Bird communities after 37 years in a rural area of NW Spain

Comunidades de aves despois de 37 anos nunha zona rural do noroeste de España

Comunidades de aves después de 37 años en una zona rural del noroeste de España

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Abstract

In a globalized world, changes in human activities are negatively affecting biodiversity at different scales. Long-term monitoring of bird communities can inform about changes in biodiversity over time. We explored how bird species richness, and abundance changed after a 37-year period at 5 sites in O Courel Mountains, a well conserved region of NW Spain. We also analyzed the abundance changes over time in the 15 most abundant species and whether these changes relate to the phenotypes of these species. Repeated bird surveys were performed in the same locations of five different sites in 1977 and 2014. Our results showed species richness and overall bird abundance did not change after 37 years within the five studied sites. Although, within species analyses showed 8 species changed their abundances. Overall, *Cyanistes caeruleus, Garrulus glandarius, Parus major, Prunella modularis* and *Sylvia atricapilla* increased their abundances and *Erithacus rubecula, Phylloscopus ibericus*, and *Troglodytes troglodytes* decreased over time. We did not find any relationship between the change in species abundances and bird phenotypes. This study shows that, despite the specific changes in the abundance of eight species over nearly four decades, overall bird species richness and abundance may be maintained in well preserved natural areas.

Keywords: bird diversity; long-term diversity changes; bird traits; well preserved areas.

INTRODUCTION

Birds are excellent biodiversity indicators because their population trends are affected by many ecological factors, such as the niche breadth (SEOANE, LAIOLO, & OBESO, 2017) and the climatic niche (JIGUET ET AL., 2010). They are very sensitive to environmental changes (BLAIR, 1999; FULLER ET AL., 1995; RUSSO, 2007), although sensitivity differs among species (MCGILL ET AL., 2015; SIRAMI, ET AL., 2008). But also birds constitute a conspicuous and cosmopolite animal group generally easy to sample (ESCANDELL, 2013). Due to these reasons, birds are commonly used as model species in long-term monitoring studies of diversity changes (ALLEN ET AL., 2019; PARODY ET AL., 2001; SIRAMI ET AL., 2008) or population trends (ŞEKERCIOĞLU ET AL., 2019; TRABA & MORALES, 2019).

Human-induced environmental changes are impacting biodiversity (BOWLER ET AL., 2020; JETZ ET AL., 2007; KERR & CURRIE, 1995; SHIVANNA, 2020), such as bird species richness and abundance (DA SILVEIRA ET AL., 2016; FONDERFLICK ET AL., 2013; REDLICH ET AL., 2018). For example, many western humanized areas have seen a gradual rural abandonment of traditional agriculture throughout the 20th century (BEILIN ET AL., 2014; CORBELLE-RICO ET AL., 2012; MACDONALD ET AL., 2000; REGOS ET AL., 2016), while others have experienced the process of industrial agricultural intensification (DONALD ET AL., 2001; GAO ET AL., 2019). As a consequence, in both cases, biodiversity levels might decrease as has already been observed in plant communities in different regions of Europe (BUHK ET AL., 2017; FLOHRE ET AL., 2011; GUITIÁN ET AL., 2012; SIRAMI ET AL., 2007) but also in bird communities (BATÁRY ET AL., 2018; DONALD ET AL., 2001; FLOHRE ET AL., 2011; FULLER ET AL., 2007; GUERRERO ET AL., 2012; SALAVERRI ET AL., 2019; SIRAMI ET AL., 2008).

Over the last 50 years, rural Europe, and within it, the NW of the Iberian Peninsula, have undergone a strong process of rural abandonment. Within the natural region of northwestern Spain, O Courel (42° 34′ 59.99″ N, 7° 10′ 0.01″ W; 21,020 ha), the number of inhabitants was reduced (-60%) and with it, the livestock (-80%) and number of farmlands (-36%) decreased as well (LÓPEZ-BAO ET AL., 2015; MUNILLA ET AL., 2008). All these changes have modified vegetation patterns favoring woodland areas (LÓPEZ-BAO ET AL., 2015; MUNILLA ET AL., 2008), with an associated loss of bird diversity (SALAVERRI ET AL., 2019) which may be linked to a landscape homogenization (BUHK ET AL., 2017; SUÁREZ-SEOANE ET AL., 2002).

However, within O Courel region, areas which have not been cultivated remained stable, thus a vast majority of the region has not locally changed (VALERO ET AL., 2019). We do not know whether and how bird richness and abundance may have changed in the well-preserved areas of this region after a 37-year period. Analyzing changes in the richness and abundance of bird communities after several decades in well preserved plots in NW Iberia would help us understanding bird diversity trends at undisturbed sites, i.e. which have not undergone abandonment or industrialization.

We investigated changes in bird diversity and species trends after a long-term period in different habitats which have remained well preserved within O Courel region. Here, we assessed changes in overall bird species richness and abundance within five sites (two chestnut woodlands, a montane forest, a holm oak forest and a heathland) after 37 years, using data obtained from bird surveys performed in the same locations with the same methodology in July 1977 and July 2014. Bird populations might show different trends over time, and this could be related to their specific traits (ALLEN ET AL., 2019; FONDERFLICK ET AL., 2013; LEHIKOINEN ET AL., 2019; MORELLI, ET AL., 2020; SIRAMI ET AL., 2008). Thus, we additionally analyzed whether species phenotypes are related to the abundance trends of the

15 most abundant species overall in this area. We hypothesized that (*i*) the overall number of species and bird abundance varied after a 37-year period, (*ii*) and these changes may differ among sites, and (*iii*) changes in species abundances may be explained by bird phenotypic traits.

MATERIALS AND METHODS

Study area

The study was performed in O Courel Mountains (Galicia, NW Spain), mostly located within the municipality of Folgoso de Courel (Lugo: 42° 35' 20" N -7° 11' 43" W; 193 km^2), and part of the EU Natura 2000 network included in the "Ancares-Courel" Site of Community Importance (Nat-2000 Site Code ES1120001). Annual rainfall exceeds 1,500 mm, snow warnings are probable between November and April, and the annual average temperature oscillates between 8 and 10ºC, although it can even reach 23ºC (GUITIÁN ET AL., 2004). About 750 species of higher plants are present in this 21,020-ha region, as well as, rare or very rare plant species in Galicia (GUITIÁN, 2006). One of the most remarkable vegetal units are the heathlands covering 70% of the total surface, the common hawthorn woodlands (*Crataegus monogyna*) over the limestone outcrops; the montane mixed forests mainly composed by Pyrenean oaks (*Quercus pyrenaica*) and Holm oaks (*Quercus rotundifolia* Lam.) occupying 20% of the total area; but also the chestnuts woodlands (*Castanea sativa*). Furthermore, this region is home to 114 bird species (GUITIÁN ET AL., 2004; MUNILLA ET AL., 2008), and it is also important to mention the secular human presence in this area. The most notable human land uses were croplands on the less steep slopes, logging, and grazing activities in the scrubland areas (GUITIÁN ET AL., 2004).

We selected 5 sites belonging to 4 habitats for this study (three different leaf deciduous forests and a heathland), mostly located in the Moreda valley, with the exception of the heathland in the Ferreirós valley: (1) Devesa da Rogueira (hereinafter montane forest) is a montane mixed forest (900 - 1,400 m.a.s.l.) with a dense undergrowth (*Erica arborea* and *Vaccinium myrtillus)* and a great tree diversity (*Fagus sylvatica, Quercus petraea, Sorbus aucuparia* and *Taxus baccata*; GUITIÁN ET AL., 2004). (2) Moreda's holm oak forest (from now on, holm oak forest) is dominated by *Quercus ilex* subsp*. rotundifolia L.* on a limestone substrate (800 - 900 m.a.s.l.) and accompanying *Quercus pyrenaica* and *Crataegus monogyna* tree species. (3) De Lomba's heathland (hereinafter, heathland) is mainly composed of *Erica australis* and *Genista tridentata*, growing on skeletal soil (1,200 - 1,400 m.a.s.l.) and forming very low but dense heaths due to consecutive fires. (4) Fuente Parada's chestnut woodland and (5) Moreda's chestnut woodland (hereinafter) are located on a valley floor slope (approximately 900 m.a.s.l.), primarily composed of *Castanea sativa* trees (see Table SIa, for more site details in Supplementary materials section).

Bird surveys

This study used bird survey data collected on July 1977 (BAS ET AL., 1978) and July 2014, using an identical methodology in the five locations (Data S1 in Supplementary materials section). The transects were surveyed in 1977 (3-8 times) and in 2014 (twice) following the same itinerary and walking the same distance (montane forest: 500 m; Holm oak forest: 530 m; heathland: 615 m; Parada's chestnut woodland: 330 m; Moreda's chestnut woodland: 360

m) with the exception of the holm oak forest since the original trail disappeared and an alternative route (156 m longer) was performed in the same forest plot in 2014 (Table SIb in Supplementary materials section). During each survey, all the individuals observed and heard within a 25-m band on each side of a finish transect were recorded maintaining a constant walking speed (JÄRVINEN & VÄISÄNEN, 1976). All the surveys were performed by expert ornithologists (José Guitián in 1977 and jointly Luis Salaverri in 2014) early in the morning and under windless and rainless weather conditions.

Bird traits

Bird phenotypic data were extracted from the "*Life-history characteristics of European birds*" open-access dataset (STORCHOVÁ & HOŘÁK, 2018) and available at *Dryad*: https://datadryad.org/stash/dataset/doi:10.5061/dryad.n6k3n. We selected 27 numeric trait variables with complete cases for all the 15 most abundant species in our study (*Cyanistes caeruleus, Erithacus rubecula, Fringilla coelebs, Garrulus glandarius, Phylloscopus ibericus, Parus major, Prunella modularis, Periparus ater, Regulus ignicapilla, Sylvia atricapilla, Sitta europaea, Serinus serinus, Sylvia undata, Turdus merula, Troglodytes troglodytes*). The phenotypic traits included were the mean bird length (cm); the mean wing length (mm), the mean tail length (mm), the mean bill length (mm), the mean tarsus length (mm), the mean weight during breeding (g), and the corresponding means of all these traits by sex. With regard to the reproductive traits, we considered the minimum, the maximum and the mean of clutch size (no. of eggs), the mean brood size per year (as the average no. of broods per breeding season), the mean length and mean width of the eggs (mm), the mean egg mass (g), the incubation period (as the average egg incubation period, days), the fledging period (as the average age of youngs when fledgling, days), the feeding independence (as the average age of youngs when being independent of parental feeding, days) and the age of first breeding (as the average age of first breeding event, years).

Statistical analyses

Changes in the number of species between years and among sites, were analyzed by a generalized linear model (GLM) where the response variable was the total number of bird species observed per site and year (n= 10), fitted to a normal error distribution with an identity-link function. Overall bird abundance differences between years and among sites were also analyzed by a generalized linear model (GLM) where the response variable was the sum of individuals recorded per site and year (n=10), corrected by the number of surveys (see Table SIb in Supplementary materials section) fitted to a normal error distribution with an identity-link function. In both models, year (1977 and 2014) and site (montane forest, holm oak forest, heathland, Parada's and Moreda's chestnut woodlands) were included as fixed effects. This approach allows us to analyze the global variation in the number of species and bird abundance between sites and between years (the objective of our study), and not only the variability of bird richness and abundance per site, in which case we would only have one annual replicate per site, both for overall species richness and bird abundance. In addition, number of species and birds per survey was low and not representative of each site (Supplementary Data S1). Thus, we aggregated richness and abundance data as the survey sum of species and individuals per site and year. This is why the interaction between site and year factors was not included in both models.

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Considering the 15 most abundant bird species (i.e.10 or more individuals recorded; Table II, Fig. 1), we analyzed the abundance change between 1977-2014 and among the five study sites by constructing an independent generalized linear model (GLM) for each species, in which the response variable was the sum of individuals observed per site and year, corrected by the number of surveys (Table SIb in Supplementary materials section), fitted to a normal error distribution with an identity-link function and including the year and site as fixed effects.

For the analysis of the relationship between abundance changes and bird phenotypes, we first created a variable at the species level with three categories for the abundance change factor accordingly to the sign of the estimated year effect ("+": species with statistically significant increase in abundance, "-": species with statistically significant decrease in abundance, "ns": species with non-significant change in abundance) based on the results of the per species abundance analysis explained above. Second, we selected 27 numeric avian phenotypic traits from *Dryad* open-source dataset (STORCHOVÁ & HOŘÁK, 2018; see above bird traits sub-section for more details) to perform a Principal Component Analysis (PCA) for dimensional reduction. We extracted three Principal Components, with initial eigenvalues from the matrix of variance above 1.0 and which explained a total of 91.66% variance of 27 phenotypic traits among our 15 more abundant species (PC1: 72.33%; PC2: 15.38%; PC3: 3.95%). PC factor loadings were included in the Supplementary materials section (see Table SII).

Change in abundance per species as coded above (increase, decrease and non-significant change) in function of bird phenotypic traits was analyzed by means of a generalized linear model (GLM) in which the response variable was the factorial abundance change (three levels: increase in five species, decrease in three species, non-significant change in seven species) per species (n= 15), fitted to a multinomial error distribution with a log-accumulated link function (the total change in species abundance was analyzed in a similar manner and gave equivalent results, not shown). The scores of three Principal Components extracted from PCA were included as explanatory covariates (analyses of individual phenotypic traits were additionally tested and gave equivalent results, not shown).

All analyses were performed using the SPSS for Windows, version 25.0 (IBM CORP. 2017). Error distribution, link function and model's structure were chosen by means of the AICc criterion starting with saturated models (BURNHAM & ANDERSON, 2004).

RESULTS

Overall, 392 individuals of 31 bird species were recorded.

The number of bird species varied among sites but did not change overall from 1977 to 2014 (Table I, Fig. S1a). The heathland was the site with the lowest specific richness (6 species in total for both years). Similarly, the overall abundance of birds (sum of individuals per site and year corrected by the number of surveys) has not changed after the 37-year period although it differed among sites (Table I, Fig. S1b), being the heathland the site with lower bird abundance (8 birds in total for both years).

Table I. GLMs results for richness (total no. of species observed per site and year) and abundance (sum of birds observed per site and year, corrected by the corresponding no. of surveys) variation in function of the year (1977, 2014) and the site (Paradas's chestnut woodland, Moreda's chestnut woodland, heathland, holm oak forest, and montane forest) factors included as fixed effects into the models (n = 10). Marked in bold are the statistically significant effects.

| Response variable	Fixed effects	Wald Chi-square	d.f.	*P-value*
Richness (no. of species)	Year	1.434	1	0.231
	Site	19.242	4	**0.001**
Abundance (no. of individuals)	Year	0.802	1	0.370
	Site	19.156	4	**0.001**

Among the 15 more abundant species (i.e. more than 10 individuals observed in both years), only eight species showed a change in their abundance over time and 13 species differed in their abundance among sites (Table II). In particular, the abundance of *Cyanistes caeruleus, Garrulus glandarius, Parus major, Prunella modularis* and *Sylvia atricapilla* increased between 1977-2014, and *Erithacus rubecula, Phylloscopus ibericus*, and *Troglodytes troglodytes* decreased in their abundances after the same 37-year period (Table II, Fig. 1). Among the seven species that did not differ in abundance between years: *Fringilla coelebs, Periparus ater, Regulus ignicapilla, Sylvia undata* and *Turdus merula* showed differences in the number of individuals detected per species among sites, as did the 8 species that varied in abundance over time (Table II, Fig. 1).

Table II. GLM results for species abundance (sum of individuals observed per site and year, corrected by the no. of surveys) variation in function of the year (1977, 2014) and the site (Paradas's chestnut woodland, Moreda's chestnut woodland, heathland, holm oak forest, and montane forest) included as fixed effects in the independent models performed for the 15 most abundant species, i.e. 10 or more individuals (n = 10). We marked in bold the statistically significant effects, and specified the sign of the significant changes between years ("+": increase; "-": decrease, "ns": non-significant change).

Response variable		Species	Fixed effects	Wald Chi-square	d.f.	P-value	Change
Abundance (no. of individuals)		*C. caeruleus*	**Year**	5.330	1	**0.021**	+
			Site	26.408	4	**<0.001**	
		E. rubecula	**Year**	5.358	1	**0.021**	-
			Site	225.432	4	**<0.001**	
		F. coelebs	Year	0.357	1	0.550	**ns**
			Site	14.988	4	**0.005**	
		G. glandarius	**Year**	24.323	1	**<0.001**	+
			Site	223.990	4	**<0.001**	
		P. ibericus	**Year**	6.265	1	**0.012**	-
			Site	10.000	4	**0.040**	
		P. major	**Year**	18.045	1	**<0.001**	+
			Site	13.068	4	**0.011**	
		P. modularis	**Year**	10.808	1	**0.001**	+
			Site	31.557	4	**<0.001**	

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| Response variable	Species	Fixed effects	Wald Chi-square	d.f.	P-value	Change
	P. ater	Year	0.908	1	0.341	**ns**
		Site	14.571	4	**0.006**	
	R. ignicapilla	Year	3.623	1	0.057	**ns**
		Site	24.371	4	**<0.001**	
	S. atricapilla	**Year**	6.552	1	**0.010**	+
		Site	38.620	4	**<0.001**	
	S. europaea	Year	2.071	1	0.150	**ns**
		Site	9.142	4	0.058	
	S. serinus	Year	0.000	1	0.986	**ns**
		Site	8.349	4	0.080	
	S. undata	Year	2.500	1	0.114	**ns**
		Site	20.408	4	**<0.001**	
	T. merula	Year	0.873	1	0.350	**ns**
		Site	11.695	4	**0.020**	
	T. troglodytes	**Year**	12.59	1	**<0.001**	-
		Site	13.59	4	**0.009**	

Figure 1. Change in species abundance (sum of individuals per site and year, corrected by the number of surveys) of the 15 more abundant species (i.e. ≥ 10 individuals observed overall) by site: montane forest (light green-colored bars), holm oak forest (yellow-colored bars), heathland (dark green-colored bars), Moreda's chestnut woodland (red brown-colored bars) and Parada's chestnut woodland (brown-colored bars).
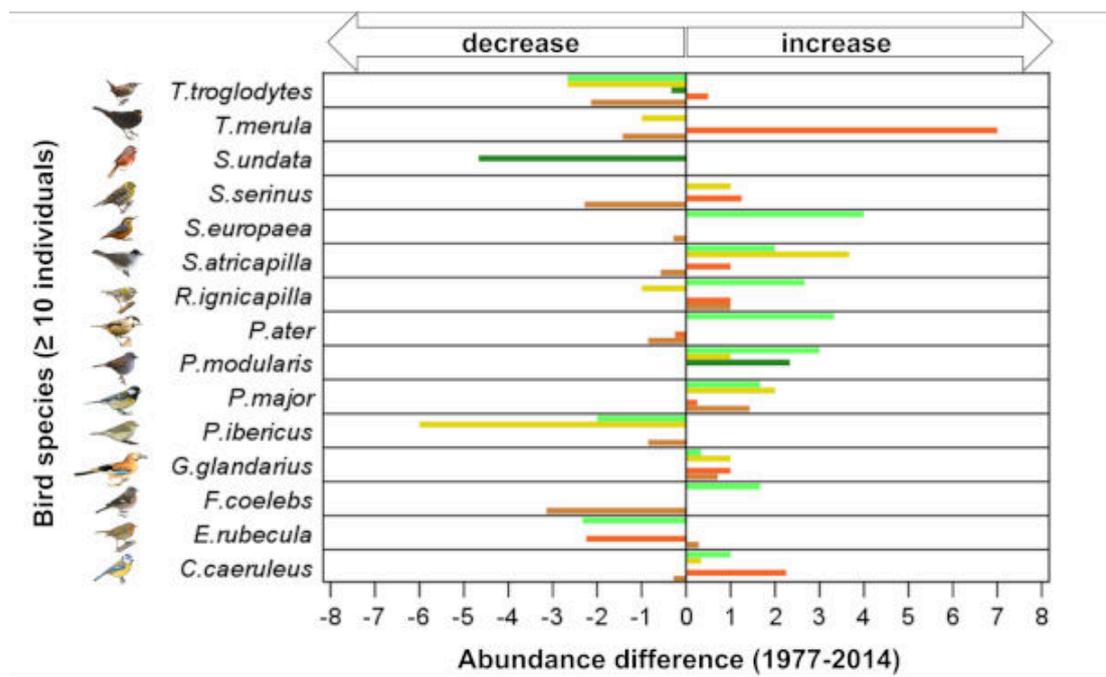
With regard to bird traits analysis, we did not find any relationship between the phenotypes of bird species (measured by PCA from the phenotypic space using 27 traits, Table

SII in Supplementary section) and the specific change in species abundance over 37 years for the 15 more abundant species (Table SIII, Fig. 2).

Figure 2. PC2 factor (15.38 % of variance explained) in function of PC1 factor (72.33 % of variance explained) extracted from PCA for phenotypic traits variables reduction (n= 15 species), according to the factorial abundance change (green dots: increasing species, red dots: decreasing species, blue dots: species with non-significant change).
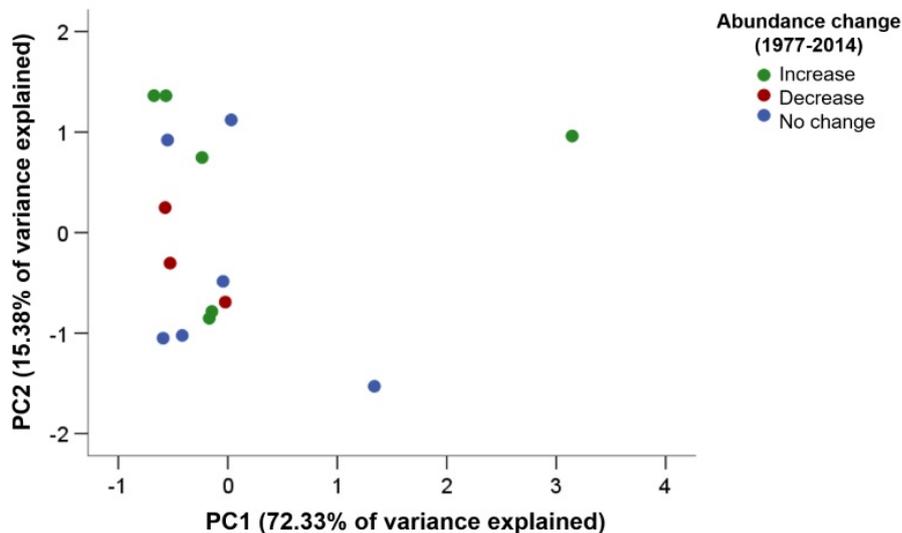
DISCUSSION

The overall number of bird species and individuals did not change after 37 years, in well-preserved areas from NW Spain (O Courel mountains) but we found specific changes in abundance of 8 of 15 most abundant species. These species specific trends may depend on their characteristics, their preferences for a certain land cover, their migration patterns or their biogeographical origin (SUÁREZ-SEOANE ET AL., 2002). For example, species traits may determine their level of success in particular habitats, where certain level of specialization is required for breeding and surviving (ALLEN ET AL., 2019; COETZEE & CHOWN, 2016; LEHIKOINEN ET AL., 2019). However, we did not find a relationship between species traits and abundance change in 15 most abundant bird species after 37 years, maybe due to the lack of sufficient phenotypic variation among these 15 species compared here.

We found differences in species richness and overall bird abundance among sites, being the heathland the site with the lowest number of species and abundance compared to the other sites. These differences observed among sites may be linked to differences in floristic composition and vegetation structure (DÍAZ, 2006; GUITIÁN ET AL., 2004; ROSENVALD ET AL., 2011), as well as, land cover (DA SILVEIRA ET AL., 2016). Thus, the higher number of species observed corresponds to mature deciduous forests (i.e. with a more diverse plant community and complex vegetation structure): Moreda's (20 species in total) and Parada's (19 species) chestnut woodlands, the montane forest (17 species overall), and the holm oak forest (14 species in total), but the lowest species numbers was found in the heathland (6 species overall), the site with lower plant diversity and more simple vegetation structure. However, bird species numbers found in our mature deciduous forests were rather lower than those found in other NW Iberian forests (30-37 species; BAS ET AL., 2018; CALVIÑO-CANCELA, 2013; GODED ET AL., 2019), which may be explained by altitudinal differences with regard to our study sites, that have already accounted for a decrease in bird species at higher

elevations (SALAVERRI ET AL., 2019), specially forest-dwelling species (TELLERÍA, 2019), but also by the landscape structure, in particular when considering the surrounding areas (FONDERFLICK ET AL., 2013). Thus, marked habitat differences among sites may explain the reduced number of bird species and abundance found in the heathland.

Moreover, the greater numbers of birds (as the sum of individuals per site and year corrected by the number of surveys) were found in the Moreda's chestnut woodland (28 birds in total for both years), montane forest (27 birds in total), and the holm oak forest (23 birds in total), and these numbers are rather lower than those observed in the already mentioned NW Iberian forests (60-140 total birds; BAS ET AL., 2018; CALVIÑO-CANCELA, 2013; GODED ET AL., 2019). If we compare bird abundance among study sites, our results may suggest that mature deciduous forests could be acting as bird diversity reservoirs due to a possible landscape homogenization of the surrounding plots (BRANDT ET AL., 2013), as a consequence of the ongoing farmland abandonment process (HERZON ET AL., 2014; SALAVERRI ET AL., 2019; VERHULST ET AL., 2004), but also the increase of woodland areas in this region (LÓPEZ-BAO ET AL., 2015; MUNILLA ET AL., 2008). These results may be supported by the fact that O Courel still maintains well preserved areas given the landscape heterogeneity provided by a mosaic of large patches, mainly dominated by leaf deciduous forests and scrublands (VALERO ET AL., 2019).

Therefore, the bird richness and abundance remained stable after 37 years at the study sites in O Courel Mountains, despite the specific changes in species trends of 8 most abundant species found within our study area. Although we were not able to analyze the effect of the year*site interaction (given the level of our analysis), it seems that these eight species specific trends might differ when we separate the change in species abundance by site (Fig. 1). One possible explanation to the specific changes in species abundance is the habitat preference of these species (GARCÍA ET AL., 2014). The forest-dwelling species (*Cyanistes caeruleus, Garrulus glandarius,* and *Parus major*) showed a generalized increase, which is consistent with the increased area occupied by forest in this well preserved region over the study period (LÓPEZ-BAO ET AL., 2015; MUNILLA ET AL., 2008). In contrast, bird species highly associated with the underbrush (such as *Prunella modularis, Sylvia atricapilla,* and *Troglodytes troglodytes*) have increased in the Moreda's chestnut forest, the montane forest and the holm oak forest, which could indicate that the shrub substrate has increased in these deciduous forests. Surprisingly, *Phylloscopus ibericus* consistently decreased in all the study sites, which might be explained by the relevant population fluctuations of trans-Saharan migratory species observed (PAYEVSKY, 2006). Lastly, the general declined observed in *Erithacus rubecula* and *Troglodytes troglodytes* (excepting at the Moredas's chestnut woodland), but also the site differences observed in other species with no changes over time (*Fringilla coelebs, Periparus ater, Regulus ignicapilla, Sylvia undata* and *Turdus merula*) are difficult to interpret, partly due to site-specific factors that could be acting at each site and promoting different dynamics of species population trends.

Finally, the absence of a significant effect of species phenotypic traits on the change in abundance experienced by the 15 most abundant species can be explained by the fact that these 15 species did not differ enough from each other (in the phenotypical space studied with 27 avian traits, which were mainly body size and breeding strategy) to detect a relationship of temporal patterns in species abundance and bird phenotypic traits. This result might suggest that different bird traits to that included in our species phenotypes analysis, could explain specific changes observed in our 15 species over time, such as the habitat preference or breeding habitat specialization (MORELLI ET AL., 2020), but also migration

distance (JIGUET ET AL., 2010; SIRAMI ET AL., 2008) or even biogeographical origin (SUÁREZ-SEOANE ET AL., 2002).

CONCLUSIONS

To conclude, our study shows no changes in bird richness and overall bird abundance after 37 years in a well conserved mountain area of NW Iberia (O Courel) and finds changes in species specific trends (increasing trends in 5 from the 15 more abundant species, mainly forest-dwelling species, and decreasing trends in 3 species) which are unrelated to the species phenotypic traits. Our results indicate that bird communities in this well conserved region are maintaining their levels of overall diversity, despite possible site-specific shifts in species abundances. Further investigations in well preserved areas long-term linked to human presence will be relevant to understand the rate of change in biodiversity at local scales in the context of a globalized world.

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Supplementary Materials

Figure S1. GLMs results for the variation of (a) species richness (total no. of species) and (b) abundance (sum of individuals corrected by the nº of surveys) per site and year. No significant changes were found between years, despite the significant global differences among sites (a) heathland: p-value<0.010; (b) heathland: p-value<0.001).

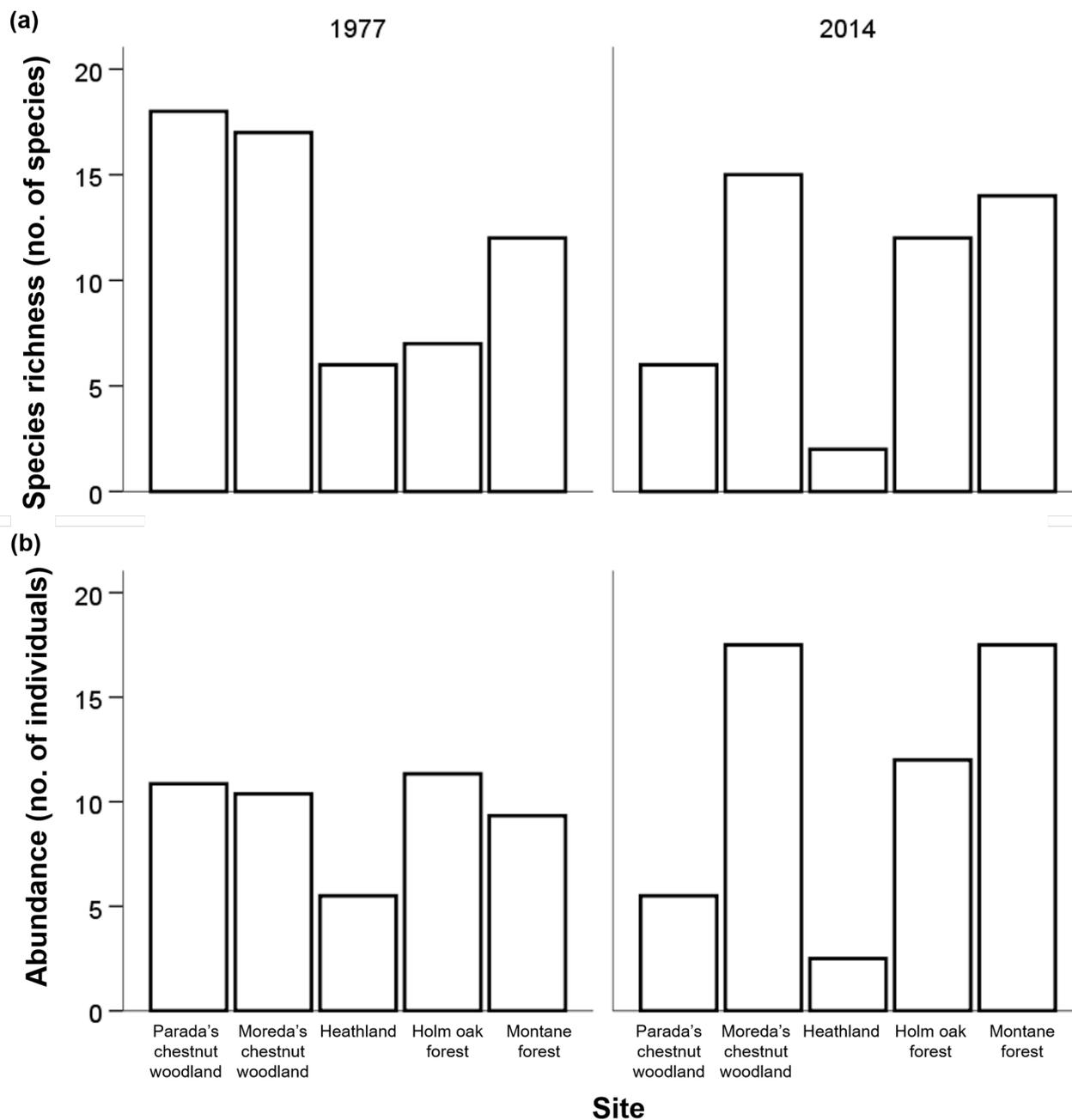María Losada, Luis Salaverri, María Docampo, José Guitián, Mar Sobral

Table SI. Summary of (a) site characteristics (Bas et al. 1978), and (b) bird surveys details per site (montane forest, holm-oak forest, heathland, Parada's chestnut woodland, Moreda's chestnut woodland) and year (1977, 2014).

	Site	Montane forest		Holm oak forest		Heathland		Parada's chestnut woodland		Moreda's chestnut woodland	
(a)	Area (ha)	2.50		3.04		3.08		1.80		1.65	
	Orientation	N		S		S		W		NO-N-NE	
	Elevation (m.a.s.l.)	1,230-1,320		650		1,000		750-770		760-780	
	Tree cover (%)	100		70		100		100		90	
	Tree richness / 400 m² plot	4		3		0		2		4	
	Main human influences	Timber harvesting		Firewood collection		Regular fires		Annual chestnut collection + Timber harvesting		Occasional chestnut collection	
	Surrounding land uses	Oak copses + Heathlands + Mowing fields		Pasturelands + Heathlands + Mowing fields		Rye fields + Oak copses		Croplands and gardens + Mowing fields + Urban		Poor croplands + Meadows	
	Year	1977	2014	1977	2014	1977	2014	1977	2014	1977	2014
(b)	Length (m)	500	500	530	686	615	615	360	360	330	330
	No. of surveys	6	2	3	2	6	2	7	2	8	2

Table SII. PC factor loadings extracted from the PCA for dimensional reduction of avian phenotypic traits (27 variables with complete cases for the 15 most abundant bird species). The PC loadings correspond to the three PCs extracted from PCA with eigenvalues >1 and which explained a total 91.66% of variance in phenotypic traits among bird species.

Phenotypic traits	PC1	PC2	PC3
Bird length - mean (cm)	0.992	-0.051	0.076
Wing length - mean (mm)	0.980	0.012	0.024
Wing length - mean - males (mm)	0.978	0.009	0.026
Wing length - mean - females (mm)	0.981	0.015	0.023
Tail length - mean (mm)	0.959	-0.131	0.168
Tail length - mean of males (mm)	0.958	-0.129	0.169
Tail length - mean of females (mm)	0.960	-0.133	0.168
Bill length - mean (mm)	0.926	0.120	-0.315
Bill length - mean of males (mm)	0.926	0.131	-0.312
Bill length - mean of females (mm)	0.927	0.108	-0.318
Tarsus length - mean (mm)	0.962	-0.063	0.135
Tarsus length - mean - males (mm)	0.963	-0.055	0.147
Tarsus length - mean of females (mm)	0.962	-0.071	0.123
Weight during breeding - mean (g)	0.991	0.002	0.070
Weight during breeding – mean of males (g)	0.991	0.013	0.058
Weight during breeding – mean of females (g)	0.990	-0.009	0.081

Phenotypic traits	PC1	PC2	PC3
Clutch size - minimum (eggs)	-0.277	0.813	0.124
Clutch size - maximum (eggs)	-0.123	0.838	0.402
Clutch size - mean (eggs)	-0.216	0.868	0.395
Brood size per year - mean (broods)	-0.188	-0.522	0.366
Egg length - mean (mm)	0.953	-0.218	0.070
Egg width - mean (mm)	0.955	-0.213	0.074
Egg mass - mean (g)	0.973	-0.143	0.123
Incubation period (days)	0.408	0.717	-0.248
Fledging period (days)	0.367	0.861	-0.068
Feeding independence (days)	0.783	0.460	-0.096
Age of first breeding (years)	0.870	0.266	-0.197

Table SIII. GLM results for the factorial abundance change (increase, decrease and non-significant change) between years (1977-2014) in function of the three PCs extracted from PCA (PC1, PC2, PC3) for the phenotype analysis (27 phenotypic traits of the 15 most abundant bird species), included as covariates (n=15 species). No statistically significant effects were found.

Response variable	Factors	β	SE	Wald Chi-square	d.f.	*P-value*
	PC1	-0.263	0.579	0.207	1	0.649
Factorial abundance change	PC2	-0.908	0.595	2.325	1	0.127
	PC3	-0.490	0.571	0.735	1	0.391