Effectiveness of the Natura 2000 network in protecting Iberian endemic fauna

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Abstract

The Iberian Peninsula is a major European region of biodiversity, as it harbours more than 30% of European endemic species. Despite a number of studies having evaluated the ability of nature reserves to protect certain taxa, there is still a lack of knowledge on how Iberian endemic fauna are represented in these reserves. We detected biodiversity hotspots of Iberian endemicity and evaluated the effectiveness of the Natura 2000 network (N2000) in representing 249 endemic species from eight animal taxonomic groups (amphibians, mammals, freshwater fishes, reptiles, water beetles, butterflies, lacewings and dung beetles). We found that only the 10% of these Iberian endemic species are considered species of community interest (i.e. species included in the Annexes of the Habitats Directive). We conducted gap analyses and null models of representativeness in N2000. Generally, N2000 is effective in its representation of Iberian endemic fauna, although we detected species and few hotspots of endemism that were still not represented. It is necessary to declare a few new protected areas, thus enhancing N2000's effectiveness in the conservation of the Iberian endemic fauna. Although the aim of N2000 is to protect species listed in the Birds and Habitats Directives, the conservation status of endemic species from one of the most important areas of Europe in terms of biodiversity, could be also a concern for the European Union. Our results are useful in the context of the recent European Commission mandate calling for a 'fitness check' of the Birds and Habitats Directives. This approach could be also applicable to other regions with high value of endemicity.

Introduction

Biodiversity loss associated with human activities is a major concern due to its pervasive effects on ecosystem functioning and services (Purvis & Hector, 2000; Baumgärtner, 2007; Cardinale et al., 2012; Castro et al., 2015). Thus, the conservation of biodiversity has been assumed to be a main challenge in this century [see Aichi Biodiversity Targets, European Union (EU) Biodiversity Strategy for 2020]. The different levels of biological diversity are not homogeneously distributed across the planet, and the most diverse areas are known as biodiversity hotspots (Myers et al., 2000; Myers, 2003). The Mediterranean basin is one of these global biodiversity hotspots (Myers et al., 2000; Cuttelod et al., 2008), and within it, the Iberian Peninsula is a major area, harbouring more than 50% of the European vertebrate and plant species (Médail & Quézel, 1997; Williams et al., 2000, Araújo, Lobo & Moreno, 2007; IUCN, 2013a, b). The endemicity rate in Iberia is also high (c. 31% for endemic plants and vertebrates; Williams et al., 2000). However, biodiversity within the Iberian Peninsula is not distributed homogeneously. Since resources for conservation are limited, the identification of biodiversity hotspots within global hotspots (see Gómez & Lunt, 2004) could represent a key strategy for allocating conservation resources.

To prevent biodiversity loss, the EU has created the largest network of protected areas up to date: the Natura 2000 network (hereafter N2000), which covers more than 18% of the EU (EEA, 2012). N2000 includes sites designated under the Birds Directive (special protection areas, SPAs) and the

Habitats Directive (Special Areas of Conservation, SACs). The designation of these areas is based on the presence of certain bird species included in Annex I of the Birds Directive, as well as certain habitats and species (others than birds) included in Annexes I (habitats) and II (species) of the Habitats Directive. However, both criteria for the inclusion of species in these annexes and the designation process for N2000 sites have been criticized, arguing that the establishment of priorities should be more dynamic and based on scientific criteria (Hochkirch *et al.*, 2013; Orlikowska *et al.*, 2016; Lisón *et al.*, 2017). Moreover, annexes are biased towards charismatic species (Cardoso, 2012). Even so, the Habitats Directive is the main tool of the EU for reducing the loss of biodiversity, and plays an important role in diverse areas such as the Iberian Peninsula.

An important task in conservation biology is to evaluate the effectiveness of protected areas in the representation of biodiversity. Many studies have approached these analyses using different taxonomic groups and different spatial scales. For example, Rodrigues *et al.* (2004) considered vertebrates on a global scale; Abellán & Sánchez-Fernández (2015) and Kukkala *et al.* (2016) considered herpetofauna and vertebrates, respectively, at the European scale. In the same way, the effectiveness of N2000 and other protected areas has been evaluated within the Iberian Peninsula using dung beetles (Martín-Piera, 2001), vertebrates (Rey Benayas & De la Montaña, 2003; López-López *et al.*, 2011), lichens (Martínez *et al.*, 2006), water beetles (Sánchez-Fernández *et al.*, 2008*a*), herpetofauna (Lobo & Araújo, 2011), endangered invertebrates (Hernández-Manrique *et al.*, 2012), butterflies (Romo, Munguira & García-Barros, 2007; Romo *et al.*, 2014) and bats (Lisón, Sánchez-Fernández & Calvo, 2015). The effectiveness of protected areas with regard to climate change has also been examined both at the European level for plant species (Araújo *et al.*, 2004), plants and vertebrates (Araújo *et al.*, 2011) and, at the national scale, for terrestrial vertebrate species (Aragón *et al.*, 2010).

Despite this large amount of research devoted to assess protected area networks even considering different taxonomic groups (mostly vertebrates and plants see e.g. Maiorano, Falcucci & Boitani, 2006; Araújo *et al.*, 2007; López-López *et al.*, 2011), there is a scarcity of studies including insects (the most important taxonomic group in terms of biodiversity) in their evaluations. Moreover, in almost all of these studies, the distributional range of most of the species exceed the studied area, leading to partial estimates of the conservation status of species, since we do not know how far a given species is protected outside the studied area in question. Thus, the interest to conduct the present work focussing on endemic species is clear, since (1) they allow assessing the effectiveness of protected areas considering the entire range of the species distributions, and (2) the conservation responsibility of these species falls exclusively on the public agencies sharing the study area (i.e. in the case of the Iberian Peninsula, only in Portugal and Spain). However, there is no study focussing exclusively on the assessment of protected areas effectiveness for endemic fauna, especially considering both vertebrate and invertebrate species jointly.

The main objective of this study was to assess how Iberian endemic fauna are represented in the N2000. Specifically, we aimed (1) to generate an updated distributional database of Iberian endemic fauna from eight taxonomic groups; (2) to study the distribution patterns and to detect hotspots for each group; (3) to identify hotspots of Iberian endemic fauna, integrating by the first time all available taxonomic groups; (4) to evaluate the effectiveness of the N2000 regarding the representation of both species and hotspots; and finally; (5) to detect conservation gaps and propose new areas for inclusion in the Iberian N2000.

Materials and methods

The distribution data of the endemic Iberian species belonging to eight faunal groups were compiled in a database. These taxa include four vertebrate groups (amphibians, terrestrial mammals, freshwater fishes and reptiles) and four invertebrate groups (water beetles, dung beetles, Papilionoidea butterflies (hereafter butterflies) and lacewings). Although birds are one of the groups with better information about their distribution, there are only two endemisms within the study area (*Aquila adalberti* and *Cyanopica cooki*); thus, birds were not included in this study. Only strict Iberian endemisms were considered (species with geographic ranges restricted to the study area, which is the continental territories of Portugal and Spain), excluding those species whose distributions extend along the north face of the Pyrenees or southern France. The reason for the exclusion of these species lies in the difficulty of establishing a threshold for the northern range of their distributions and for coherence in their management (Rodrigues & Gaston, 2002), as the conservation responsibility of the selected species falls exclusively to the environmental agencies of Spain and Portugal.

Distributional database

In a first step, distributional data on endemic vertebrates were obtained from available state agencies databases. In Spain, we used the Spanish Inventory of Terrestrial Vertebrate Species of the Ministry of Agriculture, Food and Environment (http://www.mapama.gob.es/es/biodiversidad/temas/inventarios-nacionales/inventario-especies-terrestres/default.aspx; accessed January 2016), which includes the information contained in atlases for amphibians and reptiles (Pleguezuelos, Márquez & Lizana, 2002), mammals (Palomo, Gisbert & Blanco, 2007) and freshwater fishes (Doadrio, 2002), as well as other data obtained in further surveys. The Instituto da Conservação da Natureza e das Florestas database was used for Portugal (http://www.icnf.pt/portal/naturaclas/patrinatur/especies; accessed January 2016), including data for mammals, amphibians and reptiles (Loureiro *et al.*, 2008) and continental fishes. For invertebrates, we used the most recent published atlases for water beetles (Millán *et al.*, 2014; Sánchez-Fernández *et al.*, 2015); butterflies (García-Barros *et al.*, 2004); lacewings (Monserrat & Triviño, 2013) and dung beetles (Lobo & Martín-Piera, 1991). All data was processed and integrated into a single database with a resolution of 100 km^2 UTM squares.

For the second step, all the distributions were checked and updated by the authors (at least one specialist for each one of the selected groups), including all distributional data available so far. Thus, a final version of the database with the most updated and accurate geographical information was generated (database available upon request). For each species, we compiled information about its conservation status, including its presence in the International Union for Conservation of Nature (IUCN) red list or Annexes II and IV of the Habitats Directive.

Protected areas

This study is based on the terrestrial N2000 in the Iberian Peninsula (Fig. S1 in Supplementary Material). Four GIS data layers (SPAs and SACs for Spain and Portugal) supplied by national conservation agencies were processed and combined to produce a single layer of the current N2000 in the Iberian Peninsula. Then, overlapping proportions between each 100 km^2 UTM square and N2000 were calculated.

Distribution patterns and hotspots

We generated maps of endemic species richness for each group at a resolution of 100 km^2 UTM squares. In addition, we calculated a geographic rarity index for each square and each species, defined as the inverse of the number of squares in which each species appears (1/n; being n the number of UTM squares where a species appears). We calculated an average rarity for each square, which was defined by the sum of the rarity values of all species that appear in that square divided by the total number of species occurring there [i.e. ($\Sigma 1/n$)/N; being N the total of species that appear in that square]. Then, to identify hotspots for each group, squares were sorted according to their richness values and the first 100 squares were selected (c. 2% of Iberian squares). In the event of equal richness, priority was given to those squares with higher geographic rarity values. Although it could be some hypothetical cases in which the cutoff coincides with the change in richness value, in our case, rarity was considered in all cases, as we always had to choose among a number of squares with the same richness value (and different values of rarity). Thus, we identified the top 100 squares in terms of both richness and geographic rarity as hotspots for each taxon. Finally, we identified those squares with hotspots for at least two of the eight taxonomic groups as Iberian endemic fauna hotspots. Because the threshold of the first 100 squares could be arbitrary, we used also different cut offs (i.e. the first 50, 150 and 200 squares) to identify hotspots, obtaining (excepting fishes) similar results as with the first 100 squares (see Table S17 and Fig. S27 in Supplementary Material).

Effectiveness of protected areas

We conducted both a classical gap analysis and null models of representativeness. Previously and as a part of an exploratory data analysis, we calculated the mean and standard deviation of the overlapping values between N2000 polygons and the set of squares in which the species of each taxonomic group appears.

Gap analysis

This analysis allows for the exploration of the amount and nature of biodiversity falling within or outside protected areas and the identification of species and/or areas that need further protection (Scott *et al.*, 1993).

Once identified, the hotspots for each taxon and for endemic Iberian fauna jointly were overlapped with the N2000 polygons. Subsequently, three types of squares identified as hotspots were defined as a function of the calculated overlapping values: squares 'represented' within N2000 (overlapping value ≥25%), squares 'marginally represented' (from 1 to 25%), and squares 'outside' the N2000 (<1%). In addition, for each species, the level of representativeness in N2000 was calculated as the mean percentage overlap (MPO), which is computed as the mean percentage of spatial overlap between those squares in which the species occurs in the study area and the N2000 polygons (see Sánchez-Fernández & Abellán, 2015). This value (using the same threshold as above) allowed us to classify species according to the degree of representation offered by N2000 (i.e. represented, marginally represented and species outside N2000).

Null models

Null models allow for the identification of species and hotspots that are under- or overrepresented in the protected area network, regardless of the size of their distribution range (Sánchez-Fernández & Abellán, 2015). Thus, a combination of both approaches (gap analysis and null models) provides valuable information for detecting underrepresented species (or the identified hotspots) and improving the effectiveness assessment of protected areas.

Once the MPO was calculated for each species, null models were used to test whether these values differed significantly from those expected by chance according to the size of species distribution ranges (number of squares in which they appear). For this, the observed MPO value for each species was compared with the MPO values obtained from 10 000 random distributions with same number of squares in which each species appears. A species is considered to be underrepresented when more than 95% of the random distributions have a higher level of representativeness than the MPO observed, while a species is considered to be overrepresented when less than 5% of these randomizations show a higher level of representativeness than the observed value. This analysis was carried out in R, version 3.0.3 (R Development Core Team, 2012) (for details, see Sánchez-Fernández & Abellán, 2015).

Results

Iberian endemic fauna

In the Iberian Peninsula, a total of 1160 species belong to the eight taxonomic groups considered, of which 249 were

Iberian endemisms (21.3%). Water beetles was the group with the highest number of endemic species (118), followed by freshwater fishes (38), while mammals represented only eight endemic species (Table 1). The highest percentages of endemicity (number of endemic species over the total number of Iberian species) were found in freshwater fishes (65.5%), amphibians (42.3%) and reptiles (38.5%), while the lowest values were found in mammals (8.8%) and butterflies (7.3%) (Table 1). The final database contained 39 932 records (taxonomic group/code/species/UTM 100 km^2 square) for the 249 endemic Iberian species (Tables S1-S8 in Supplementary Material). Freshwater fishes was the group with the highest number of records (14 507), while endemic lacewings and dung beetles had only 464 and 519 records respectively (Table 1). Only 25 out of these 249 species (10%) are included in the Annexes of the Habitats Directive (II and/or IV). Mammals were the group that, in proportion, had a greater number of endemic species included in the annexes of the Habitats Directive (50%). Only one Iberian endemic invertebrate of the studied groups, the butterfly *Polyommatus golgus*, was included in the Habitats Directive (Table 1).

Distribution patterns and hotspots

The richness patterns of endemism for each group and the selected hotspots are shown in Supplementary Material, in Figs S2–S9 and S10–S17 respectively. A total of 115 squares were selected as hotspots of Iberian endemic fauna in the Iberian Peninsula (see Figs 1 and S18 in Supplementary Material), that is, those that were identified as hotspots for at least two taxonomic groups (Figs S10–S17 in Supplementary Material). Only two of these squares, located in the Cantabrian Mountains and Central Mountain System, are hotspots for five groups. Four squares were identified as hotspots for four groups, all located in the same mountain ranges. Nearly identical distributions are present for the 23 squares that were hotspots for three taxonomic groups; but

Table 1 Information on the eight taxonomic groups studied in the Iberian Peninsula

Group	NS	NE	%E	NE Ann. (II, IV)	NR
Amphibians	26	11	42.3	(5, 5)	7642
Mammals	91	8	8.8	(4, 4)	5914
Freshwater fishes	58	38	65.5	(11, 1)	14507
Reptiles	39	15	38.5	(2, 4)	5558
Water beetles	476	118	24.8	(0, 0)	3083
Dung beetles	59	17	28.8	(0, 0)	519
Butterflies	220	16	7.3	(1, 1)	2245
Lacewings	190	26	13.7	(0, 0)	464

NS, total number of species in each group present in the Peninsula; NE, number of endemisms in each group; %E, percentage of endemicity (NE × 100/NS); NE Ann. (II, IV), number of endemic species listed in the Annexes (II, IV) of the Habitats Directive; NR, number of records for the endemic species of each group in the database.

in this case, these squares were also found in Sierra Nevada (Figs 1 and S18).

Effectiveness of protected areas

Gap analysis

We found 214 species represented in N2000, 32 marginally represented, and just three species outside the N2000: one freshwater fish (*Iberochondrostoma olisiponensis*, Critically Endangered), one lacewing (*Mantispa incorrupta*) and one dung beetle (*Onthophagus coenobita*). These latter two species are not listed in the IUCN Red List (Tables S7 and S8 in Supplementary Material). The 32 marginally represented species included one amphibian, one reptile, 15 freshwater fishes, one butterfly, eight water beetles, two lacewings and four dung beetles (Tables S9–S16 in Supplementary Material).

The overlap between hotspots of different groups and N2000 is shown in Figs S19–S26 in the Supplementary Material. In general, hotspots for butterflies, water beetles and mammals were better represented than those of the other groups, while the worst represented were freshwater fishes and amphibians (Table 2, Figs S19–S26 in Supplementary Material).

The representativeness of hotspots of Iberian endemic fauna in N2000 was high, with 104 (out of 115) squares represented in N2000 (i.e. having an overlapping value greater than 25%, see Fig. 2). The remaining 11 squares were marginally represented (5) or outside N2000 (6). The squares outside the network were located in the Cantabrian Mountains (two squares), Central Mountain System (two squares) and the low Guadiana river valley in Portugal (two squares).

Null models

In general, hotspots for each taxonomic group and for the Iberian endemic fauna were over-represented in N2000 (see Table S17 and Fig. S27 in Supplementary Material). Most endemic vertebrates were also overrepresented by N2000 (Figs S28–S31, Tables S9–S12). However, the majority of freshwater fishes, the Iberian frog *Rana iberica*, and three reptiles (*Iberolacerta aranica*, *Iberolacerta aurelioi* and *Iberolacerta galani*) were represented at random (i.e. these species show MPO values falling within the confidence interval of the MPO values obtained from the 10 000 random distributions with same number of squares). On the other hand, the golden-striped salamander *Chioglossa lusitanica*, the Bocage's wall lizard *Podarcis bocagei* and seven freshwater fishes (*Achondrostoma occidentale*, *Achondrostoma oligolepis*, *Iberochondrostoma lusitanicum*, *I. olisiponensis*, *Iberochondrostoma oretanum*, *Pseudochondrostoma duriense* and *Squalius carolitertii*) were significantly underrepresented (Supporting Information Figs S28–S31, Tables S9–S12).

None of the invertebrate species were underrepresented. Seventy-one endemic water beetles were overrepresented, and the rest (47 species) did not show differences from the null model (Supporting Information Fig. S32, Table S13). Similarly, only the representativeness values for two butterfly
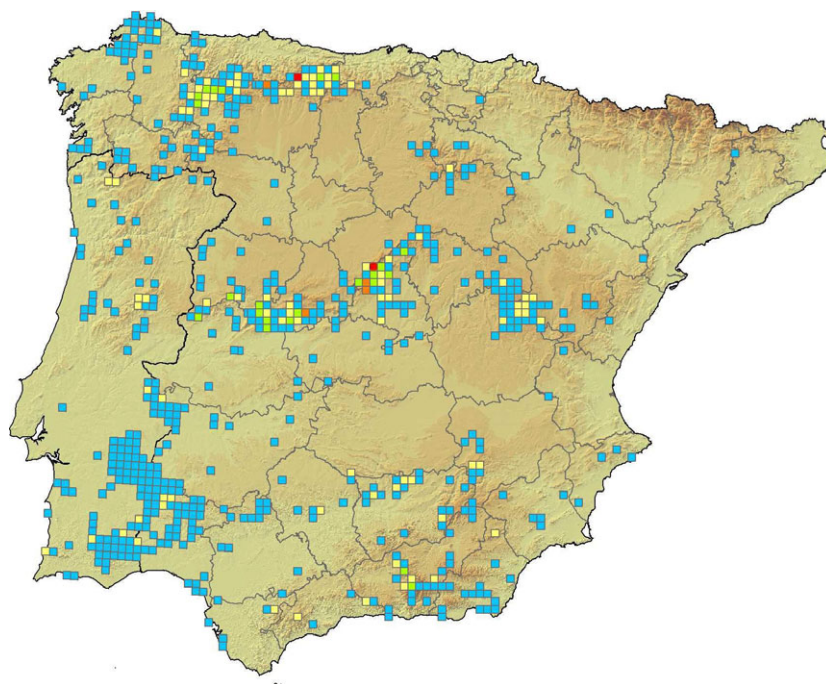
Figure 1 Map resulting from the overlapping of the maps of hotspots for each taxonomic group. Each colour indicates the number of taxa for which a given square is considered a hotspot: one group (blue); two groups (yellow); three groups (green); four groups (orange) and five groups (red). Note that hotspots of Iberian endemic fauna are those squares that are hotspots for at least two groups. [Colour figure can be viewed at wileyonlinelibrary.com]

Table 2 Results of the gap analysis for the different groups of Iberian endemic species

Hotspots (100 squares)	NSR	NSMR	NSO
Amphibians	55	16	29
Mammals	89	6	5
Freshwater fishes	36	24	40
Reptiles	60	24	16
Water beetles	69	18	13
Butterflies	72	11	17
Lacewings	69	21	10
Dung beetles	68	21	11
Iberian endemic fauna[a] (115 squares)	104	5	6

NSR, number of squares well represented by the Natura 2000 network (overlap ≥ 25%); NSMR, number of squares marginally represented (1–25% overlap); NSO, number of squares outside the network (overlap < 1%).

[a]Identified as hotspots for at least two of the eight groups considered in this study (see Materials and methods for details).

species fell within the values expected by chance (*Euchloe bazae* and *Polyommatus fulgens*) (Supporting Information Fig. S33, Table S14). Regarding lacewings, approximately half of the species were overrepresented, while the other half were within the confidence interval of the null model (Supporting Information Fig. S34, Table S15). Finally, the majority of the endemic dung beetles were represented randomly, except for seven species that were overrepresented by the N2000 (Supporting Information Fig. S35, Table S16).

Discussion

The assessment of the effectiveness of protected areas in the preservation of biodiversity is a research focus that has received much attention during the past two decades (Hockings, Stolton & Dudley, 2000; Chape *et al.*, 2005; Abellán & Sánchez-Fernández, 2015). However, despite the high conservational interest of endemic species (e.g. Burlakova *et al.*, 2011) and the widely acknowledged importance of the Iberian biodiversity in a European context (Williams *et al.*, 2000; Schuldt & Assmann, 2010), this is the first comprehensive analysis focused on the effectiveness of N2000 in the protection of Iberian endemic fauna (but see López-López *et al.*, 2011).

It is worth to note that only the 10% of the Iberian endemic species considered are acknowledged as species of community interest (i.e. those species listed in the Habitats Directive). Thus, if these species have not protection at a national level, the only protection available for most of them (especially invertebrates) is the extent to which they occur in protected areas designated on the basis of other taxa or habitat features (i.e. those species and habitats of community interest). Although the aim of N2000 is to protect species listed in the Birds and Habitats Directives, the conservation status of endemic species in one of the most important areas of Europe in terms of biodiversity, could be also a concern for the EU, and hence a secondary objective of N2000 sites. In this sense, our results could be useful in the context of the recent European Commission mandate calling for a
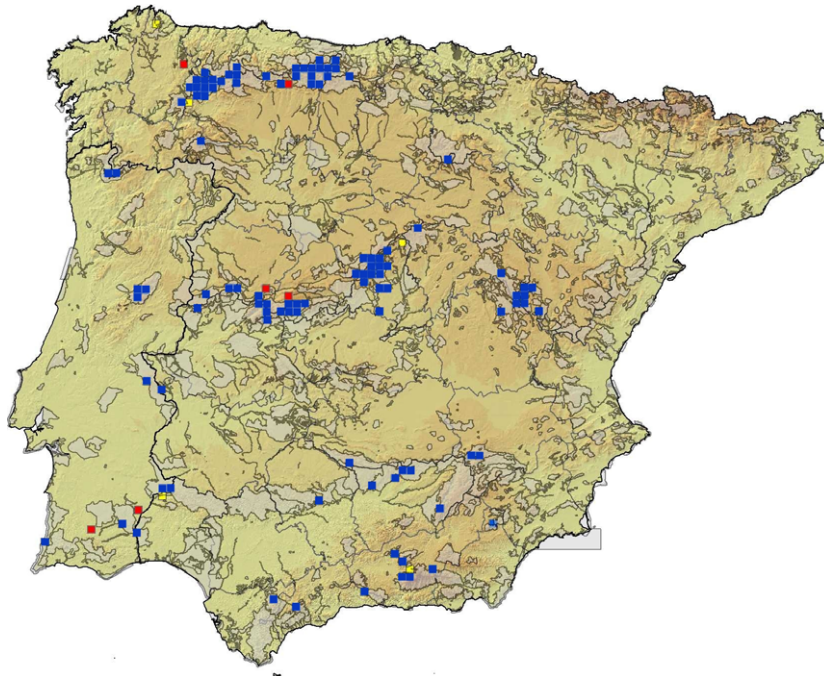
Figure 2 Gap analysis for the hotspots of Iberian endemic fauna. Represented hotspots are in blue (SR), marginally represented hotspots are in yellow (SMR), and those hotspots outside the Natura 2000 Network are in red (SO). [Colour figure can be viewed at wileyonlinelibrary.com]

'fitness check' of the Birds and Habitats Directives (European Commission, 2015).

We are aware that this study does not incorporate estimates of the quality of the inventories while it is likely that there is heterogeneity in the sampling efforts across taxonomic groups or regions within the study area. Some areas lack complete distributional information for some groups (e.g. mammals, water beetles or lacewings in some areas of Portugal, but also in some regions of Spain, or even dung beetles in most part of the Guadiana basin, including parts of both Spain and Portugal). However, rather than compare between taxonomical groups or political regions, the main aim is to identify hotspots for the whole Iberian endemic fauna using, to our knowledge, the best distributional information available so far on Iberian endemic species (after a refinement process conducted by specialist in each group, see Materials and methods). Thus, although, it is likely that some important areas for conservation had not been identified here due to lack of sampling effort, the areas identified here are certainly important, and their conservation should be prioritized.

Most of the hotspots (especially for invertebrates groups and for all Iberian endemisms considered here) are concentrated in some of the main mountain ranges of the Iberian Peninsula (Cantabrian Mountains, Central Mountain System, Iberian System, and Baetic System; García-Barros *et al.*, 2002), which could comprise a number of separate glacial refuges during the Pleistocene Ice Ages (see Gómez & Lunt, 2004; Schmitt, 2007), linked to a Late Quaternary climate stability (Abellán & Svenning, 2014). However, the number

of hotspots for Iberian endemism in other mountain ranges (e.g. Pyrenees) is notably lower, in agreement with other studies using endemic flora (Domínguez-Lozano *et al.*, 2000). The low number of endemism in the Pyrenees could be also related to the way that endemic species were defined.

Although the threshold for considering an occurrence square as represented by N2000 might be more restrictive, the results show that most of the 115 squares identified as hotspots of endemic fauna in the Iberian Peninsula (*c.* 90%) are represented by N2000 according to our criteria. Besides, the six squares identified as the most important hotspots for Iberian endemic fauna (i.e. those squares that are hotspots for at least four taxonomic groups; Fig. 1) are well covered by N2000 (mean 75%, ranging from 27 to 100%). It is interesting to note that the two squares of the Cantabrian Mountains and the four from the Central System are already connected by N2000 sites. However, the gap analysis showed that there were still areas that were only marginally protected, or even outside this network (11 squares), in some of the main mountain systems and along the Guadiana River near the border between Spain and Portugal (Fig. 2). Thus, we propose the inclusion of these 11 squares in N2000. Within these 11 hotspots, we must highlight six of them (located in the Galician Massif, Cantabrian Mountains, and the Central Mountain System), harbouring some species that are only marginally represented by N2000. These species include four endemic fishes (*Achondrostoma arcasii*, *Luciobarbus bocagei*, *P. duriense* and *S. carolitertii*), one reptile (*P. bocagei*) and one amphibian (*C. lusitanica*) (Tables S9,

S11 and S12 in Supplementary Material). According to the IUCN, *P. duriense*, *A. arcasii* and *C. lusitanica* are listed as Vulnerable. If there is a possibility to expand the Iberian N2000, these six hotspots should be prioritized. However, declaring them as Sites of Community Importance is difficult in terms of legislation, as only three of these six species appear in Annex II of the Habitats Directive (*A. arcasii*, *C. lusitanica* and *P. bocagei*). There are two ways to overcome this difficulty: (1) to focus on the habitats of these spaces in order to find habitats included in the Annex I of the Habitats Directive, and (2) to propose the inclusion of these endemic species in the Annex II of the Habitats Directive. However, as these requests would be long and tedious, and the lists in the annexes are overly static (Hochkirch *et al.*, 2013), the urgent designation of micro-reserves could be the most practical solution in the short term to protect these important areas for the Iberian endemic fauna (Sánchez-Fernández *et al.*, 2008a).

It is surprising that the representation values for invertebrates in N2000 are in general higher than for vertebrates (Supporting Information Table S18; $t = 36.9$; $X_{invertebrates} = 48.4$, $X_{vertebrates} = 29.9$; $P < 0.001$), which could have several interpretations. It is possible that this network exerts an umbrella effect over Iberian endemic invertebrates, being effective in representing other species that have not been taken into account for its declaration. However, perhaps the most logical explanation is related to the lower sampling effort performed for invertebrates (especially outside protected areas). The distributional databases for arthropods are usually more incomplete and biased (Romo, García-Barros & Lobo, 2006; Sánchez-Fernández *et al.*, 2008b) than those of vertebrates. It is likely that endemic invertebrates have been mainly detected in those regions that are more intensely studied, that is, in protected areas (Lisón *et al.*, 2015), as these regions necessarily have more detailed inventories than others (Hochkirch *et al.*, 2013). This 'false effectiveness', as a consequence of an insufficient sampling effort, may have biased the conclusions of many entomological studies performed to date. However, a recent study examining the location of newly described Iberian species shows that most of them are invertebrates and, more importantly, that these species can be found both within and outside N2000 reserves (Payo-Payo & Lobo, 2016).

Although most of the areas of interest for the conservation of endemic species are within protected areas, this is not a guarantee for their long-term survival (Sánchez-Fernández *et al.*, 2013) because management measures in SPAs and SACs are primarily directed towards the conservation of habitats and/or species for which they have been declared. Theoretically, the N2000 should provide protection mechanisms to prevent the degradation of the natural habitats of listed endemic species. However, these may only provide 'virtual protection', as SPAs are declared mainly to conserve birds, and only a few endemic species are listed in Annex II of the Habitats Directive, which is considered in the declaration of SACs.

The N2000 provides effective coverage of the Iberian endemic fauna studied. However, the management plans within these spaces should consider effective measures to guarantee the conservation of these species. On the other hand, there are still few endemic species and hotspots of endemism outside this network. To ensure the preservation of endemic biodiversity, it is advisable to consider extending the network in order to protect these areas and to propose the inclusion of those endemic species underrepresented in the Habitats Directive. Our approach could also be applicable to other countries or regions with high value of endemicity (e.g. other Mediterranean peninsulas or islands) in order to preserve their endemic species.

Acknowledgements

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Supporting information

Additional Supporting Information may be found in the online version of this article at the publisher's web-site:

Table S1. General information on Iberian endemic amphibians: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S2. General information on Iberian endemic mammals: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S3. General information on Iberian endemic

freshwater fishes: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S4. General information on Iberian endemic reptiles: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S5. General information on Iberian endemic water beetles: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S6. General information on Iberian endemic butterflies: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S7. General information on Iberian endemic lacewings: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

Table S8. General information on Iberian endemic dung beetles: species code, scientific name, author, world IUCN category in which each species is listed, and presence or absence in Annexes II and/or IV of the Habitats Directive.

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Table S10. Results of the null model for mammals.

Table S11. Results of the null model for freshwater fishes.

Table S12. Results of the null model for reptiles.

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Table S17. Results of the null model for hotspots using different cut offs for different taxonomic groups (the first 50, 100, 150 and 200 cells), and the subsequent hotspots for endemic Iberian fauna using all groups jointly.

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Figure S2. Map of species richness of endemic amphibians (10 × 10 km grid size).

Figure S3. Map of species richness of endemic mammals (10 × 10 km grid size).

Figure S4. Map of species richness of endemic freshwater fishes (10 × 10 km grid size).

Figure S5. Map of species richness of endemic reptiles (10 × 10 km grid size).

Figure S6. Map of species richness of endemic water beetles (10 × 10 km grid size).

Figure S7. Map of species richness of endemic butterflies (10 × 10 km grid size).

Figure S8. Map of species richness of endemic lacewings (10 × 10 km grid size).

Figure S9. Map of species richness of endemic dung beetles (10 × 10 km grid size).

Figure S10. Hotspots of endemic amphibians.

Figure S11. Hotspots of endemic mammals.

Figure S12. Hotspots of endemic freshwater fishes.

Figure S13. Hotspots of endemic reptiles.

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Figure S20. Results of the GAP analysis for mammals. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S21. Results of the GAP analysis for freshwater fishes. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S22. Results of the GAP analysis for reptiles. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S23. Results of the GAP analysis for water beetles. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S24. Results of the GAP analysis for butterflies. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S25. Results of the GAP analysis for lacewings. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S26. Results of the GAP analysis for dung beetles. SR (squares represented), SMR (squares marginally represented) and SO (squares outside) the Natura 2000 Network.

Figure S27. Representativeness according to the null models for hotspots for each group identified using different thresholds (i.e., the first 50, 100, 150 and 200 squares).

Figure S28. Representativeness according to the null models for amphibians.

Figure S29. Representativeness according to the null models for mammals.

Figure S30. Representativeness according to the null models for reptiles.

Figure S31. Representativeness according to the null models for freshwater fishes.

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Figure S33. Representativeness according to the null models for butterflies.

Figure S34. Representativeness according to the null models for lacewings.

Figure S35. Representativeness according to the null models for dung beetles.