



Preserving the evolutionary history of freshwater biota in Iberian National Parks



Pedro Abellán^{a,b,*}, David Sánchez-Fernández^{b,c}, Félix Picazo^c, Andrés Millán^c, Jorge M. Lobo^d, Ignacio Ribera^b

^a Department of Bioscience, Aarhus University, Ny Munkegade 114, DK-08000 Aarhus, Denmark

^b Institut de Biologia Evolutiva (CSIC-UPF), Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Spain

^c Departamento de Ecología e Hidrología, Universidad de Murcia, Campus de Espinardo, 30100 Murcia, Spain

^d Departamento de Biogeografía y Cambio Global, Museo Nacional de Ciencias Naturales (CSIC), José Gutiérrez Abascal 2, 28006 Madrid, Spain

ARTICLE INFO

Article history:

Received 12 November 2012

Received in revised form 27 March 2013

Accepted 2 April 2013

Keywords:

Phylogenetic diversity

Protected areas

Evolutionary distinctiveness

Iberian Peninsula

Water beetles

Endangered species

Area selection

ABSTRACT

The establishment of protected areas is one of the main strategies to reduce losses of biodiversity. While a number of studies have evaluated the effectiveness of existing reserves in preserving representative samples of ecosystem and species diversity, there has been no systematic assessment of their effectiveness in terms of conserving evolutionary history. We used comprehensive phylogenies of four lineages of aquatic Coleoptera to investigate (i) the performance of National Parks (NPs) in representing the phylogenetic diversity (PD) of the Iberian Peninsula; (ii) the representation in NPs of the species with the highest conservation priority, as identified from a combination of their evolutionary distinctiveness and vulnerability; and (iii) whether species richness may be a good surrogate of PD when selecting new conservation areas. Our results show that Iberian NPs perform poorly in the preservation of freshwater PD. In most cases PD was not different from a random expectation, but when it did differ, PD in NPs was always lower than that obtained by a random selection of the same number of species. We also found that most of the highly evolutionarily distinct and vulnerable taxa were not covered by any NP. Finally, when additional conservation areas were selected maximizing the number of unrepresented species, the variation in PD could be very high, and as a consequence, depending on the group and the number of areas added, they could preserve much less evolutionary history than when they were specifically selected to maximize PD.

© 2013 Elsevier Ltd. All rights reserved.

1. Introduction

Conservation biologists are increasingly incorporating phylogenetic information when evaluating conservation priorities, both using species-based and area-based approaches (Rolland et al., 2012). When the focus is on species, the assumption is that not all species are equal in terms of evolutionary distinctiveness, as the extinction of phylogenetically singular taxa would result in a larger loss of evolutionary history (Vane-Wright et al., 1991; Redding and Mooers, 2006). These measures of evolutionary distinctiveness can also be extended to incorporate extinction risk for assessing conservation worth (e.g., Redding and Mooers, 2006; Isaac et al., 2007).

When the focus is the conservation of an area, the evolutionary relationships of the species it contains reveal their shared evolutionary history. One of the most frequently used statistics, phylogenetic diversity (PD), can be quantified by summing the branch

lengths of a phylogeny that subtend all the species in the subset to be measured (Faith, 1992). Conservation efforts can then be directed towards those areas hosting the subset of species that maximizes PD (see e.g., Forest et al., 2007). The rationale underlying this approach is the assumption that, since closely related taxa will tend to be also similar in their physiologies and ecologies (Harvey, 1996), by maximizing PD we likely maximize the representation of genotypic, phenotypic and functional diversity, thus providing biological systems with the best options to respond to a changing world (Vane-Wright et al., 1991; Faith, 1992). Despite evidently strong theoretical grounds for incorporating PD into conservation prioritization schemes, the benefits of the use of PD metrics has been called into question because it tends to scale in a predictable way with taxon richness, which is more easily obtained. In practical terms, conservation decision making based on richness or PD might be largely indistinguishable (Polasky et al., 2001; Rodrigues and Gaston, 2002; Rodrigues et al., 2005, 2011). Nevertheless, empirical studies (e.g., Forest et al., 2007; Devictor et al., 2010) have shown that taxon richness maybe decoupled from PD (i.e. some areas have more or less PD than expected given their number

* Corresponding author at: Department of Bioscience, Aarhus University, Ny Munkegade 114, DK-08000 Aarhus, Denmark. Tel.: +45 87156128.

E-mail address: pabellan@um.es (P. Abellán).

of species), and this decoupling could have important implications for conservation planning (Forest et al., 2007; Strecker et al., 2011).

Although protected areas play a key role in conservation strategies to reduce losses of biological diversity (Chape et al., 2005), they are often not selected to meet specific biodiversity objectives, and historical, socio-economic or aesthetic criteria have dominated the choice of their locations (Pressey, 1994). While a number of studies have evaluated the effectiveness of protected areas in preserving representative samples of ecosystem and species diversity (e.g. Rodrigues et al., 2004; Araújo et al., 2007; Branquart et al., 2008), there has been no systematic assessment of their effectiveness in preserving evolutionary history (but see Devictor et al., 2010) nor the extent to which the PD captured by existing reserves shows departures from what it would be expected based solely on their species richness. This is particularly the case for non-charismatic groups – such as invertebrates – and for freshwater biota, which is especially threatened but generally neglected (Abellán et al., 2007; Cardoso et al., 2011).

Here we investigate how the existing network of National Parks (NPs) represents the evolutionary history of the Iberian freshwater biota. In the Iberian Peninsula, a global biodiversity hotspot (Brooks et al., 2006), NPs are at the core of the conservation policies and are committed to preserve the best representation of its natural heritage (Morillo and Gómez-Campo, 2000). We use water beetles as a surrogate of the wider freshwater biota, as it is one of the most diverse and best known groups of aquatic invertebrates in this region (Ribera, 2000; Sánchez-Fernández et al., 2008b). They exhibit a high level of endemism, but also include species widely distributed across the Palearctic and Holarctic regions. They have been shown to be good indicators of the wider diversity in aquatic ecosystems (Bilton et al., 2006; Sánchez-Fernández et al., 2006) and to be useful to select priority areas for conservation (Sánchez-Fernández et al., 2004; Abellán et al., 2005).

More specifically, we use comprehensive phylogenies of four lineages of aquatic Coleoptera to investigate: (i) the performance of the Iberian NPs in representing PD (i.e. do NPs include more or less PD than expected given their number of species or their area?); (ii) the representation in NPs of the species with the highest conservation priority, as identified from a combination of its evolutionary distinctiveness and vulnerability; and (iii) whether species richness is a good surrogate of PD in the selection of new protected areas. Since NPs are not the only protected areas in Spain and Portugal, which have several other heterogeneous regional or international categories of protection, our aim was not to evaluate the extent to which the whole phylogenetic diversity of the Iberian Peninsula is protected. We rather focused on the performance of this concrete reserve network, which represents the most charismatic and exigent protection category in the region and whose areas are linked by a common focus and similar management approaches.

2. Methods

2.1. Studied groups

We used four monophyletic lineages of aquatic Coleoptera belonging to three different families in two suborders, representing three independent invasions of the aquatic medium. Sampling aimed to maximize the presence of western Palearctic – and in particular Iberian – species, but with the inclusion of species from other geographical areas when morphological or molecular data suggested they could be closely related to some Iberian ones. The full list of taxa and data used in this study is provided in the Appendix A.

1. Suborder Adephaga, family Dytiscidae, subfamily Agabinae: in the West Palearctic it includes the genera *Agabus*, *Ilybius* and *Platambus* (Nilsson, 2001). They are mostly species inhabiting standing water and with generally wide geographical ranges throughout the Palearctic or Nearctic realms, although they also include a number of narrow-range endemics (Table 1).
2. Suborder Adephaga, family Dytiscidae, Hydroporini *sensu lato*: a clade including tribes Hydroporini and Hygrotini (Ribera et al., 2008), with 20 genera in the western Palearctic (Nilsson, 2001; Appendix A). It encompasses a heterogeneous set of species inhabiting a wide spectrum of aquatic habitats and geographic ranges.
3. Suborder Polyphaga, family Hydraenidae: in the western Palearctic it includes six genera (Hansen, 1998) encompassing a heterogeneous set of species inhabiting a wide spectrum of aquatic habitats, with a high number of narrow endemics but also with widespread species.
4. Suborder Polyphaga, family Hydrochidae: includes a single genus (*Hydrochus*) with ca. 180 described species. In the west Mediterranean (Iberian Peninsula, Italy, south France and North Africa) the species of the genus form a monophyletic group that also includes one species (*H. roberti*) so far recorded only from the Caucasus and Turkey (Hidalgo-Galiana and Ribera, 2011).

In the phylogenies we included all Iberian species of Agabinae, Hydroporini and Hydrochidae (Table 1). Missing endemics of Hydraenidae were in general very rare, some only known from the types and never collected since their description. All the endemic species present in the NPs were included in the phylogenies with the exception of *Ochthebius cantabricus*, although we included specimens from a morphologically very similar species from Turkey recorded as *O. cantabricus* but likely to be a separate species (M.A. Jäch per.com., 2011). We did not consider *Agabus nevadensis*, an endemic to Sierra Nevada, as it is nested within the widespread *A. bipustulatus* (Drotz et al., 2010).

2.2. Species inventories in the National Parks

Our study focused on the NPs (IUCN category II) located within the Iberian Peninsula (Fig. 1). In mainland Spain, the National Park network is an integrative system for the protection and management of eight areas selected to represent the Spanish natural heritage (Morillo and Gómez-Campo, 2000). It started in 1918 with the NP of Covadonga (now Picos de Europa) and Ordesa (Fig. 1), and new parks had been added in a process still underway (the last one, Monfragüe, in 2007, although a new one – Guadarrama – is planned to be established in 2013). We also included in the study the only designated NP in Portugal (Peneda-Gerês) (Fig. 1).

We obtained species distribution data for the NPs from fieldwork and from ESACIB, an exhaustive database of Iberian water beetle occurrences (Sánchez-Fernández et al., 2008b). Field data were collected during 2008–2010 from a total of 111 localities which represent the diversity of water body types present within

Table 1

Number of Iberian species, Iberian endemics, Iberian subspecies (all endemic), and total number of taxa included in the phylogenies in the four studied lineages (as for August 2012). All Iberian species and subspecies were included in the phylogenies with the exception of the Hydraenidae (with the included number in parentheses). See Appendix A for a complete species list.

Lineage	Iberian sp	Endemic sp	Iberian ssp	Total
Agabinae	26	4	0	98
Hydroporini s.l.	96	41	8	280
Hydraenidae	148 (128)	62 (49)	1	245
Hydrochidae	11	4	0	12

Download English Version:

<https://daneshyari.com/en/article/6300527>

Download Persian Version:

<https://daneshyari.com/article/6300527>

[Daneshyari.com](https://daneshyari.com)