Are predators negative or positive predictors of farmland bird species community on a large geographical scale?

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ABSTRACT

Species distribution models (SDMs) are numerical tools that combine species occurrence/density or species richness with environmental data in order to predict particular species' distribution. In most cases only abiotic environmental parameters are used as predictors, while biotic interactions which control distribution of species and influence the goodness of fit of the SDM, such as predator–prey systems, have been broadly neglected. For this reason, we tested the usefulness of easy to detect predators, such as the Common Buzzard and the Common Raven, as positive and negative predictors, respectively, of farmland bird species richness. We analyzed factors affecting the density of both predators and farmland bird species using data from 958 1×1 km^2 study plots in Poland and a set of 22 environmental variables. Next, we also included these predators' densities as additional predictors of farmland bird species. Habitat and climatological predictors were aggregated using the Principal Components Analysis and then related to the Common Raven's and the Common Buzzard's densities as well as farmland bird species richness using General Additive Models. Finally, completed models were assessed according to information – theoretic criteria. Our results showed that all the analyzed groups occurred in open areas; the Common Buzzard and passerine bird species preferred traditional farmland, while the Common Raven reached its highest density in modern intensive farmland. Importantly, we documented a significant increase in the goodness of fit of SDMs for farmland bird species, having added the density of predators as negative (Common Raven) and positive (Common Buzzard) predictors. Consequently, our findings suggest that species' specific models can improve the predictive power of SDMs and can be used as an effective tool for predicting bird diversity with higher accuracy.

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1. Introduction

Biodiversity loss observed in recent years across Europe is probably one of the most widely documented patterns in conservation biology (Krebs et al., 1999; Donald et al., 2001; Benton, 2007). Generally linked to agriculture management, it spawned a large body of research on possible drivers, i.e. mechanization and agrochemicals, of the observed changes especially on farmland birds (Chamberlain and Fuller, 2000; Donald et al., 2001; Benton et al., 2002; Gregory et al., 2004; Newton, 2004; Donald et al., 2006; Wretenberg et al., 2006; Butler et al., 2010). However, the observed patterns of biodiversity change differ between regions, hampering our understanding of exact mechanisms driving the observed changes, especially at a large geographical scale (Fox, 2005; Wretenberg et al., 2006; Reif et al., 2008; Tryjanowski et al., 2011). Therefore, a study on a trans-regional scale is one of the key elements enhancing conservation strategies in the European Union as a whole (Sanderson et al., 2009). The most desirable data should be derived directly from field study, however, covering large areas solely by fieldwork is basically unrealistic (Spanhove et al., 2012), because data collection is time consuming, and hence costly. That is why conservationists pay a lot of attention to developing analytical tools, especially predictive modeling, which may indirectly estimate species density and/or richness at a large geographical scale.

Species distribution models (SDMs; e.g., Franklin, 2010; Kosicki and Chylarecki, 2012a,b; Morelli and Tryjanowski, 2014) are numerical tools based on the ecological niche concept that links

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observations of species occurrence/density or species richness with environmental variables. Generally, they are used to predict species distribution/density or species richness at a large geographical scale (Elith and Leathwick, 2009), but most importantly they show environmental suitability for species or target groups (Guisan et al., 2013). In many cases, data from the Geographic Information Systems (GIS) and also small scale habitat data are used as predictors, i.e. the Corine Land Cover, NDVI dataset, WordClim, topography as well as the distribution of vascular plants (e.g., Guisan and Zimmermann, 2000; Giordano et al., 2010; Kosicki and Chylarecki, 2012a,b). However, recent studies highlight that patterns of species distribution are not only a result of a complex interplay between environmental estimates, but also interactions between species themselves (Le Roux et al., 2013; Wisz et al., 2013; Morelli and Tryjanowski, 2014). In some cases, predator–prey relationships used as additional predictors significantly improved the goodness of fit of SDMs and made them more biologically realistic (Seoane et al., 2005; Carrascal et al., 2006; Aráujo and Luoto, 2007; Morozova et al., 2008; Schweiger et al., 2008, 2011; Heikkinen et al., 2007; Meier et al., 2010; Pellissier et al., 2012; Wisz et al., 2013). Still, despite extensive knowledge of relationships between species occurrence, this kind of information is rarely used in SDMs, especially in modeling species richness (Kissling et al., 2012; Wisz et al., 2013). Therefore, we decided to extend the usual approach and to analyze factors shaping distribution of farmland bird species, using not only environmental variables but also density of predatory birds considered as surrogates.

The effectiveness of surrogates is still debatable (Lindenmayer et al., 2002; Roberge and Angelstam, 2004; Kéry et al., 2007; Roth and Weber, 2008). The most severe criticism concerns the methodological approach, where indicators are defined on the basis of a simple positive correlation between potential surrogates and target species or a group of species, while the context of environmental preferences of species is often overlooked (Carroll et al., 2001). Thus, surrogates will be useful only if they have met objective criteria (Caro and O'Doherty, 1999), i.e. geographic range must be similar to target groups (Sebek et al., 2012); surrogates must respond to the same habitat variable as target groups (Murphy et al., 2011); they must be widely applicable in nature (Tryjanowski and Morelli, 2015); and should be capable of providing a continuous assessment independent of sample size. In addition, ideal surrogates should be quickly recognizable (Magierowski and Johnson, 2006) and their identification handled by non-experts (Sebek et al., 2012). Following these principles, we decided to use the Common Buzzard's and the Common Raven's densities as surrogates of farmland bird species richness in the open landscape of Poland. Both species are among most common and easily distinguishable large birds in the Palearctic (Cramp and Simmons, 1980). They are easy to detect during the breeding season because they often soar above farmland and their nests are relatively large and easy to spot. Although they are not taxonomically closely related, they are quite similar with regards to some aspects of their ecology. Both predators are associated with mixed open habitats where arable fields and meadows are interspersed with small forests, where these species are predators of many animals, e.g. mammals, reptiles and also birds. For these reasons, we expected that these predators' densities might correlate with farmland bird species richness. Additionally, predators' densities and farmland bird species diversity were also expected to vary, depending on different habitat types and/or other environmental aspects, e.g. climate, topography and vegetation. Bearing the above in mind, we developed two kinds of models for farmland bird species: the first based on the same environmental predictors as both predators, and the second one with the Common Raven's and the Common Buzzard's densities as additional variables. By comparing both models, i.e. with and without the predator's densities, the potential effect of their densities treated as

surrogates can be evaluated. So our analytical approach should indicate not only the relationship between environmental components and species diversity, but also show whether the predator's density reflects farmland bird species richness or not. In other words, we tested the usefulness of the two predatory species as surrogates of farmland bird species on a large geographical scale. Recent papers describing spatial patterns of farmland species richness in Poland (e.g., Kosicki and Chylarecki, 2012b) did not address the issue, as they did not examine surrogates among biotic predictors.

The aims of this study are to: (1) find possible relationships between diversity of farmland bird species and densities of the Common Buzzard and the Common Raven; (2) develop species distribution models of the Common Buzzard, the Common Raven and farmland bird species richness based on environmental predictors; and (3) develop a predictive model of farmland bird species richness, in which densities of both predators are used as additional predictors.

2. Materials and methods

2.1. Bird data

The predators' densities and farmland species richness data were derived from the Common Breeding Birds Monitoring Scheme (Chylarecki and Jawińska, 2007) and collected in Poland in years 2000–2013 in 958 1 km^2 grid cells (see Appendix A, Fig. S1). Survey plot squares had been chosen at random out of 311.664 1 km^2 squares covering the whole territory of Poland. In each breeding season each plot was surveyed twice. The first visit took place between 10 April and 15 May and the second between 16 May and 30 June. The bird census within each square consisted of two parallel 1 km transects along either an east–west or north–south axis. Each transect was divided into five 200 m sections, in which birds were noted within three distance categories (<25 m, 25–100 m, >100 m). Birds were noted perpendicular to the transect line. Each survey started between the dawn and 9 am and lasted for about 90 min. The surveys were carried out by volunteers, but regrettably many squares were not regularly monitored. During a ten-year period each square was inspected on average (±SD) in 6.5 ± 3.9 breeding seasons.

Only the 14 most common birds species were considered when determining the farmland bird species richness index (Kuczyński and Chylarecki, 2012). Most of them (11 species) are considered as the focal species (Gregory et al., 2007) (see Appendix A).

2.2. Environmental data

Various environmental data, expected to correlate with the Common Raven' and the Common Buzzard's densities as well as farmland species richness, were used as explanatory variables. These data were converted into GRASS GIS file format (Neteler and Mitasova, 2008) with the grid size of 1 km^2 and reprojected to the coordinate system EPSG4284 projection (http://spatialreference.org/ref/epsg/4284/).

Mean altitude and the difference between the highest and the lowest point (meters above sea level) data come from the Digital Evaluation Model (DEM) dataset (GTOPO30, resolution of 1 km^2), originally provided by the U.S. Geological Survey's EROS Data Center (Sioux Falls, South Dakota). Climate data were derived from the WorldClim database (www.worldclim.org), which is a set of global climate layers (climate grids) with spatial resolution of 1 km^2. When compared to previous large-scale climatological data, these data demonstrate the highest spatial resolution (Hijmans et al., 2005) and they have already been successfully used several times as a predictor for modeling animal distributions (e.g.,