How well do protected area networks support taxonomic and functional diversity in non-target taxa? The case of Iberian freshwaters

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ABSTRACT

Protected area networks represent one of the mainstays of global conservation polices and are therefore central to current efforts to maintain biodiversity. However, a major limitation of most conservation strategies is their bias towards particular taxonomic groups and ecosystems, meaning that many taxa and habitats are often only incidentally protected as a by-product of inclusion within reserves. Here we investigate how effectively protected area networks, not specifically designated for freshwaters, support aquatic biodiversity in the Iberian Peninsula (Spain and Portugal), using data for water beetles, surrogates of overall macroinvertebrate diversity in these habitats. We explore the behaviour of different measures (α, β and γ) of both taxonomic and functional diversity at different spatial scales. Overall our findings highlight the contrasting performance of reserve systems in the maintenance of either taxonomic or functional diversity, as well as the importance of spatial scale. Iberian reserves perform relatively well in supporting taxonomic diversity of water beetles at the peninsular scale, but the same protected areas poorly represent functional diversity. Such a mismatch cautions against the use of any one diversity component as a surrogate for others, and emphasizes the importance of adopting an integrative approach to biodiversity conservation in aquatic ecosystems. Furthermore, our results often show contrasting patterns at smaller spatial scales, highlighting the need to consider the influence of scale when evaluating the effectiveness of protected area networks.

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1. Introduction

Protected area networks represent one of the mainstays of worldwide conservation polices and are therefore central to current efforts to maintain biodiversity (Chape et al., 2005). Numerous species are highly dependent on protected areas for their continued persistence; occurring either entirely or largely within their bounds (Jackson and Gaston, 2008). However, the implementation of nature reserves is only the start of the task and evaluating how effective they are is a global research priority to better understand their effectiveness in protecting wider biodiversity (Bertzky et al., 2012). A major limitation of most conservation strategies is their bias towards particular taxonomic groups (Martín-López et al., 2009), meaning that many taxa and habitats are often only incidentally protected as a by-product of their inclusion within reserves. Freshwaters, for example, are key hotspots of biodiversity (Strayer and Dudgeon, 2010), and are recognized as amongst the most endangered habitats in the world with important needs of protection, research and public awareness (e.g. Dudgeon et al., 2006; Geist, 2011; Kingsford and Neville, 2005; Monroe et al., 2009; Strayer and Dudgeon, 2010). Despite this, very few protected areas have been planned specifically for freshwaters (Abell et al., 2007) and the effectiveness of incidental protection in representing aquatic features and taxa remains poorly and incompletely known (e.g. Abellán et al., 2007). Additionally, the groups which have been the focus of most conservation efforts (e.g. vertebrates or plants) are likely to be poor surrogates for diversity patterns in many freshwater organisms (see Darwall et al., 2011). Given this, assessing the extent of both intentional and incidental representation of freshwaters within existing protected area networks is a major prerequisite for identifying and plugging conservation gaps (Herbert et al., 2010).

To date, most conservation efforts have focused on protecting areas that ensure adequate representation of taxonomic diversity (TD), such as species richness (e.g. Rodrigues et al., 2004).

Despite this, it is increasingly well recognized that protected areas should strive to preserve all components of biodiversity including the ecological and evolutionary processes that generate and maintain it and the goods and services that humans obtain from nature (Mulongoy and Chape, 2004). Functional diversity (FD), which reflects the range of biological, physiological and ecological traits within natural communities (Petchey and Gaston, 2006), has been advocated as an important facet of diversity for ensuring the provision of goods and services (Díaz et al., 2006), and has been shown to be a key driver of ecosystem processes (e.g. Mokany et al., 2008); essential in understanding relationships between biodiversity, ecosystem functioning and environmental constraints (Mouchet et al., 2010). In addition, incorporating functional information into conservation strategies allows for this approach to go beyond simple species representation. Indeed, human activities may have an impact on FD and alter species interactions and ecosystem functioning regardless of the change in taxonomic diversity (Díaz et al., 2006). Similarly, regions of high TD may be incongruent with regions of high FD (Cumming and Child, 2009), and such spatial mismatch between different aspects of diversity may result in protected area networks that do not fully represent biodiversity (Abellán et al., 2013; Devictor et al., 2010).

Effective protected area systems in a changing world should also ensure the maintenance of species and functional processes at different spatial scales (Brooks et al., 2006; Devictor et al., 2010; Gering et al., 2003). Both taxonomic and functional diversity can be broken down into local, regional and among-site components (so-called alpha, gamma and beta diversities; Whittaker, 1972). Whilst the effectiveness of protected areas in representing alpha (e.g. species richness in a given site, or local diversity) and gamma biodiversity (the total taxa represented in a protected area network, or regional diversity) have often been assessed (e.g. Araújo et al., 2007; Branquart et al., 2008; Rodrigues et al., 2004), very few studies have explored how well existing protected area networks represent beta diversity (and its components), despite the fact that it is the rate of species (or trait) turnover between sites that dictates the optimal spatial arrangement of conservation areas (Nekola and White, 2002). As beta diversity quantifies the change in species (or traits) across space, it provides information about variation in species assemblages, which can be very useful to preserve ecological and evolutionary processes as well as the underlying environmental heterogeneity necessary for long-term persistence (Fairbanks et al., 2001; Margules and Pressey, 2000). Furthermore, beta diversity itself is comprised of two components: spatial turnover and nestedness (see Baselga, 2010). Whilst both nestedness (i.e. a pattern characterised by depauperate sites being strict subsets of richer ones) and turnover (i.e. species/trait replacement from site to site) are components of beta diversity, they have different conservation implications (Wright and Reeves, 1992). A preponderance of nestedness within a network would permit the prioritization of just a small number of the richest sites, whilst high turnover would require conservation of a larger number of different sites, not necessarily the richest ones (Baselga, 2010).

In this study we investigate how effectively protected area networks, not specifically designated for freshwaters, support aquatic macroinvertebrate biodiversity in the Iberian Peninsula. We explore the behaviour of both taxonomic and functional diversity measures, at local (α), inter-site (β) and regional (γ) scales. In addition to making up the bulk of freshwater animal biodiversity, macroinvertebrates play a key role in freshwater ecosystem processes (Covich et al., 1999) but are still less studied and protected compared to other, more publicly appealing, taxa (Strayer, 2006). We specifically use water beetles as a surrogate of overall macroinvertebrate diversity, as these represent one of the most diverse and best known groups of aquatic invertebrates in the region (Millán

et al., 2014; Ribera, 2000), living across the complete spectrum of inland water habitats. Aquatic beetles have been shown to be excellent surrogates for wider macroinvertebrate biodiversity in Iberia (Guareschi et al., 2012; Sánchez-Fernández et al., 2006) and elsewhere (Bilton et al., 2006) and have been used to select priority areas for aquatic conservation (Foster et al., 1989; Sánchez-Fernández et al., 2004). Furthermore, aquatic Coleoptera show considerable diversity in life histories and ecological strategies (Jäch and Balke, 2008), and are therefore functionally important in aquatic habitats, being involved in ecosystem processes such as biomass production, nutrient cycling and recourse processing.

Specifically, we use aquatic beetle data from the Iberian Peninsula to address the following questions: (i) do protected areas have significantly higher α-diversity than non-protected areas? (ii) do protected area networks include more total diversity (γ) than expected by chance, given their area? and (iii) do protected area networks include more inter-site diversity (β) than expected by chance alone, given their area? Addressing the first question we explore whether protected areas include those cells with the highest diversity (e.g. species richness), whilst answering the second question provides information about the effectiveness of the whole network in representing overall freshwater diversity. Finally, the third question deals with dissimilarity amongst protected sites within the network, which is related to their complementarity, a principle widely used in conservation planning (Justus and Sarkar, 2002). Our study has wider implications for the design of protected area networks, being the first investigation to explore how well such networks support both taxonomic and functional measures of biodiversity in a non-target group across different spatial scales.

2. Methods

2.1. Study area and data

This study focuses on the Iberian Peninsula, a biodiversity hotspot located in south-western Europe, which is mainly composed of the mainland territories of Portugal and Spain (Fig. 1). The region, which extends nearly 600,000 km^2, includes a variety of biomes, relief, climates, and soil types, where altitude ranges from sea level to 3483 m. The study area is one of the richest European regions in terms of animal species diversity (Williams et al., 2000) and is characterised by a wide variety of ecosystem types, including aquatic environments, some of which are rare on a European context (Millán et al., 2011).

Distributional data of Iberian water beetles at 10×10 km resolution were obtained from the ESACIB database (see Sánchez-Fernández et al., 2008a; Millán et al., 2014), which represents the most complete information available for a group of freshwater macroinvertebrates in the study area. The database currently contains over 60,000 records with associated location data (10×10 km UTM cells) for 484 water beetle species. Species level was used for taxonomic diversity measures whilst genus level information was used to assess functional diversity (Dolédec et al., 2000; Gayraud et al., 2003).

Two different protected area networks were investigated: the extant regional and national protected area network (RNAs) and the wider and incompletely implemented Natura 2000 network of protected areas (N2000) (see Fig. 1). RNAs are at the core of national and regional conservation policies, and include National and Natural Parks, Natural Reserves, Natural Monuments, Protected Landscapes, Protected Marine Areas (not included in this study) as well as different types of local protected areas (i.e. those included in Spanish and Portuguese laws). The N2000 network