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European Bird distribution is “well” represented by Special Protected Areas: Mission accomplished?

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ABSTRACT

Based on spatial distribution maps for 495 breeding bird species inhabiting mainland Europe, we examined whether bird richness is well represented by the protected areas under the European Birds and Habitats Directives. The former regulates the designation of Special Protected Areas (SPAs) for birds, whereas the latter focuses on habitats through the Sites of Community Importance (SCI) and Special Areas of Conservation (SAC). All together, these areas conform the Natura 2000 network. To achieve our goal, we identified high-value richness areas by assessing the geographic distribution of all bird and important bird species (IBS, according to the Birds Directive) occurring in European Union (EU) countries, and investigated how well bird richness were represented in the current protected areas network. Our assessments showed little association between bird richness patterns and the cover of protected areas (PAs) across EU countries. The congruence between high-value richness areas of all bird species and IBS with PAs cover was moderate, suggesting that different conservation planning targets should be taken into account to safeguard IBS, or the composition of bird species. Our results also showed that 16 (3.9%) threatened species were present in gaps of PAs. The poor relationship between PAs cover and bird richness pattern found herein may provide evidence that the establishment of SPAs across Europe may not be fully accounting for richness patterns to enhance the performance of the current network.

1. Introduction

In the face of the alarming threats (i.e. human actions) affecting species distribution patterns, a key issue to halt species loss is to establish priority areas for conservation, regarded as areas selected to represent maximum biological diversity (Margules and Pressey, 1988). Protected areas (PAs) are considered as beachheads against biological extinction.

However, it is becoming increasingly recognised that a large proportion of PAs around the world receive ineffective enforcement (Margules et al., 2000; Wiersma and Nudds, 2009). The deficiency of well-defined goals, governmental interpretations of conservation objectives and misrepresentation of decision processes in favour of satisfying economic interests are important barriers for the implementation of PAs (Apostolopoulou and Pantis, 2009). Rather than bureaucratic issues, biodiversity conservation planning should focus more on natural processes (Maiorano et al., 2007). Conservation planning should be established in accordance with biodiversity patterns (Pressey et al., 2003). Recently, studies at different grains and spatial scales have attempted to identify PAs highlighting the importance of the spatial patterns of species distribution of different taxonomic groups (Myers et al., 2000; Rey Benayas and de la Montaña, 2003; Jelaska et al., 2010).

There have been various attempts to identify the effectiveness of PAs network (Maiorano et al., 2007; Wiersma and Nudds, 2009). This has yielded several studies recommending that further efforts are still necessary to provide adequate representativeness of biodiversity (Rodrigues et al., 2004; Wiersma and Nudds, 2009). An effective PAs network should encompass the maximum biodiversity represented by a minimum number of sites (Wiersma and Nudds, 2009). Furthermore, a particular gap analysis in current PAs networks is an important tool to assess biological representation and, therefore, help conservationists to identify priorities for the establishment of new PAs or restoration of existing ones (Wiersma and Nudds, 2009).

In Europe, the Natura 2000 network of PAs aims to conserve species and special habitat types (habitats with distinguished geographic, abiotic and biotic features) across the 27 European Union (EU) countries. Natura 2000 comprises areas under the Habitats Directive (Directive EEC/92/43) – including Sites of Community Importance (SCI) and Special Areas of Conservation (SAC) – and

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sites under the Birds Directive (Directive Directive 2009/147/EC) – including Special Protected Areas (SPAs). Specifically, SCI/SAC aim to conserve biodiversity through the persistence of most patrimonial species and habitats across Europe, whereas SPAs aim to create a comprehensive scheme for all wild birds naturally occurring in the EU countries (EC, 2009). Both directives are regarded as keystone of Europe's natural conservation.

In the present study, we tested whether PAs under the Birds and Habitats Directives network represent the patterns of breeding bird species richness across EU countries. Specifically, we aimed to: (1) identify patterns of bird species richness across Europe, (2) verify whether the spatial distribution of protected areas under the Birds and Habitats Directives follow the spatial distribution pattern of bird species richness, (3) identify the geographical location of high-value richness areas of bird species across Europe, and (4) investigate the congruence between high-value bird richness areas and PAs cover.

2. Methods

2.1. Data

Distribution data for bird species were obtained from the European Bird Census Council Atlas of European Breeding Birds (EBCC) (Hagemeijer and Blair, 1997). These data integrates 25 years of continuous field surveys by ornithologists in more than 40 countries, and comprises 495 European Bird species (Hagemeijer and Blair, 1997). After excluding all those species not occurring in all EU countries, a total of 416 bird species were used in the analysis. We recognise that more recent data (i.e. Birds of Western Palearctic Interactive (BWPi), 2006) could be also used in this analysis. However, BWPi provides bird species range maps and this approach imposes some limitations. First, range maps produces less reliable information than survey data and contain less information, especially at finer scales (Hurlbert and Jetz, 2007). Second, range maps tend to overestimate the presence of species (generating false positives), inflating the error of commission (Hurlbert and Jetz, 2007). This overestimation may affect conclusions in the identification of high-value richness areas, making results unreliable. Consequently, the atlas of the EBCC seems to be the most suitable tool for broad scale analyses.

The Birds Directive (Directive 2009/147/EC) provides a list of 193 bird species that shall be subject of species conservation measures to safeguard their survival and reproduction. For analyses, we grouped birds into: (1) all bird species and (2) important bird species (IBS), comprising those species listed in the Birds Directive Annex I (139 species). Additionally, bird species were classified according to the categories defined by the International Union for Nature Conservation (IUCN 2010) into unthreatened (i.e. species considered of least concern (LC), 358 species) and threatened species, including those considered as endangered (En, 2 species), vulnerable (Vu, 12 species), and near threatened (NT, 17 species). 27 species were not found in the IUCN (2010) database.

Next, we overlapped all bird species distributions onto a UTM grid cell of 50 × 50 km each (1695 cells) to generate cell richness values for all species and IBS in UTM grid cells. Also, we used Natura 2000 data network (EEA 2012) to generate maps of PAs under the Birds Directive (SPAs) and a map of combined PAs – including SPA, SAC and SCI. Finally, we superimposed the 50 × 50 km grid to the Natura 2000 data network map to calculate the percentage and number of SPAs and combined PAs for each cell.

2.2. Data analyses

Relationship between bird species richness (all and IBS species) and protected areas cover, including SPA, SAC and SCI areas, were investigated by means of Poisson regression models. We also calculated the likelihood ratio index proposed by McFadden (1974). This index is a pseudo R-squared measure and is often used to measure the explained variation or coefficient of determination when data are not normally distributed (Cameron and Windmeijer, 1996). McFadden index was expressed as:

$$R_{\mathrm{MF}} = 1 - \frac{\ln(L_{\mathrm{M}})}{\ln(L_0)} \tag{1}$$

where L_{M} represents likelihood for the model containing all variables and L_0 represents the likelihood with intercept only.

To identify local spatial clusters of cells of high-richness value of bird species we used G^* spatial statistics (Getis and Ord 1992). This technique allows the identification of spatial clusters of similar values that are high or low relative to the mean (Getis and Ord 1992, Nelson and Boots, 2009). Also, G statistics produces a Z value, used as diagnostic tool. High Z values represented spatial aggregation of high bird richness values whereas low Z values represented spatial aggregation of low bird richness values. Values greater than two were used to indicate spatial clusters of values that were extreme and high relative to the mean (Nelson and Boots, 2008). Additionally, we used Bonferroni tests to assess whether these values were statistically significant. Those significant cells were considered as hotspots of richness for bird species, hereafter high-value richness areas (hvra).

Finally, we superimposed the maps of hvra on the maps of SPAs and the combined PAs. Those cells without SPAs but with SAC/SCI cover were classified as partial gaps of bird species richness. Cells without any PA cover were considered total gaps. Complementary, we investigated the distribution of threatened bird species occurring in areas without SPA cover, by describing the spatial distribution of such species. All statistical analyses were performed in R (R Development Core Team, 2009), including its packages 'spdep' (Bivand et al., 2012) and 'pscl' (Jackman, 2012), and Geographic Resources Analysis Support System (GRASS GIS 6.4, Neteler et al. 2012).

3. Results

The spatial distribution of SPA and combined PAs showed similar patterns (Appendix A.1 and A.2). A high PAs cover was observed especially in the North (Finland) and Mediterranean area (Spain and France). About 10% of cells (166) remained without SPA cover (SPA gaps) and 0.8% (14) cells without combined PAs cover (combined PAs gaps). Most of them were located in Sweden, France and Finland.

The overall geographic distribution of bird species richness showed similar trends, with richness increasing eastwards. Considering all bird species, the richest cells were mostly located in Bulgaria (201 species), Poland (190 species), Lithuania (184 species) and the Czech Republic (181 species) (Fig. 1A). The highest richness cells of IBS were mostly located in Greece and Bulgaria, representing 66 and 60 bird species; whereas the lowest was found in United Kingdom, with 1 species (Fig. 1B).

Poisson regression models indicated that the relationship between bird spatial richness patterns and Natura 2000 protected areas (SPA and combined PA cover) were in general weak (Table 1). Similarly, the relationship between richness and the number of PAs was low (Table 1). In general, models explained very low variance of bird richness patterns. The regression coefficient of these models showed that the PA cover and the number of PAs were both positively correlated with bird richness.

A total of 248 (14.6%) hvra cells for bird species were observed (Fig. 2A). From these, 143 cells were hvra of all bird species richness and 189 cells were hvra of IBS richness. The congruence between hvra cells for all bird and IBS was moderate. From the 248