas of high-value diversity identified according to the standardized biodiversity index of all taxa together (units in bold type) and natural protected areas (symbols as in Fig. 1).

4. Discussion

4.1. Distribution of areas of high-value diversity

Within taxa, there were overall significant correlations between species richness, rarity, vulnerability, and a combined index of biodiversity, with the exception of richness and vulnerability, which were not correlated for any taxa, and richness and rarity, correlated just for mammals. This mismatch has been reported for many taxa in different parts of the world (Drinkrow and Cherry, 1995; Lombard, 1995; Williams et al., 1996; Fagan and Kareiva, 1997; Hacker et al., 1998; Fjeldsa, 2000). Conversely, Swengel (1998) found in Midwestern USA that within a habitat type, site rankings based on total numbers of butterfly species significantly tended to agree with site rankings based on numbers of specialist butterfly species. The combined index of biodiversity provided significant correlations with its components but “failed” in the cases of species richness of amphibians and vulnerability of mammals. More importantly, we found that among taxa the correlations between criteria were very different. Species richness was always significantly correlated across taxa, but for vulnerability only amphibians and reptiles were correlated. These results indicate that, whereas there are certainly some macroecological patterns of species diversity that are consistent for different taxa, other determinants of the various components of species diversity differ. Overall, the balance leads to a moderate to low congruence between areas of high-value diversity identified according to different criteria and/or for different taxa. For analysis of congruence between taxa in other areas of the world, see Prendergast et al. (1993), Gaston et al. (1995), Lombard (1995), Balmford and Long (1996), Williams et al. (1997), Simmons et al. (1998), and Araujo (1999).

The effects of biogeography in areas of high-value diversity distribution are relevant, mostly for ectotherm species (Fig. 2). Biogeographic effects in Iberia include climate differences in the northern fringe of the Iberian Peninsula as compared to the rest of the country, and the insular effect in the Balearic Islands. Increased regional species diversity in climate transition zones is consistent with the analyses for plant species of Castro et al. (1997) and Rey Benayas and Scheiner (2002). These patterns may also be due, in part, to refugia in a land with over a millennium of varied agricultural, silvicultural, and pastoral practices. The peaks in species richness of amphibian, reptile and bird species in the central-western mountain ranges that we found (Fig. 2a–c) supports this interpretation. In the analysis of these authors, areas of high species richness were also rich in endemic species. At the scale of our analysis, we have found, though, a lack of relationship between species richness and rarity. Both ecotones and refugia may

contribute to the higher regional species diversity of transitional zones.

Island biogeographic effects are also evident in our maps. These effects are very relevant for amphibian and reptile species (Fig. 2a,b), moderate for bird species (Fig. 2c), and inexistent for mammals (Fig. 2d). The explanations for these patterns may lie in the differences in dispersion capabilities and speciation and extinction rates of the taxa (Blondel and Aronson, 1999). Mammals are poor colonizers of islands, and humans drove to extinction all autochthonous mammal species in the Balearic Islands. Currently, all mammals except bats have been introduced by humans in these islands (Alcover et al., 1998; Palmer et al., 1999).

Besides biogeographic and refugia effects, patterns of areas of high-value diversity distribution have additional explanations that are relevant at regional and local scales. Differences in the ecological requirements for the taxa contribute to these patterns. Thus, a large proportion of areas of high-value diversity of amphibian species concentrate in northern Spain (Fig. 2a) since the higher precipitation and lower evaporation rates provide a greater moisture in air and soil as well as flooded habitats suitable for reproduction. Conversely, there is an aggregation of areas of high-value diversity of reptile species in the dry southern part of the Iberian Peninsula (Fig. 2b) (Meliadou and Troumbis, 1997; James and Shine, 2000). Large wetlands in the country are consistently associated to areas of high-value diversity of bird species, since many of them are specific of this kind of habitats. Fortunately, all large wetlands have legal protection (natural protected areas 6, 8, 45, 61 and others in Appendix A, Fig. 1).

4.2. Identifying areas of high-value diversity as a tool for nature conservation

This study attempted to provide decision makers data needed to identify areas especially worthy of conservation (Prendergast et al., 1999), but our approach can be applied anywhere. We acknowledge that definitions of areas of high-value diversity are to some extent arbitrary, and our results are obviously scale dependent. A finer scale of resolution would likely result in a diminished areas of high-value diversity congruence among taxa (J.M. Rey Benayas, unpublished data). Overall, the areas of high-value diversity using the combined index of biodiversity had the best performance, capturing over 93% of the species and with fewer than 10% of threatened species uncaptured (Table 5). The greater effectiveness of the rarity criterion, as compared to the richness criterion, is in agreement with other studies (Haeupler and Vogel, 1999). Congruence of areas of high-value diversity of the different taxa was moderate to low. This makes conservation strategies more difficult.

Our Standardized Biodiversity Index of all taxa resulted in a site selection that included all amphibian and mammal species, all but one reptile species and all but six bird species (four out of these seven species are endangered, Table 6; Appendix B). Elsewhere in the world, where species distribution data are often sparse and mapped at even larger scales, and where decision making on reserve placement usually has to be very rapid, we suggest that a strategy based solely on one or two criteria, and on only one or a limited number of taxa, may fail to provide adequate protection for many organisms. The areas of high-value diversity approach could benefit from adding human threats (especially vegetation destruction) and land ownership and value to the geographical analysis of biodiversity (Dobson et al., 2001; Scott et al., 2001). Areas harboring high levels of species diversity and that are also under severe threat are usually defined in the literature as hotspots (Myers, 1988, 1990; Prendergarst and Eversham, 1995; Beisinger et al., 1996; Harcourt, 2000; Myers et al., 2000).

In our study, when one looks at the coincidence between areas of high-value diversity according to the various criteria and natural protected areas, the scenario is discouraging (see Table 7). However, only 30% of areas of high-value diversity based on the Standardized Biodiversity Index of all taxa did not include any natural protected area (Fig. 3). In agreement with other authors, we suggest that this gap should be corrected urgently (Barnard et al., 1998; Simonetti, 1999). Spain's vertebrate fauna could be more effectively protected with only moderate acquisition of new, well-sited protected areas. While 70% of the areas of high-value diversity (modal area of 2500 km²) included natural protected areas, these average only 274.6 km². Natural protected areas occupy a small fraction of areas of high-value diversity, and there is no guarantee that the species found in a areas of high-value diversity site will be present in a fraction of natural protected area. Unfortunately, very few natural protected areas have complete lists of their species. Only for these sites is it possible to compare the diversity of protected areas and associated areas of high-value diversity. We urge that all natural protected areas be surveyed in order to strengthen nature conservation, and assess the effective long-term viability of the species in these areas (Hansen et al., 1993). Other studies on the coincidence between areas of high-value diversity and natural protected areas are those of Scott et al. (1993), Fearnside and Ferraz (1995), Lombard (1995), Jaffre et al. (1998), Savitsky and Lacher (1998), Araujo (1999), Maddock and Benn (2000), and Scott et al. (2001).

Biodiversity should not be the only target of conservation of natural protected areas (Gómez-Limón and de Lucio, 1995; Burger, 2000). Water and nutrient cycles, ecological processes such as productivity, and many other values and functions (landscape, geological,

anthropological, aesthetical, spiritual, recreational, cultural) have been recognized in the scientific literature as important elements for conservation (Franklin, 1993; De Leo and Levin, 1997; Ettema et al., 1998; Rothley, 1999). Charismatic organisms such as some vertebrate groups may not always be the most appropriate surrogates for biodiversity (Prendergast et al., 1993; Araujo, 1999). This study did not consider either areas of high-value diversity for migratory, non-breeding birds, which add nearly 400 species to the avian fauna. The approach taken in this paper should be applied to as many other taxa as possible, in order to aid the formulation of the National Strategic Plan for Biodiversity Conservation. It is also useful for designing the Natura 2000 European Network of Special Conservation Areas, which pursues the preservation of representative and threatened habitats and species in the European Union (IUCN, 1994; European Commission, 1996).

Biodiversity conservation must not depend solely on natural protected areas. Management of traditional agricultural systems and forests are keystones for conservation outside natural protected areas (Hawthorne, 1996; Neitlich and McCune, 1997; Martin and Eadie, 1999; Loumou et al., 2000; Aauri and de Lucio, 2001). Maps of areas of high-value diversity may be useful for ecological restoration. It is possible to identify actions to be taken in areas of high-value diversity to foster the populations of the most endangered species. Some examples are habitat reconstruction (e.g. ponds), revegetation (e.g. riverine forests or island forests), refuge sites and food supply (e.g. rabbits for predators such as the lynx and the Iberian imperial eagle) (St. Clair et al., 1998; Brooker et al., 1999). These maps may also be useful for environmental impact assessment and mitigation (Ayensu et al., 1999). We overlapped a map of areas of high-value diversity and a map of natural protected areas. Next, we will overlap our map of areas of high-value diversity with the planned road, high-speed train railway and reservoir maps. Many recommendations will then arise. For instance, five large reservoirs are planned to be built in the Pyrenean Mountains, a zone of areas of high-value diversity concentration and important for migratory birds.

Margules and Pressey (2000) pointed to six stages in systematic conservation planning: (1) compile biodiversity data, (2) identify conservation goals, (3) review existing conservation areas, (4) select additional conservation areas, (5) implement conservation actions, and (6) maintain the required values of conservation areas. We took a first step for biodiversity conservation planning in the studied region, and point out the following conclusions from our study. Since the results are scale dependent, we advise that biodiversity data should be compiled with higher resolution, particularly for the natural protected areas (stage 1). For the goal of conservation of the largest pools of vertebrate diversity that

takes into account rarity and vulnerability criteria (stage 2), our study has highlighted a gap in the existing natural protected area network (stage 3) within areas of high-value diversity. Their identification is the starting point to undertake stage 4 and set priorities related to stages 5 and 6 such as ecosystem management and restoration and environmental impact assessment and mitigation. The question is: will politicians finally pay attention to take notice of ecological research? (Brusard, 1991; Mooney, 1991). Time will tell.

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Appendix A

List of national, natural and regional parks that were considered in this study. Numbers match Fig. 1. Source: Europarc-España database.

National Parks (IUCN category II): 1. Picos de Europa, 2. Ordesa y Monte Perdido, 3. Aigüestortes i Estany de Sant Maurici, 4. Cabañeros, 5. Tablas de Daimiel, 6. Archipiélago de Cabrera, 7. Doñana, 8. Sierra Nevada.

Natural Parks (IUCN category V): 9. Fragas do Eume, 10. Complejo Dunar de Corrubedo e Lagoas de Carregal e Vixán, 11. Islas Cíes, 12. Monte Aloia, 13. Baixia Limia-Serra do Xurés, 14. O Invernadeiro, 15. Somiedo, 16. Redes, 17. Oyambre, 18. Dunas de Liencres (Piélagos), 19. Saja-Besaya, 20. Macizo de Peña Cabarga, 21. Collados del Asón, 22. Urdabai (Biosphere Reserve), 23. Área de Gorbeia, 24. Urkiola, 25. Aralar, 26. Valderejo, 27. Pagoeta, 28. Izki, 29. Aiako Harria, 30. Señorío de Bértiz, 31. Urbasa y Andía, 32. Bardenas Reales, 33. Sierra de Cebollera, 34. Moncayo, 35. La Sierra y Cañones de Guara, 36. Posets-Maladeta, 37. Cadí-Moixeró, 38. Zona Volcánica de la Garrotxa, 39. Aiguamolls de l'Empordà, 40.

Cap de Creus, 41. Montseny, 42. Sant Llorenç del Munt i l'Obac, 43. Montserrat, 44. Delta de l'Ebre, 45. Lago de Sanabria y alrededores, 47. Cañon del Río Lobos, 48. Hoces del Río Duratón, 50. Monfragüe, 51. Cornalvo, 52. Cumbre, Circo y Lagunas de Peñalara, 56. Hayedo de Tejera Negra, 57. Lagunas de Ruidera, 58. Prat de Cabanes-Torreblanca, 59. Sierra Espadán, 60. La Albufera, 61. Marjal de Pego-Oliva, 62. El Montgó, 63. Penyal d'Ifac, 64. Carrascal de la Font Roja, 65. El Hondo, 66. Salinas de Santa Pola, 67. Sa Dragonera, 68. S'Albufera de Mallorca, 69. Mondragó, 70. L'Albufera des Grao, la illa d'en Colom i el cap de Favàritx, 71. Sierra de Aracena y Picos de Aroche, 72. Sierra Norte de Sevilla, 73. Sierra de Hornachuelos, 74. Sierra de Cardeña y Montoro, 75. Sierra de Andujar, 76. Despeñaperros, 77. Sierras de Cazorla, Segura y las Villas, 78. Sierra de Castril, 79. Entorno de Doñana, 80. Sierras Subbéticas, 81. Sierra de Huétor, 82. Sierra Mágina, 83. Sierra de Baza, 84. Sierra de María-Los Vélez, 85. Bahía de Cádiz, 86. La Breña y Marismas del Barbate, 87. Sierra de Grazalema, 88. Los Alcornocales, 89. Sierra de las Nieves, 90. Montes de Málaga, 91. Sierras de Tejeda, Almijara y Alhama, 92. Sierra Nevada, 93. Cabo de Gata-Níjar.

Regional Parks (IUCN category V): 46. Picos de Europa, 49. Sierra de Gredos, 53. Cuenca Alta del Río Manzanares, 54. Curso Medio del Río Guadarrama y su entorno, 55. Entorno de los ejes de los cursos bajos de los Ríos Manzanares y Jarama, 94. Sierra de La Pila, 95. Sierra Espuña, 96. Carrascoy y El Valle, 97. Cabo de Cope-Puntas de Calnegre, 98. Salinas y Arenales de San Pedro, 99. Calblanque, Monte de Las Cenizas y Peña del Aguila.

Appendix B

Species excluded from the high-value diversity areas identified according to different criteria and their vulnerability status according to the *Red Book of Spanish Vertebrates* (Blanco and González, 1992).

Abbreviations are the following: E=endangered, V=vulnerable, R=rare, U=undetermined, I-K=insufficiently known, I=introduced, and N-T=non-threatened.

According to species richness. **Amphibians:** *Alytes muletensis* (E), *Bufo viridis* (R), and *Hydromantes ambrosii*; **reptiles:** *Podarcis lilfordi* (V); **breeding birds:** *Amandava amandava* (I), *Bucanetes githagineus* (N-T), *Estrilda melpoda* (I), *Falco eleonora* (R), *Numenius arquata* (R), *Pandion haliaetus* (E), *Plegadis falcinellus* (N-T), *Psittacula krameri* (I), *Puffinus mauretanicus* (N-T), *Rissa tridactyla* (R), *Sylvia sarda* (N-T), and *Uria aalge* (E); **mammals:** *Ammotragus lervia* (I).

According to rarity. **Amphibians:** *Alytes cisternasii* (N-T), and *Peurodeles waltl* (N-T); **breeding birds:**

Amandava amandava (I), *Aythya fuligula* (N-T), and *Corvus frugilegus* (R).

According to vulnerability. **Amphibians:** *Alytes cisternasii* (N-T); **reptiles:** *Algyroides marchi* (R), *Lacerta monticola* (N-T), and *Lacerta schreiberi* (N-T); **breeding birds:** *Acrocephalus schoenobaenus* (N-T), *Aegolius funereus* (R), *Anthus pratensis* (N-T), *Anthus spinoletta* (N-T), *Anthus trivialis* (N-T), *Aythya fuligula* (N-T), *Bucanetes githagineus* (N-T), *Carduelis spinus* (N-T), *Certhia familiaris* (N-T), *Circus cyaneus* (I-K), *Corvus frugilegus* (R), *Crex crex* (U), *Cygnus olor* (I), *Charadrius morinellus* (R), *Dendrocopos leucotos* (E), *Dendrocopos medius* (V), *Dryocopus martius* (R), *Emberiza citrinella* (N-T), *Estrilda melpoda* (I), *Fidecula hypoleuca* (N-T), *Gallinago gallinago* (I-K), *Gypaetus barbatus* (E), *Lagopus mutus* (E), *Lanius collurio* (N-T), *Lanius minor* (E), *Locustella naevia* (N-T), *Luscinia svecica* (N-T), *Montifringilla nivalis* (N-T), *Myiopsitta monachus* (I), *Nume-nius arquata* (R), *Parus palustris* (N-T), *Perdix perdix* (V), *Phalacrocorax carbo* (N-T), *Phylloscopus sibilatrix* (I-K), *Phylloscopus trochilus* (N-T), *Plegadis falcinellus* (N-T), *Prunella collaris* (N-T), *Psittacula krameri* (I), *Pyrhcorax graculus* (N-T), *Rissa tridactyla* (R), *Saxicula rubetra* (N-T), *Scolopax rusticola* (I-K), *Tetrao urogallus* (V), *Tichodroma muraria* (N-T), *Turdus torquatus* (N-T), and *Uria aalge* (E); **mammals:** *Ammodragus lervia* (I), *Apodemus flavicollis* (N-T), *Arvicola terrestris* (N-T), *Chionomys nivalis* (N-T), *Glis glis* (N-T), *Lepus castroviejo* (R), *Lepus europaeus* (N-T), *Marmota marmota* (I), *Martes martes* (N-T), *Micromys minutus* (N-T), *Microtus gerbei* (N-T), *Mustela lutreola* (E), *Myocastor coypus* (N-T), *Rupicapra pyrenaica* (N-T), *Sorex araneus* (N-T), *Sorex coronatus* (N-T), *Sorex minutus* (N-T), *Talpa europaea* (N-T), and *Ursus arctos* (E).

According to the combined index of biodiversity. **Amphibians:** *Alytes cisternasii* (N-T); **reptiles:** *Lacerta monticola* (N-T), *Lacerta schreiberi* (N-T), and *Vipera seoanei* (N-T); **breeding birds:** *Aythya fuligula* (N-T), *Corvus frugilegus* (R), and *Estrilda melpoda* (I).

According to the standardized biodiversity index of all taxa. **Reptiles:** *Algyroides marchi* (R); **breeding birds:** *Amandava amandava* (I), *Bucanetes githagineus* (N-T), *Corvus frugilegus* (R), *Estrilda melpoda* (I), *Rissa tridactyla* (R), and *Uria aalge* (E).

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