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Congruence between breeding and wintering biodiversity hotspots: A case study in farmlands of Western Poland

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ABSTRACT

Farmland landscapes are recognized as important ecosystems, not only for their rich biodiversity but equally so for the human beings who live and work in these places. However, biodiversity varies among sites (spatial change) and among seasons (temporal change). In this work, we tested the hypothesis that bird diversity hotspots distribution for breeding is congruent with bird diversity hotspots for wintering season, focusing also the representation of protected areas for the conservation of local hotspots. We proposed a framework based on the use of species richness, functional diversity, and evolutionary distinctiveness to characterize avian communities.

Although our findings show that the spatial distribution of local bird hotspots differed slightly between seasons, the protected areas' representation was similar in both seasons. Protected areas covered 65% of the most important zones for breeding and 71% for the wintering season in the farmland studied. Functional diversity showed similar patterns as did bird species richness, but this measure can be most effective for highlighting differences on bird community composition. Evolutionary distinctiveness was less congruent with species richness and functional diversity, among seasons.

Our findings suggest that inter-seasonal spatial congruence of local hotspots can be considered as suitable areas upon which to concentrate greater conservation efforts. However, even considering the relative congruence of avian diversity metrics at a local spatial scale, simultaneous analysis of protected areas while inter-seasonally considering hotspots, can provide a more complete representation of ecosystems for assessing the conservation status and designating priority areas.

KEYWORDS

Avian communities; Evolutionary distinctiveness; Farmland; Protected areas; Seasonality; Spatial congruence

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INTRODUCTION

Identification and protection of biodiversity hotspots constitute one of the most important tools for conservation planning (Bellard et al., 2014; Midgley et al., 2002; Myers et al., 2000). For several decades, hotspots of richness, endemism, and rare species have been used in various environments as a tool to define the core zones and boundaries of protected areas networks (Barnard et al., 1998; Lascelles et al., 2012; Lombard, 1995), often while focusing selection on species occurrence and richness (Bonn and Gaston, 2005; Kati et al., 2004). The basic role of reserves is to separate elements of biodiversity from processes that threaten their existence in the wild (Margules and Pressey, 2000). Correspondingly, the monitoring of local hotspots within protected areas networks is a common

framework used to study the environmental health in determinate ecosystems. Monitoring protected areas is in fact a priority for conservation, and considerable efforts are allocated to their study and preservation (Lombard, 1995; Tellería et al., 2008). Considering that conservation resources should be used as efficiently as possible while maximizing maintenance of the most threatened areas (Murdoch et al., 2007; Tuví et al., 2011), the assessments of hotspots' spatial distribution could be used for systematic conservation planning as well as identification of locations of special importance for conservation.

The Natura 2000 Ecological Network comprises the current strategy for nature conservation implemented by the European Union Member States (Pellissier et al., 2013). This strategy is radically different in comparison with the previous protection system, because in Natura 2000 the aims are

twofold: to stop the biodiversity loss and also to maintain or recover the favourable nature conservation status while protecting natural habitat types, flora, and fauna (Grodzińska-Jurczak et al., 2012). In Poland, the initial steps to implement the Natura 2000 Ecological Network were taken during the late 1990s. Today, that network covers 19.8% of Polish territory. It includes 823 Special Areas of Conservation (SACs) and 144 Special Protection Areas (SPAs) for protecting some bird species (Grodzińska-Jurczak et al., 2012).

Notwithstanding this progress, the representation of protection offered by these reserves' networks needs to be monitored continuously (Tuvii et al., 2011). This is especially true in farmlands, the habitats within which are characterized by a simplification of the structural complexity due to the incidence of modern agricultural techniques, and which is likely greatly to diminish the biodiversity (Benton et al., 2002; Morelli et al., 2014; Ryszkowski et al., 2002; Stoate et al., 2009; Tscharntke et al., 2008). The effectiveness of these efforts may be hampered by the fact that the criteria often used to identify protected areas can be biased by several methodological issues. For example, the concept of local hotspots (rather frequently used in identifying areas that deserve to be protected) is commonly based on the species richness measured during a fixed period, sometimes repeated through several years. For bird species, the breeding season (from spring to early summer) is used as the main period for survey, because it coincides with the greater species richness present within an area and the detectability of species is heightened at that time due to the birds' territorialism. For these reasons, many studies directed to the establishment of priority conservation areas have focused exclusively on breeding species distribution (Herrando et al., 2009; O'Dea et al., 2006; Virkkala and Rajasarkka, 2007). At local scales too, the majority of papers are focused on just one season, typically that for breeding (Berg, 2002; Santana et al., 2014; Wuczyński et al., 2011) or winter (Kasprzykowski and Goławski, 2012; Tryjanowski, 1995). Only a few studies have dealt with winter species distribution in order to evaluate the effectiveness or representation of conservation reserves (Chitante and Meriggi, 2016; Gaston et al., 2008; Marfil-Daza et al., 2013). Then too, the conservation criteria currently applied in farmlands regarding protected areas are designed mainly with a view to the distribution of breeding birds while seasonal changes and shifts from wintering to breeding grounds are generally not taken into account. Potentially, therefore, important conservation criteria are neglected. In fact, the occurrence of species during breeding season provides only a partial overview of the environment, and a study on hotspots examines just a restricted spatial pattern of the biodiversity distribution. Because the wintering situation could be different, the hotspots could be mismatched if compared with the spring data.

Therefore, improved diversity measures are needed in order to assess the real diversity contained in a protected area. Today, it is widely recognized that not only the number of species but also the particular species present and their phenotypes can provide critical information for determining the na-

ture and strength of the relationships between species diversity and a range of ecological functions (Stuart-Smith et al., 2013). Indices quantifying functional diversity, for instance, are essential in understanding relationships between biodiversity, ecosystem functioning, and environmental constraints (Mouchet et al., 2010). Moreover, phylogenetic diversity – which means the total evolutionary history or phylogenetic branch lengths of all species in a community – has potential for quantifying biodiversity at the finest scale (Faith, 1994), and so this is now recognized as reflecting intrinsic conservation value (Frishkoff et al., 2014; Morelli et al., 2016).

We studied the patterns of bird diversity hotspots in agroecosystems across sites (spatial approach) and seasons (temporal approach) in order to understand how a spatio-temporal approach can help to most accurately capture the distribution of local hotspots of bird diversity. We also tested the hypothesis that a portion of the Polish protected areas within farmlands are equally effective containing both breeding and wintering local hotspots. To assess bird diversity, we applied a complementary set of diversity measures: species richness, functional diversity index, and phylogenetic diversity scores for each bird community. Finally, we endeavoured to determine the overlapping hotspot areas between breeding and wintering seasons.

1. METHODS

1.1. Study location and protected areas

The study was conducted in an agricultural landscape of Western Poland, near Odolanów (51°34'N, 17°40'E). This area was selected because it had already been a subject to previous studies (Hromada et al., 2002; Tryjanowski and Morelli, 2015). The study location (38,000 ha) is an extensively used agricultural landscape and comprises a mosaic of meadows and pastures (44%), arable fields (42%), midfield woodlots of different ages (6%), plus scattered trees and discontinuous linear habitats, mainly consisting of mixed rows of trees and shrubs (see details in Hromada et al. 2002). Protected areas in the study location occupy a total surface of 18,000 ha, or 47.3% of the overall location. The Polish protected areas are classified into two categories: grounds covered by the landscape park (*Dolina Baryczy*) and the areas protected by Natura 2000. The two protected area types partially overlap. For a more detailed explanation about the protection level of each kind of area, see Grodzińska-Jurczak et al. 2012.

1.2. Bird data collection

A total of 64 sampling sites in agricultural landscapes were visited at least two times per season during the breeding and wintering seasons in the year 2010. The year of study was divided into two seasons, following the phenology of bird species: i) breeding season (April–June 2010), and ii) wintering season (December 2009–February 2010). In our study, wintering bird community consisted mainly of resident species, but we also

included two overwintering migrants from northern Europe. The selection of the study area and sampling sites was based on the local knowledge of researchers involved in the project and trying to visit the same places visited during a previous study (Kwieciński et al., 2017).

Of the total, 44 sites (68.75%) were sampled within the protected areas, while 20 sites (31.25%) were sampled outside the protected areas. Sampling involved taking 5-minute point counts at each sample site, extending from half an hour after sunrise until 4.5 hours after sunrise. Counts were taken only during favourable weather conditions. Point counts provide highly reliable estimates of relative population density, and this is a standardized and practical method for comparing bird communities between different habitats and times (Bibby et al., 1992; Voříšek et al., 2010).

1.3. Biodiversity measures

Three measures of biodiversity were used to describe the bird communities at each sample site: bird species richness (BSR), functional diversity (FD), and community evolutionary distinctiveness (CED). Within each sample site, the species richness, which is a basic surrogate for ecological diversity (Magurran, 2004), was calculated as the maximum number of species observed, considering all visits. The average BSR was calculated for each season, considering all sample sites monitored in each season. An index of functional diversity was calculated for each bird community based on the species-trait approaches focused on the functional aspects of biodiversity. This provides an additional tool to complement the traditional taxonomic approach (Aubin et al., 2013; de Bello et al., 2010). In this study, FD was calculated using the avian niche traits provided by Pearman et al. (2014) on feeding ecology. This information was considered adequate for characterizing the bird communities, even if those authors had focused the bird description on the breeding season. The table with bird traits consists of 35 variables that describe the trophic niche of each bird species, including variables across 1) food type (14 variables), 2) behaviour's in acquiring food (9 variables), 3) substrate from which food is taken (9 variables) and 4) period of day during which a species forages actively (3 variables) (Pearman et al., 2014). Based upon these bird traits, we calculated the Petchey's functional diversity using the 'vegan', 'ade4', and 'picante' packages in R (Dray and Dufour, 2007; Kembel et al., 2010; Oksanen et al., 2016). Petchey's FD measures diversity by constructing a dendrogram of similarity among species of the community while considering the species traits (Petchey and Gaston, 2006, 2002).

Evolutionary distinctiveness (ED) score is a measure of the species uniqueness based on the phylogeny or evolutionary tree of species (Jetz et al., 2014). Phylogenetic diversity is estimated by summing the branch lengths of all species present in an assemblage, and then the ED score for each species is calculated by dividing the total phylogenetic diversity of a clade amongst its members (Faith, 1992). In this study, we used the ED scores of bird species available from www.edgeofexistence.org (EDGE of Existence, 2015). In order to characterize the ED

level for the bird community at each sample site, ED scores for all species present were summed; that sum was divided by the species richness, and thus, an averaged per site or community ED (CED) was obtained.

1.4. Hotspots classification

All sample sites were classified using a binary system: sites with higher values of BSR and FD for each season (values within the 75–100 percentile range) were classified as local hotspots (value = 1) and sites with lower values of BSR or FD (values within the 0–74 percentile range) were classified as non-hotspots (value = 0). The percentage of local hotspot within the protected areas was calculated. A comparison was made between local hotspot within the protected areas and outside the protected areas while taking into account the relative percentage of sample sites within versus outside those protected areas. The CED and average FD were used to compare the bird communities among protected versus unprotected areas and between seasons.

1.5. Statistical analysis

Because the data were not normally distributed, the Spearman's rank correlation coefficient was calculated for paired sample sites in order to assess the correlation between BSR and FD values for breeding and wintering seasons. Comparison of FD and CED between seasons was made using the Welch's paired *t*-test, and comparison between bird communities from protected and unprotected areas was performed using the Welch's two-sample *t*-test (Sokal and Rohlf, 1995). Temporal differences in the number of local hotspots within and outside the network of protected areas during the two seasons were compared using a chi-square test (Sokal and Rohlf, 1995).

We used the Mantel test to check for spatial autocorrelation of data (Mantel, 1967). This test evaluates the similarity between two matrices: one measuring ecological distance (BSR among sample sites) and one as the geographical distance among the sample sites (Legendre and Legendre, 2012). The Mantel statistic (r_m) is a measure of the correlation that results from the cross-product of the matrix elements after standardization; it lies between -1 and $+1$, and it behaves like a standard correlation coefficient (Legendre and Legendre, 2012). We used Monte Carlo permutations with 9999 randomizations in testing for significance (Oksanen et al., 2016).

Generalized linear mixed models were used to describe the relationships between BSR (response variable with Poisson error distribution), FD, CED (both modelled specifying a Gaussian distribution), and protected areas and seasons (modelled as predictor variables). Sample sites were added as random factors because they repeated during seasons. Models were fitted with the 'lme4' package in R (Bates et al., 2014) using the Akaike's information criterion for model selection (Burnham and Anderson, 2002).

A graphical exploration as to the spatial distribution of the local hotspots between seasons based on the distribution of BSR, FD, and CED values was carried out using inverse

distance weighting (IDW) for interpolation (Lu and Wong, 2008). Even if interpolation techniques are penalized due to the fact that landscape and environmental conditions can be dishomogeneous, IDW was considered suitable in the case study because it was applied in a relatively uniform landscape (e.g., extensive farmlands). In order to test the statistical significance of differences in spatial patterns of hotspots during breeding and wintering season, the Mantel test (Mantel, 1967) was performed using the values of BSR, FD, and CED, rearranged as a matrix of distances among pairwise sample sites. If a significant correlation existed, it indicated that the pattern of values was similar.

All statistical tests were performed using the R software (R Development Core Team, 2017).

2. RESULTS

2.1. Bird species richness, functional diversity, and evolutionary distinctiveness

During the field work, a total of 143 different bird species were observed. Among these, 98% of the species were classified as of Least Concern (LC) and only the remaining 2% belonged to the Near Threatened (NT) category of IUCN (BirdLife International, 2014). During the breeding season, 150 contacts of 134 species were collected, while during the wintering season, 228 contacts of 63 species were collected. The average BSR was higher during the breeding than wintering season, and a similar pattern was detected for functional diversity (FD) ($t = 7.67$, $df = 34$, p -values < 0.05 , Table 1). The BSR and FD were strongly and positively correlated in the two seasons ($r = 0.97$, $n = 50$ paired sites for breeding season, and $r = 0.94$, $n = 50$ paired sites for wintering seasons, all p -values < 0.05).

No differences were detected in FD between the avian communities within or outside the protected areas during the breeding season ($t = 0.23$, $df = 26.7$, p -values > 0.05), but those differences were significant during the wintering season. In winter, the avian community FD values were higher within the protected areas ($t = 2.85$, $df = 27.36$, p -values < 0.05 , Fig. 2).

The CED values were unrelated with BSR and FD in the two seasons (all p -values > 0.05). Bird communities in protected areas did not have significantly higher values on average for evolutionary distinctiveness than in the unprotected areas in either season ($t = 0.18$, $df = 16.14$, p -value = 0.86 and $t = -0.02$, $df = 13.05$, p -values > 0.05 for breeding and wintering, respectively). The CED values were, however, significantly higher during the breeding season ($t = 2.49$, $df = 34$, p -values < 0.05 , Table 1, Fig. 1). While BSR and FD were slightly higher in the protected than unprotected areas during wintering season, CED was slightly higher in the unprotected areas during this season (Table 1, Fig. 1).

2.2. Hotspots spatial mismatch between seasons

Similar proportions of local hotspots were located within the network of protected areas during the breeding and wintering

seasons. The percentage of local hotspot within the protected areas was 65% for breeding season and 71% for wintering season (Fig. 2), and the differences were not statistically significant ($\chi^2 = 0.068$, $df = 1$, p -value > 0.05). The total convergence of hotspots was near 24%, indicating that almost one-quarter of the breeding local hotspots were also hotspots during the wintering season (Fig. 2). Shown in Fig. 3 are the convergent areas obtained by using the intersect operator on IDW interpolation based on biodiversity measures between the breeding and wintering seasons. Despite a similar spatial pattern of biodiversity distribution between the seasons (Fig. 4), these similarities were not statistically significant (Mantel test, all p -values > 0.05 , based upon 9999 permutations).

The results of the generalized linear mixed models have shown that all the diversity measures studied have responded to inter-seasonal changes, with overall lower values during the wintering season (Table 2). Furthermore, the model on bird species richness confirmed that this measure is higher in the protected areas than the unprotected areas during winter (Fig. 1, Table 2). Table 2 presents all the parameter estimates, standard errors, and significance levels of GLMM performed using bird species richness, functional diversity, and community evolutionary distinctiveness as response variables, according to the interactions between season and protected/unprotected areas.

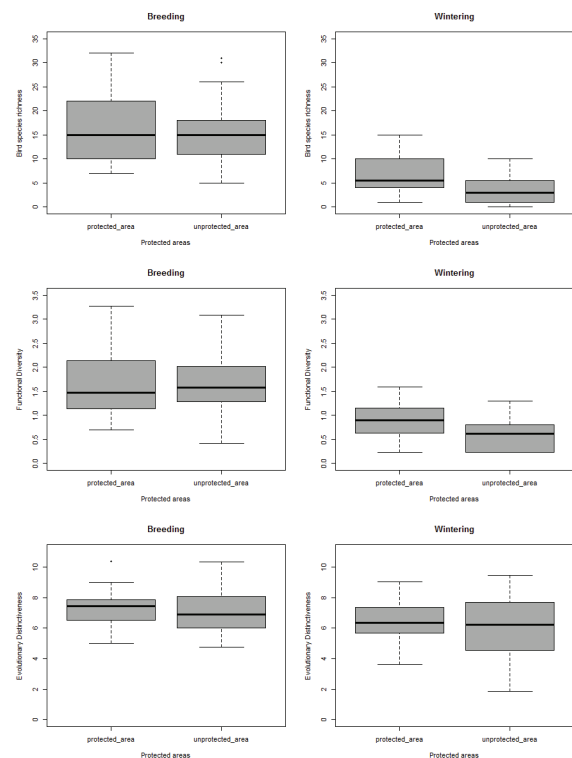


Figure 1. Comparison of bird species richness, functional diversity, and community evolutionary distinctiveness between breeding and wintering bird communities in protected and unprotected areas in farmlands of Western Poland. The boxplots show median (black bar in the middle of the grey rectangles), upper and lower quartiles, and extreme values.

3. DISCUSSION

Even if effective protection of local hotspots is considered as the fundamental aim of conservation policies (Rodrigues et al., 2004), the efficacy of protected areas could be different for breeding, wintering or migratory birds (Chiatante and Meriggi, 2016; Runge et al., 2015, 2014). In this study, we incorporated the data on inter-seasonal changes, to assess the congruence, and then to compare the relative representation of the protected areas for protecting local hotspots of species richness, functional diversity, and evolutionary distinctiveness of bird communities. From this point of view, our findings provide complementary information to a study previously published (Kwieciński et al., 2017), but focused mainly on a long term trend of avian communities than on the spatial mismatch analysis between inter-seasonal hotspots of avian diversity.

In some landscapes, hotspots of bird diversity can be associated to different land use characteristics for each season. For example, Chiatante and Meriggi 2016 found in South Italy that winter hotspots of bird diversity are associated with water bodies, shrublands and irrigated croplands, whilst breeding hotspots are associated with ecotonal areas, natural grasslands and not irrigated croplands, and with those results, it is possible to conclude that hotspots for breeding species cannot be used as a surrogate for the wintering species (Chiatante and Meriggi, 2016). In this work, we found more similar patterns between seasons, but remarkable differences with regard to the diversity metric used to characterize the bird community. Our results show that the pattern of bird diversity diverge slightly between seasons within intensively used farmlands in Poland, and also, that each avian diversity component can be incongruent with the others. Functional diversity pattern strongly followed the pattern of species richness, while evolutionary distinctiveness of bird communities was different. For this reason, we point out that conservation strategies need to ponder the multidimensional aspects of biodiversity (avian diversity in the specific

case of our study), considering the taxonomic and functional diversity components, as well as the phylogenetic components.

Additionally, the systematic conservation planning based on prioritization is currently the most influential paradigm to identify protection areas for conservation (Kukkala and Moilanen, 2013; Margules and Pressey, 2000); also, the inter-seasonal changes can play an important role (Chiatante and Meriggi, 2016). Then, our findings support the statement that the definition of protected areas have to not only use a prioritization approach, but also to take into account different biodiversity components, especially if the planning procedure is focused on a large spatial scale.

From a conservation planning viewpoint, we found that even if the patterns of biodiversity were different between seasons, the representation of protected areas was similar in the relative small study area. This is an interesting confirmation, considering that commonly protected areas are identified on the basis of only breeding data (Chiatante and Meriggi, 2016; O'Dea et al., 2006). Our findings support spatial and inter-seasonal representation of existing protected areas at local spatial scale in Poland, showing an inter-seasonal convergence of the local hotspots within the protected areas close to 24%. The reason for this congruence can be related to the fact that the main structure or features of farmlands remain similar between seasons, while only land use and weather parameters are changing (Tryjanowski, unpublished data). Considering the niche theory, bird species richness can be associated to some landscape metrics, surrogate of landscape heterogeneity (Kisel et al., 2011; Morelli et al., 2013; Schindler et al., 2013), and same structures offering protection or support during breeding season (for nesting, covering, or feeding) can offer also support during wintering season. In fact, other studies have already shown that farmland birds tend to overwinter in greater abundances in the same areas used by other species during the breeding season (Laiolo, 2005).

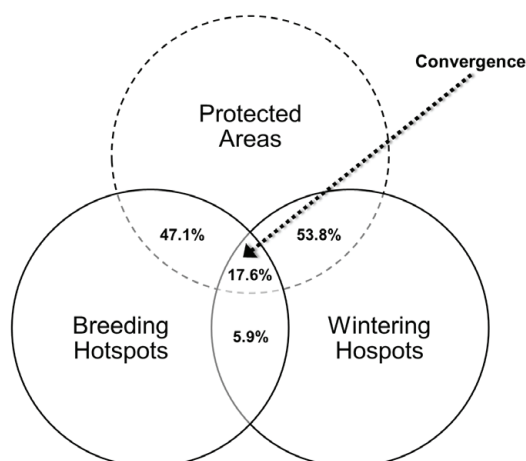


Figure 2. Venn diagram showing congruence in local hotspots within the protected areas between breeding and wintering seasons in the farmlands of Western Poland. The congruence is expressed as the percentage of sample sites and encompasses areas where breeding and wintering hotspots are shared.

Finally, the proposed methodology based on the spatial mismatch analysis can be even most adequate for studies at a large spatial scale. Inter-seasonal comparisons of local hotspots distribution on protected areas can uncover seasonal divergences in the level of protection. Convergent sites (zones where it is possible to find inter-seasonally hotspots) constitutes important conservation tools: including these zones into a protected areas network during ecological planning or setting conservation strategies can be much more efficient than to include divergent areas. Areas with high spatial congruence of local hotspots between seasons (as shown in Fig. 2) can be considered to compose the core of protected networks and then deserve greatest and most-concentrated conservation efforts.

To summarize, conservation strategies can benefit from the incorporation of inter-seasonal (i.e., temporal) comparisons, as well as to consider a multi-dimensional approach to biodiversity. An approach based upon only a single measure of biodiversity, such as species richness, could be biased because it cannot take into account the ecological role of species within the given communities (Safi et al., 2013). The complexity

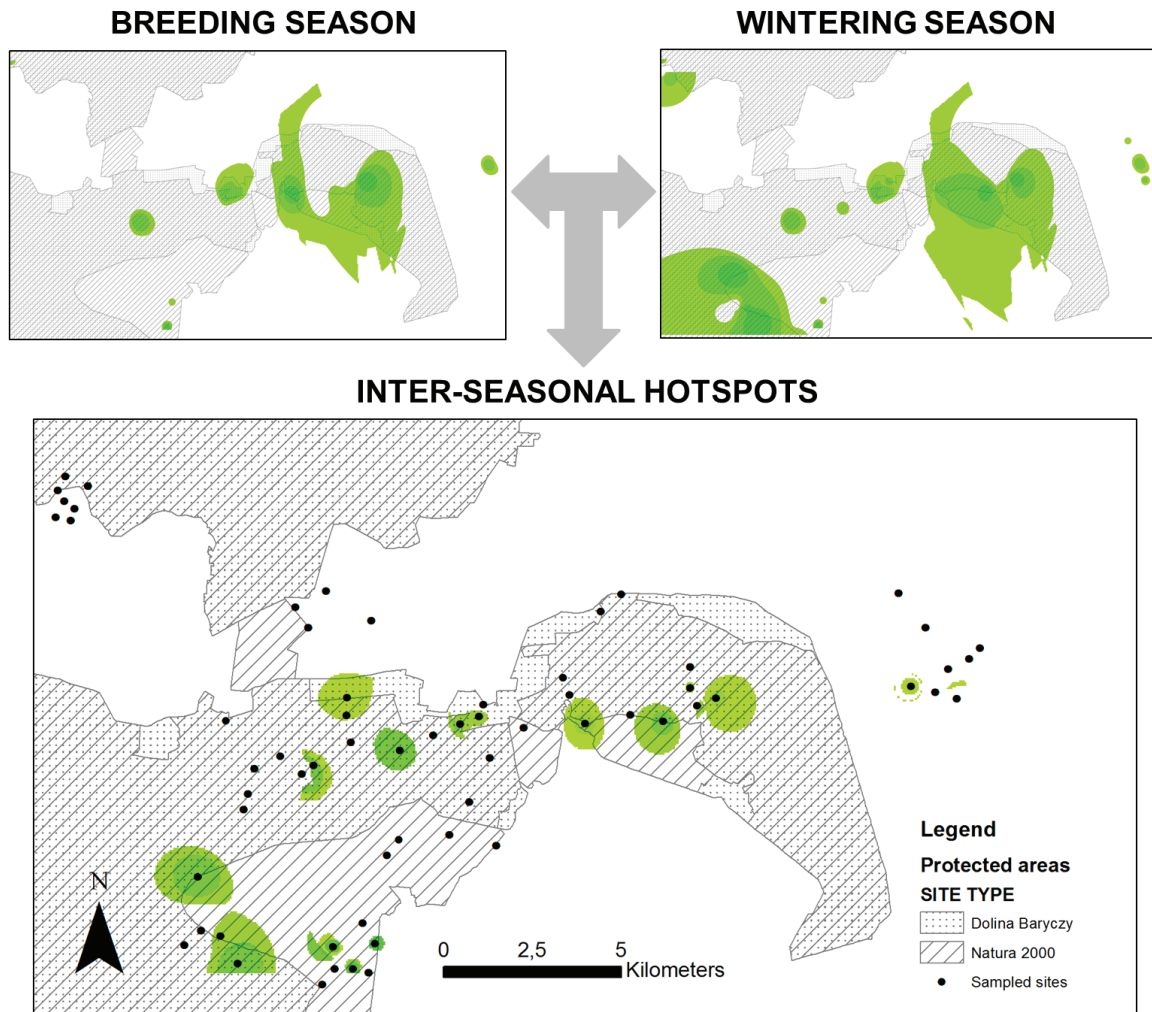


Figure 3. Spatial congruence of local hotspots of bird diversity (based on species richness and functional diversity) between breeding and wintering seasons within and outside protected areas in farmlands of Western Poland. Type of protected areas present in the study location: Dolina Baryczy and Natura 2000. The green areas are zones predicted as potential places for hotspots by applying the IDW interpolation on the basis of all local hotspots mapped.

of bird assemblages recorded during the breeding season was more underscored by the functional diversity than the taxonomic diversity approach, and indicates the need for conservation measures focused upon the community particularities, site by site. In the same way, also the phylogenetic diversity can be used to focus other particularities of bird communities, because species with higher ED scores account for large proportions of unique evolutionary history (Collen et al., 2011; Frishkoff et al., 2014) and then constitute particularly high conservation priorities.

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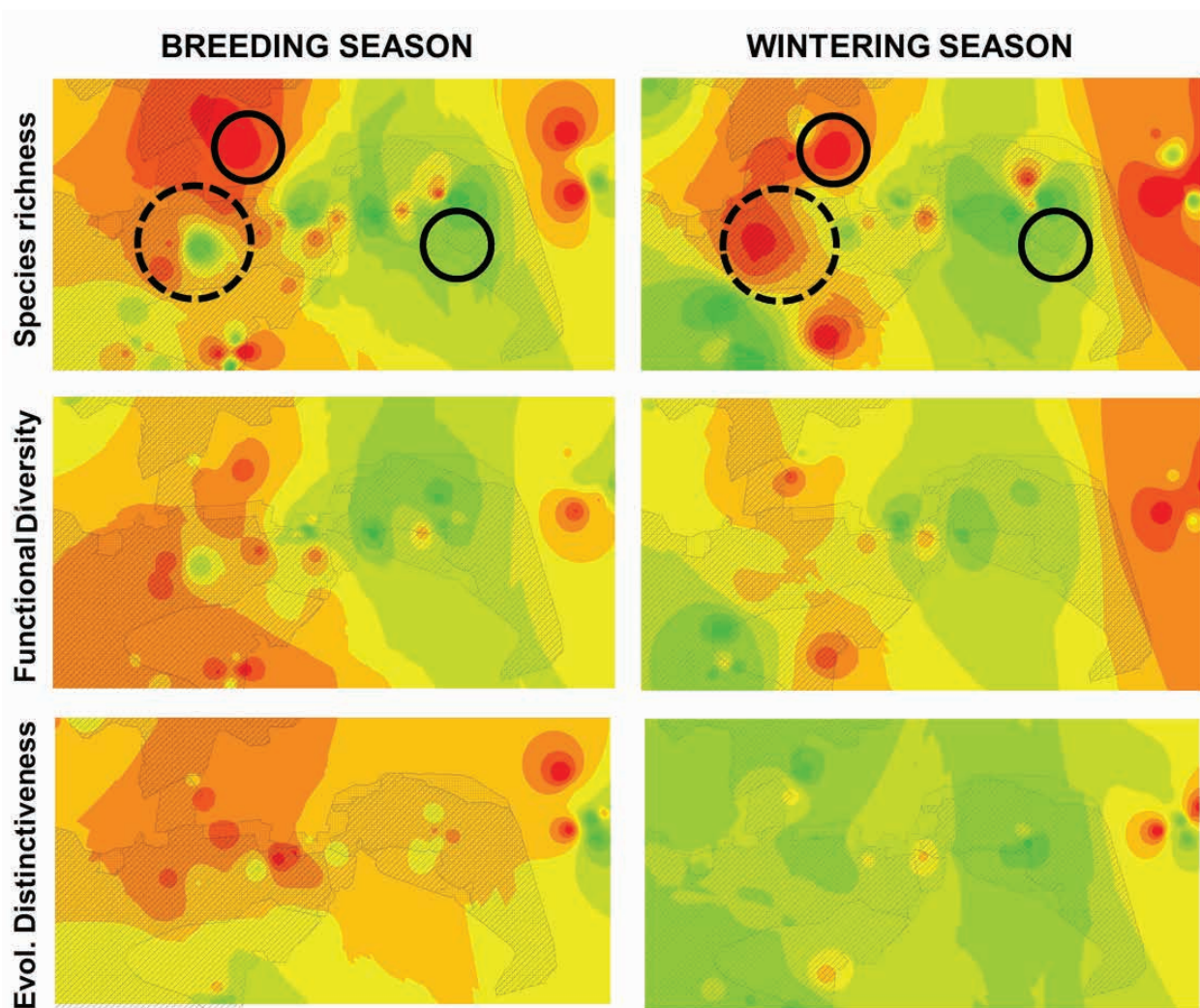


Figure 4. Spatial and temporal mismatch on biodiversity measures (bird species richness, functional diversity, and community evolutionary distinctiveness) within and outside protected areas in the farmlands of Western Poland. The measures of biodiversity were interpolated using IDW and presented in a coloured-scale from red (lowest values) to green (highest values). The circles highlight congruence areas (full line) and mismatch areas (dashed line) of species richness between seasons.

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