Towards inclusion of genetic diversity measures into IUCN assessments: a case study on birds

L. C. Vitorino, U. J. Borges Souza, T. P. F. A. Jardim, L. Ballesteros–Mejia

Abstract
Towards inclusion of genetic diversity measures into IUCN assessments: a case study on birds. The IUCN Red List categorizes species based on their geographical distribution and population size. However, attributes such as genetic information are not yet considered. We compiled information on genetic diversity (H_E, H_O) and inbreeding coefficient (f) along with their ecological attributes (IUCN category, migratory habit, forest dependence, and habitat type) from a literature survey to assess whether bird species categorized as being of highest conservation concern display the lowest genetic diversity. We used generalized linear mixed models (GLMM) to test whether avian species with less inclusive characteristics (e.g., taxa with small geographical distributions or low dispersal capability) display lower genetic diversity than those classified as Least Concern (LC). We used phylogenetic generalized least squares (pGLS) to account for phylogenetic independence of predictor variables and to verify robustness of GLMMs (generalized linear mixed models). In general, GLMM revealed more significant relationships among ecological attributes and genetic diversity patterns. After accounting for phylogenetic independence, the highest average heterozygosity values were observed in species falling under the LC category; non–migratory birds showed lower H_O and H_E average values than migratory birds, while non–forest birds showed lower heterozygosity than forest birds. Hence, we corroborate our hypothesis that genetic diversity of birds is lower in species of high conservation concern. We hope our results promote further studies on genetic diversity of bird populations. Lastly, we propose the incorporation of genetic data as metrics in the assessment of bird conservation status.

Key words: International Union for Conservation of Nature, Red List, Expected heterozygosity, Observed heterozygosity, Inbreeding coefficient

Resumen
Lograr la inclusión de las medidas de diversidad genética en las evaluaciones de la Unión Internacional para la Conservación de la Naturaleza: un estudio monográfico sobre aves. La Lista Roja de la Unión Internacional para la Conservación de la Naturaleza (UICN) clasifica las especies según su distribución geográfica y el tamaño de población. Sin embargo, todavía no se tienen en cuenta algunos aspectos como la información genética. A fin de evaluar si las especies de aves clasificadas como de máximo interés para la conservación son las que presentan la menor diversidad genética, en este estudio compilamos información sobre la diversidad genética (H_E, H_O) y el coeficiente de endogamia (f), junto con sus características ecológicas (categoría de la UICN, hábitos migratorios, dependencia de los bosques y tipo de hábitat) a partir de un estudio de las publicaciones científicas. Utilizamos modelos mixtos lineales generalizados para determinar si las especies de aves con menos características inclusivas (por ejemplo, los taxones con una distribución geográfica reducida o con escasa capacidad de dispersión) presentan menor diversidad genética que las clasificadas como de Preeocupación Menor. Utilizamos mínimos cuadrados generalizados filogenéticos para representar la independencia filogenética de las variables predictivas y para comprobar la robustez de los modelos mixtos lineales generalizados. En general, los modelos mixtos lineales generalizados revelaron la existencia de relaciones más significativas entre las características ecológicas y los patrones de diversidad genética. Al tener en cuenta la independencia filogenética, los valores máximos de heterocigosidad media se observaron en especies de la
categoría Preocupación Menor; las aves no migratorias mostraron valores medios de $H_o$ y $H_e$ más bajos que los de las aves migratorias, mientras que las aves no forestales mostraron una heterocigosidad inferior a la de las aves forestales. Por consiguiente, corroboramos nuestra hipótesis de que la diversidad genética de las aves es inferior en especies de gran interés para la conservación. Esperamos que nuestros resultados promuevan nuevos estudios sobre la diversidad genética de las poblaciones de aves. Por último, proponemos que se incorporen datos genéticos como parámetros en la evaluación de la situación de la conservación de las aves.

Palabras clave: Unión Internacional para la Conservación de la Naturaleza, Lista Roja, Heterocigosidad esperada, Heterocigosidad observada, Coeficiente de endogamia

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Introduction

The IUCN Red Lists of threatened species, hereafter Red Lists, is the source of best available information on the global conservation status of species worldwide, providing quantitative measures of extinction risks (Lamoreux et al., 2003) and associated drivers (Baillie et al., 2004). Red Lists are an important tool not only to prioritize species conservation and identification of key biodiversity areas, but also to guide conservation responses, provide support for planning or implementing biodiversity projects, and help understand potential impacts on biodiversity (Bennun et al., 2018). In this sense, Red List indicators bear the potential to quantify possible anthropogenic threats to species (e.g., Wraight and Pickering, 2018), and to strategically connect science and politics (Do et al., 2018; Rabaud et al., 2018).

Once species are identified as being at risk in the Red Lists, it might be easier to induce willingly—to-pay for nature conservation in the broader public (Tisdell et al., 2007; Jin et al., 2018). Threatened species are typically prioritized in conservation policies because of the risk of their vanishing even before we can describe their characteristics, or before we know them as important parts of ecosystems. However, non–threatened species should also receive attention, as population–level analyses may reveal the local influence of anthropogenic changes, such as habitat loss and/or fragmentation. Such changes can increase selection pressures and culminate in genetic erosion, thereby endangering population persistence in the longer term (Bijlsma and Loeschcke, 2012).

Assigning species to a given threat category is based on five data–driven criteria concerning: i) population size, ii) population fragmentation, iii) observed or projected declines in abundance, iv) geographic range size in combination with fragmentation, and v) a quantitative analysis of extinction probability (IUCN, 2001). However, there is still an important aspect of biodiversity that is largely ignored in conservation assessments of species: genetic diversity. Despite its importance for maintaining biological distinctiveness and evolutionary processes, measures of genetic diversity such as number of alleles, number of haplotypes and heterozygosity are not explicitly considered in the Red Lists. This is somewhat puzzling since there is consensus that conservation of endangered species requires deep knowledge of metapopulation dynamics and structure, which involves determining the degree of genetic diversity within and between populations.

Variability estimated using molecular markers not only helps to distinguish genetically distinct populations that may be vulnerable to environmental changes (e.g., Lee and Mitchell–Olds, 2011; Hansen et al., 2012; Limborg et al., 2012; Munday et al., 2013; Razgour et al., 2018) but also infers phylogenetic relationships between individuals both within and between species, reconstructing genealogies and gathering information on inbreeding rates (e.g., Zollinger et al., 2012; McCormack et al., 2013; Lyu et al., 2018). The current use of microsatellite markers in biodiversity conservation studies is particularly useful to address issues related to the conservation genetics of various bird species (e.g., Moura et al., 2017; Houston et al., 2018; Moussy et al., 2018; Stojanovic et al., 2018). Conservation Genetics has been defined as the discipline that applies genetic concepts and tools, including molecular markers, to small populations to reduce their risk of extinction (Frankham et al., 2002; Allendorf et al., 2012). Among its many applications, it allows to detect potential bottlenecks, measure gene flow and hybridization between populations, assess paternity, assign individuals to their population of origin, and infer population structure (e.g., Contina et al., 2018; Coster et al., 2018; Haworth et al., 2018; Kangas et al., 2018).

Birds are often used as biindicators for various reasons (Furness et al., 1993; Herrera–Dueñas et al., 2014; Padoa–Schioppa et al., 2006; Silva et al., 2018; Souto et al., 2018), including the fact that their populations are heavily affected by air pollutants and pesticides. This has put many bird populations at risk, increasing the need for studies addressing loss of genetic diversity in metapopulations. Spielman et al. (2004) compared the heterozygosity (He) of species categorized as threatened vs non–threatened taxonomically related species and found that, on average, He was 35 % lower in threatened species. Similarly, Evans and Sheldon (2008) used Phylogenetic Independent Contrast (Felsenstein, 1985) to correlate heterozygosity with the increased extinction risk, showing that genetic diversity is relatively poor in the threatened bird species category.

Here we chose to use a more robust statistical approach. Following Ballesteros–Mejia et al. (2016), we fitted GLMMs to test the influence of different ecological attributes and extinction risk on estimates of genetic diversity. GLMMs combines desirable properties of two statistical frameworks, namely linear mixed models, incorporating random effects, and GLM, which handles non–normal data (Bolker et al., 2009). Since phylogeny is known to influence ecological and morphological characteristics (Harvey and Pagel, 1991; Bennett and Owens, 2002), we used generalized least squares (pGLS) to account for phylogenetic relationships and verify the robustness of the results found by significant GLMMs. All species in a monophyletic group share a common ancestor and tend to resemble each other more than those randomly chosen across a phylogenetic tree. In light of their phylogenetic non–independence, the former cannot be considered as independent data points in statistical analyses (Garland et al., 1992)

We addressed the relationship between genetic diversity and conservation status and tested the effect of ecological attributes on patterns of genetic diversity based on data from a literature survey. Specifically, we used GLMM to test the effect of migratory habits (migratory or non–migratory), forest dependence (high, medium or low), type of habitat (terrestrial vs non–restricted to it), and extinction risk (as classified in the IUCN Red List) on the patterns of genetic diversity (H₂, observed heterozygosity; Hₑ, expected heterozygosity; f, inbreeding coefficient). Additionally, we fitted Phylogenetic Least Squares (pGLS) to
account for phylogenetic non–independence as well as to verify the robustness of GLMM predictions. Most taxa are adversely affected by genetic factors before being driven to extinction (Spielman et al., 2004), but since processes that compromise genetic diversity do not affect all bird species equally, habitat specialization may be a predictor of the demographic and genetic consequences of fragmentation (Khimoun et al., 2016). Thus, it is likely that species classified as endangered or critically endangered exhibit lower $H_e$ and higher $f$ values. Therefore, we assessed whether the genetic diversity in birds based on microsatellite data available in the literature can be used as a proxy to define their risk category and inform conservation policies.

Material and methods

Obtaining bird genetic data and ecological attributes

We conducted a survey of studies on avian population genetic based on microsatellite data. We used the Web of Science (http://www.isiknowledge.com) database with the following combinations of keywords: [birds* AND microsatellite* AND genetic diversity*], [birds* AND SSR* AND genetic diversity*], [bird* AND microsatellite* AND genetic diversity*], and [bird* AND SSR* AND genetic diversity*]. We excluded studies that used less than four microsatellite loci.

From the publications, we retrieved the following data: (i) title; (ii) year of publication; (iii) journal; (iv) study species; (v) number of individuals; (vi) number of loci; and (vii) mean values of genetic diversity, $H_e$, $H_e$ and $f$. In several studies, $f$ was not estimated. Thus, we estimate it using the equation:

$$f = 1 - \frac{H_e}{H_e}.$$

We used the database of the IUCN Red List of Threatened Species (http://www.iucnredlist.org) to extract information about the conservation status of target species. We considered the following categories: Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), Critically Endangered (CR), Extinct in the Wild (EW) and Extinct (EX) as of December 2015 to July 2016.

The Birdlife International database (http://www.birdlife.org/datazone/species) contains data on avian species worldwide, and we used it to obtain the following information for each bird species in the selected studies: (i) migratory habit (migratory or not occurring in forests) and (ii) habitat type (terrestrial or other). This information, as well as the conservation status of the species (IUCN Category), was considered here as the ecological attributes.

Data analysis

To evaluate the temporal trend in the number of articles published annually, and to correct the effect of the general increase in the number of articles over time, we use the following equation (Eq. 1):

$$\text{Number of articles in year (x)} = \frac{\text{Total number of articles in the Web of Science in year (x)}}{\text{Number of articles in year (x)}}.$$

We initially used analysis of variance and $t$–student to explore genetic variation among populations. We included bird populations of the same species analysed with the same microsatellite markers (table 1) to test whether genetic parameters $H_e$, $H_e$, and $f$ varied significantly between population pairs.

We fitted generalized linear mixed models (GLMMs) to investigate the effects of ecological attributes and conservation status on genetic diversity. IUCN category and forest dependence were treated as multistate categorical variables, whereas habitat type and migratory habit were treated as binary variables. Models were fitted for each genetic parameter ($H_e$, $H_e$, and $f$) as response variables. Ecological attributes were fitted as fixed factors, and species identity was considered as a random factor because multiple variables were measured per species. Analyses were performed using MCMCglmm package (Hadfield, 2010) implemented in R version 3.4.4 (R Core Team, 2018).

To account for phylogenetic non–independence of the effects of ecological attributes on genetic diversity, we first obtained the reference phylogenetic hypothesis of the species included in each analysis.

We gathered ten thousand phylogenies sampled from a pseudo–posterior distribution (Jetz et al., 2012) deposited in BirdTree.org website (https://birdtree.org/). We made a consensus tree using Tree annotator 1.8.2 (Drummond et al., 2012) and dropped all species without data using the 'drop.tip' function in the package 'ape' (Paradis, 2004) implemented in R version 3.4.4.

We then tested whether the studied ecological attributes showed a phylogenetic signal to account for phylogenetic relationships. We performed Abouheif’s proximity test of serial independence (Abouheif, 1999; Pavolíne et al., 2008) using the function 'abouheif.moran' from the R–package 'adephylo' (Jombart et al., 2010). We then fitted Phylogenetic Generalized Least Square Models (pGLS; Martins and Hansen, 1997) to the genetic parameters to verify whether GLMM models had resulted in robust inferences and hence the pattern persisted when accounting for phylogenetic relationships. We tested the solitary effect of each ecological attribute, as well as the effect of combining all of these in a complete model, on the genetic diversity parameters. When the same molecular marker was applied more than once to study a species the mean of the genetic parameters was used. The analyses were carried out using the package 'caper' (Orme, 2013) of the R.

Finally, Pearson’s correlation analysis was performed to assess the effect of the number of individuals and the number of loci on the genetic diversity values; the number of loci and individuals were log–transformed (base 10) to reduce the discrepancies between values. Statistical tests were performed using the R statistical package.
Because of the cumulative effect of domestication and subsequent artificial selection, *Gallus gallus* was excluded from GLMM and pGLS analysis.

**Results**

**Scientometrics**

The search revealed 359 published papers that met the criteria entered. They were published across 98 different journals between 1998 and 2015. Five of these journals (i.e., *Molecular Ecology Resources*, *Conservation Genetics Resources*, *Conservation Genetics*, *Molecular Ecology* and *PLOS One*) hosted 51.81% of the articles; 35 journals published between four and eight articles, and the remaining 58 journals published only one article.

The analysis of annual number of publications per journal revealed that 2014 was the year with the highest number of publications; 13 of the analyzed journals published studies containing genetic diversity data of bird species. The second highest mean annual publication rate occurred in 2013 and in 2015; in each of these years, nine different journals published articles that analysed the genetic diversity of birds using microsatellite markers.

After correcting for the general trend with equation 1, the number of published papers with analyses of bird genetic diversity increased significantly over time ($r = 0.740; p ≤ 0.01$), especially between 2013 and 2014.

Values of $H_e$, $H_o$ and $f$ were reported for 297 species (table 1a), 63 of which were represented more than once in the data set. *Gallus gallus* (7.80% of the total species) was the most studied species followed by *Passer domesticus* (2.40%), *Aquila chrysaetos* (1.20%), and *Tetrao urogallus* (1.20%). The total number of studied species was distributed among 94 families (table 1a) and 27 orders. The most highly represented orders were Passeriformes (44.10%), Charadriiformes (8.10%) and Galliformes (6.10%) (fig. 1A).

Most of the studied species were predominantly terrestrial (54.20%) and exhibited no migratory behaviour (62.30%). The analysis of species classification according to forest dependence showed that most species did not usually occur in forests (42.10%), followed by species with low (23.20%), medium (18.20%) and high (16.50%) forest dependence. Lastly, regarding classification according to IUCN category, the analyses showed that most of the studied bird species were categorized as LC (69.40%) (fig. 1B).

| Species                  | Microsatellite loci                                                                 |
|--------------------------|-----------------------------------------------------------------------------------|
| *Aquila chrysaetos*      | Aa15, Aa26, Aa27, Aa36, Aa39 and Aa43 (Martínez-Cruz et al., 2002)               |
| *Bubo bubo*              | B101, B111, B126 and B11 (Isaksson and Tegelstrom, 2002)                          |
| *Cyanistes caeruleus*    | Pca3, Pca4, Pca7, Pca8 and Pca9 (Dawson et al., 2000)                             |
|                          | POCC1 and POCC6 (Bensch et al., 1997)                                            |
|                          | PATMP2-43 (Otter et al., 1998)                                                    |
|                          | Ase18 (Richardson et al., 2000)                                                   |
|                          | Pdoµ5 (Griffith et al., 1999)                                                     |
|                          | Mcyu (Double et al., 1998)                                                        |
|                          | CcaTgu7, CcaTgu8, CcaTgu11, CcaTgu14, CcaTgu15, CcaTgu19,                        |
|                          | CcaTgu25 and CcaTgu28 (Olano-Marin et al., 2010)                                  |
|                          | TG05-046, TG05-053, TG13-013 (Dawson et al., 2010)                               |
|                          | Tgu07 (State et al., 2007)                                                        |
| *Nipponia nippon*        | NnNF5 (Ji et al., 2004)                                                           |
| *Passer domesticus*      | Pdoµ1 and Pdoµ4 (Neumann and Wetton, 1996)                                       |
|                          | Pdoµ5 (Griffith et al., 2007)                                                     |
|                          | Pdoµ10 (Segelbacher et al., 2000)                                                 |
| *Tetrao urogallus*       | TUD1, TUD3, TUD5 and BG15                                                         |
|                          | (Segelbacher et al., 2000, Piertney and Hoglund, 2001)                            |
Genetic diversity of bird populations

We compared the genetic diversity data obtained using the same microsatellite markers for three *Aquila chrysaetos* populations, two in Scotland and one in Slovakia, and found similar diversity patterns. $H_0$ values (0.52, 0.50 and 0.40, respectively) were always lower than $H_E$ values (0.56, 0.54 and 0.43), whereas the $f$ values were 0.34, 0.06 and 0.09 (fig. 2A). For the *Bubo bubo*, we compared data from four Spanish populations and one Norwegian population, and the highest average $H_0$ was observed in the latter (0.63), while the Spanish populations presented values of 0.4, 0.48,
0.38 and 0.51. The same pattern was observed for the mean $H_E$ with values of 0.6 in the Norwegian population and 0.39, 0.41, 0.37 and 0.55 for the Spanish populations. The $f$ value was –0.02 for the Norwegian population and 0.01, 0.07, –0.14 and –0.03 for the Spanish populations.

For *Tetrao urogallus*, we compared the average diversity values for three populations, one from the Czech Republic and two from Spain. The highest average $H_O$ was observed in the Czech population (0.67), while the Spanish populations showed $H_O$ values of 0.55 and 0.44. We observed the opposite pattern for the average $H_E$ and $f$ values, with the lowest occurring in the Czech population (0.64 and –0.03) followed by 0.66 and 0.68 for $H_E$ and 0.33 and 0.15 for $f$ in the Spanish populations. When comparing the Spanish and Czech populations we found significant differences for $H_O$ ($t = 8.06, p < 0.0001$) and $H_E$ ($t = 19.81, p < 0.0001$) according to the $t$-test.

Significant differences were found between the average $H_O$ ($F = 53.15, p < 0.001$), $H_E$ ($F = 11.57, p = 0.002$) and $f$ ($F = 86.70, p < 0.001$) values of four *Passer domesticus* populations from Scandinavia, Belgium, France and England. The average $H_O$ was highest in the French population (0.87) followed by Scandinavian (0.85), Belgian (0.79) and English populations (0.71). The highest average $H_E$ values were found in the populations from France and Scandinavia (0.88 in both) followed by those from Britain (0.85) and Belgium (0.83). The $f$ value was positive for all populations, and the lowest value was found in the population with the highest heterozygosity, the French population (0.01), followed by the Scandinavian (0.02), Belgian (0.05) and English populations (0.16).

The $t$-test also revealed a significant difference between the mean $H_O$ ($t = 11.49, p < 0.0001$) and $H_E$ ($t = 11.84, p < 0.0001$) values found in two populations of *Cyanistes caeruleus*, one Spanish ($H_O = 0.80$ and $H_E = 0.79$) and one Austrian ($H_O = 0.78$ and $H_E = 0.76$). The averages for $f$, however, were similar for the two populations with 0.03 in the Spanish population and –0.004 in the Austrian population. However, for *Nipponia nippon*, we found similar values when comparing a Japanese and a Chinese population: 0.48 and 0.46 for $H_O$, 0.37 and 0.37 for $H_E$, and 0.83 and 0.88 for $f$, respectively (fig. 2B).
Table 2. Mean values of genetic diversity of microsatellite loci and ecological attributes of avian species: N, number of species analyzed; $H_O$, observed heterozygosity; $H_E$, expected heterozygosity; $f$, inbreeding coefficient.

Tabla 2. Valores medios de la diversidad genética de los loci de microsatélites y características ecológicas de las especies de aves. N, número de especies analizadas; $H_O$, heterocigosidad observada; $H_E$, heterocigosidad esperada; $f$, coeficiente de endogamia.

| Ecological attribute | N     | $H_O$ ± 0.16 | $H_E$ ± 0.16 | $f$ ± 0.10 |
|----------------------|-------|--------------|--------------|-----------|
| IUCN category        |       |              |              |           |
| LC                   | 201   | 0.59 ± 0.16  | 0.63 ± 0.16  | 0.07 ± 0.10 |
| NT                   | 22    | 0.53 ± 0.17  | 0.54 ± 0.18  | 0.03 ± 0.20 |
| VU                   | 25    | 0.52 ± 0.13  | 0.54 ± 0.14  | 0.04 ± 0.10 |
| EN                   | 21    | 0.52 ± 0.19  | 0.54 ± 0.20  | 0.04 ± 0.07 |
| CR                   | 15    | 0.53 ± 0.12  | 0.55 ± 0.11  | 0.03 ± 0.07 |
| EW                   | 1     | 0.41 ± 0.00  | 0.40 ± 0.00  | -0.02 ± 0.00 |
| Migratory habit      |       |              |              |           |
| Migratory           | 109   | 0.59 ± 0.16  | 0.62 ± 0.16  | 0.06 ± 0.11 |
| Non-migratory       | 176   | 0.56 ± 0.16  | 0.60 ± 0.16  | 0.06 ± 0.11 |
| Forest dependence    |       |              |              |           |
| High                 | 45    | 0.58 ± 0.16  | 0.61 ± 0.15  | 0.06 ± 0.12 |
| Medium               | 52    | 0.60 ± 0.14  | 0.64 ± 0.14  | 0.05 ± 0.09 |
| Low                  | 68    | 0.56 ± 0.18  | 0.60 ± 0.18  | 0.06 ± 0.10 |
| Not occurring in forests | 120 | 0.56 ± 0.16  | 0.60 ± 0.16  | 0.06 ± 0.12 |
| Habitat type         |       |              |              |           |
| Terrestrial          | 153   | 0.57 ± 0.17  | 0.60 ± 0.17  | 0.05 ± 0.11 |
| Not restricted to    |       |              |              |           |
| the terrestrial environment | 132 | 0.57 ± 0.15  | 0.61 ± 0.16  | 0.07 ± 0.11 |

Genetic diversity, ecological attributes and conservation status

In general, we observed a large variation in the values of genetic diversity sampled, with $H_O$, $H_E$ and $f$ varying between 0.04 and 0.93, 0.08 and 0.91 and –0.61 and 0.64, respectively. When we evaluated the genetic diversity within orders, the lowest mean $H_O$ and $H_E$ values were observed in Otidiformes ($H_O = 0.44$ and $H_E = 0.49$), Accipitriformes ($H_O = 0.49$ and $H_E = 0.50$), Gaviiformes ($H_O = 0.45$ and $H_E = 0.46$) and Ciconiiformes ($H_O = 0.44$ and $H_E = 0.47$).

Regarding the conservation status, we found variation in the values of genetic diversity among the IUCN categories (table 2). The LC category showed the highest genetic diversity values ($H_O = 0.59$ and $H_E = 0.63$). However, values decreased substantially across the categories of greater concern, with 0.5 and 0.54 being the averages observed for $H_O$ and $H_E$ of all other categories combined.

Birds with migratory habits presented higher heterozygosity values ($H_O = 0.59$ and $H_E = 0.62$) than those observed in non-migratory birds ($H_O = 0.56$ and $H_E = 0.60$), but no significant variations were found in terms of $f$ ($f = 0.06$ in both). Species that do not occur in forest environments or that have low dependence on forest fragments displayed the lowest averages of heterozygosity ($H_O = 0.56$ and $H_E = 0.60$ in both). In contrast, terrestrial birds or birds not restricted to terrestrial environments did not show differences in terms of heterozygosity ($H_O = 0.57$ in both $H_E = 0.60$ and $H_E = 0.61$, respectively), although $f$ was slightly higher for birds not restricted to terrestrial environments (table 2).

When we accounted for phylogenetic relationships in the observed genetic patterns, the serial independence test showed that with the exception of the categorical variable IUCN category, all other attributes presented a significant phylogenetic signal (table 3). Phylogenetic generalized least squares performed on a complete model, with all variables combined, showed a significant relation between IUCN category and $H_O$, $H_E$ and $f$ values. We observed the highest $H_O$ values in the LC category (–0.021 ± 0.028) and the lowest for the EW category (–0.185 ± 0.089), which is the one of highest concern. The same pattern was observed for $H_E$ and $f$: the highest $H_E$ and $f$ values were also observed in the LC category (0.079 ± 0.027).
...and 0.172 ± 0.023, respectively) and the lowest in the EW category (–0.194 ± 0.086 and –0.009 ± 0.074). The migratory habit significantly affected \( H_e \) and \( f \) values, equal to 0.042 ± 0.019 and 0.058 ± 0.016 for migratory and non–migratory birds, respectively. The forest dependence significantly affected only \( f \) that turned out to be highest in birds with low dependence on forests (–0.021 ± 0.029) and lowest for species with medium forest dependence (–0.084 ± 0.030). Regarding habitat type, this significantly affected \( H_o \), \( H_e \) and \( f \) with the highest values observed in terrestrial species (–0.059 ± 0.023; –0.079 ± 0.022 and –0.041 ± 0.019) (table 4).

When we evaluated the isolated effect of each variable, similar results were found for IUCN category and \( H_o \), \( H_e \) and \( f \), so that species of the category EW had significantly lower values of \( H_o \) and \( H_e \) (tables 2, 5), but the results differed for the other categorical variables. Migratory habit, forest dependence and type of habitat affected \( H_o \) and \( H_e \). The pGLS confirmed the hypothesis that non–migratory species have lower diversity values. Likewise, \( H_e \) values may be affected in non–forest bird species. We also observed that species in terrestrial habitat showed lower levels of \( H_o \) and \( H_e \) (table 5).

A significant correlation was found between the number of loci used and the \( H_o \) (\( r = –0.183; p \leq 0.01 \)) and \( H_e \) (\( r = –0.191; p \leq 0.01 \)) estimates, but the correlations were negative (fig. 3). Conversely, no correlations were observed between the number of loci and \( f \) or between the number of individuals sampled and any estimate of genetic diversity.

**Discussion**

**Scientometrics.**

Microsatellite markers were developed in the 1980s (Tautz and Renz, 1984) and have since become increasingly popular in avian research. The observed annual increase in the number of published articles using estimates of genetic diversity for birds confirms this popularity. It should be noted that the accuracy of these indices is subject to the availability of study individuals, and is therefore favoured by larger sample sizes, which explains why most studies (69.40%) were conducted with species in the Least Concern (LC) IUCN category. However, the IUCN system categorizes species as LC based on attributes such as a wide geographical distribution and large population size (IUCN, 2015), but global conservation status may not be representative of local trends, as indicated by national Red Lists. Garcia and Marini (2006) evaluated 494 threatened or near–threatened taxa of Brazilian birds finding that the classifications of only 26% of these taxa were consistent with the global status, and revealing discrepancies between regional and global classifications. Such differences decrease the efficiency at which the IUCN list can be applied to establish national–scale conservation actions (Rodríguez et al., 2000), so studies should be conducted to evaluate the genetic diversity of bird species while considering both state and national threat levels. In addition, the ability to perform studies involving estimates of genetic diversity is also apparently influenced by the behavioural traits of the study species. Indeed, such traits may either hinder or facilitate the sampling, which may explain why most studies have been performed on predominantly terrestrial (54.20%) and non–migratory (62.30%) species with low forest dependence (23.20%) or species for which sampling was not restricted to forest environments (42.10%).

Most bird species in the studies (44.10%) belonged to the order Passeriformes (passerines), the largest and most diverse avian order. The main Passeriformes lineages diversified on all continents and now occupy almost all terrestrial ecosystems (Barker et al., 2004), and they include approximately 5,700 species that account for nearly 60% of all living birds. Passeriformes have been the focus of many ecological, behavioural, anatomical and evolutionary studies because of their ubiquity and enormous diversity (Ericson et al., 2014), generally driven by the colonization of new biogeographical regions (Kennedy et al., 2017). This order encompasses domestic species such as *Poephila cincta* and *Serinus canaria* as well as to the globally distributed *Passer domesticus* (2.40%). The most predominant species in the literature was *Gallus gallus* (7.80%), which has a large number of lineages distributed across the globe and has been widely used as a model organism in biochemical, molecular (e.g., Piekarski et al., 2015; Guizard et al., 2016) and genetic studies such as those describing

**Table 3.** Phylogenetic signal of ecological attributes for bird species included in the analyses of genetic diversity and differentiation using Abouheif's proximity test of serial independence: \( H_o \), observed heterozygosity; \( H_e \), expected heterozygosity; \( f \), inbreeding coefficient. (Significant values are denoted in bold.)

| Ecological attribute | Observed Moran’s I | p-value |
|----------------------|-------------------|---------|
| IUCN category        | –0.0457           | 0.9999  |
| Migratory habit      | 0.0412            | 0.0010  |
| Forest dependence    | 0.1519            | 0.0010  |
| Habitat type         | 0.0590            | 0.0010  |
Table 4. Phylogenetic generalized least squares for ecological attributes of bird species for each genetic parameter analysed. Data obtained considering the effect of the combination of all variables: $H_O$, observed heterozygosity; $H_E$, expected heterozygosity; $f$, inbreeding coefficient. T, T–value; P, P–value; C, coefficient ± SE. (Significant values are denoted in bold)

| Parameter | $H_O$ | $H_E$ | $f$ |
|-----------|-------|-------|-----|
| IUCN category |       |       |     |
| Intercept | 0.636 ± 0.156 | 4.086 | 0.000 |
| LC | -0.021 ± 0.028 | -0.755 | 0.451 |
| NT | -0.058 ± 0.044 | -0.136 | 0.892 |
| VU | -0.058 ± 0.045 | -1.277 | 0.202 |
| EN | -0.080 ± 0.042 | -1.886 | 0.060 |
| CR | - - - - - - - - - |
| EW | -0.185 ± 0.089 | -2.064 | 0.039 |
| Migratory habit |       |       |     |
| Migratory | - - - - - - - - - |
| Non–migratory | -0.005 ± 0.019 | -0.269 | 0.787 |
| Forest dependence |       |       |     |
| High | -0.001 ± 0.037 | -0.006 | 0.994 |
| Medium | -0.005 ± 0.035 | -0.163 | 0.870 |
| Low | -0.005 ± 0.035 | -0.031 | 0.374 |
| Not occurring in forests | 0.034 ± 0.038 | 0.902 | 0.368 |
| Habitat type |       |       |     |
| Terrestrial | -0.059 ± 0.023 | -2.572 | 0.011 |
| Not restricted to the terrestrial environment | - - - - - - - - - |

Genetic diversity of bird populations

The lack of significant differences between Aquila chrysaetos populations can be explained by the migratory nature of this species in Europe. It is categorized as LC in the European Red List with the expectation of increasing the size of local populations (European Red List, 2015). Native to mainland Europe and the Mediterranean, it currently occurs in the UK with a resident and most likely introduced population (Harrop et al., 2013). This would explain the limited differences
Table 5. Phylogenetic generalized least squares for ecological attributes of bird species for each genetic parameter analysed. Data obtained by evaluating the isolated effect of each variable: $H_O$, observed heterozygosity; $H_E$, expected heterozygosity; $f$, inbreeding coefficient; $T$, $T$–value; $P$, $P$–value; $C$, coefficient ± SE. (Significant values are denoted in bold).

Tabla 5. Mínimos cuadrados generalizados filogenéticos para las características ecológicas de las especies de aves para cada parámetro genético analizado. Datos obtenidos mediante la evaluación del efecto aislado de cada variable: $H_O$, heterocigosidad observada; $H_E$, heterocigosidad esperada; $f$, coeficiente de endogamia; $T$, valores de $T$; $P$, valores de $P$; $C$, coeficiente ± EE. (Los valores significativos se indican en negrita).

| Ecological attribute | $H_O$ | $H_E$ | $f$ |
|----------------------|-------|-------|-----|
|                       | C     | T     | P   | C   | T   | P   | C   | T   | P   |
| IUCN category         |       |       |     |     |     |     |     |     |     |
| Intercept             | 0.614 ± 0.155 | 3.969 | 0.000 | 0.580 ± 0.152 | 3.817 | 0.000 | -0.070 ± 0.128 | -0.542 | 0.588 |
| LC                   | -0.014 ± 0.026 | -0.512 | 0.609 | 0.070 ± 0.028 | 2.560 | 0.011 | 0.150 ± 0.023 | 6.462 | 0.000 |
| NT                   | -0.003 ± 0.043 | -0.062 | 0.951 | 0.026 ± 0.043 | 0.612 | 0.541 | 0.058 ± 0.036 | 1.609 | 0.109 |
| VU                   | -0.042 ± 0.045 | -0.925 | 0.356 | 0.017 ± 0.045 | 0.388 | 0.698 | 0.109 ± 0.038 | 2.879 | 0.004 |
| EN                   | -0.080 ± 0.043 | -1.847 | 0.066 | -0.008 ± 0.042 | -0.196 | 0.844 | 0.126 ± 0.036 | 3.522 | 0.001 |
| CR                   | - - - - - - - - - - - - - - - - - - - - |
| EW                   | -0.180 ± 0.091 | -1.975 | 0.049 | -0.203 ± 0.090 | -2.262 | 0.024 | -0.028 ± 0.076 | -0.367 | 0.714 |
| Migratory habit       |       |       |     |     |     |     |     |     |     |
| Intercept             | 0.598 ± 0.154 | 3.893 | 0.000 | 0.622 ± 0.154 | 4.034 | 0.000 | 0.049 ± 0.136 | 0.365 | 0.715 |
| Migratory             | - - - - - - - - - - - - - - - - - - - - |
| Non–migratory        | -0.008 ± 0.019 | -0.44 | 0.660 | 0.020 ± 0.019 | 1.022 | 0.308 | 0.025 ± 0.017 | 1.471 | 0.142 |
| Forest dependence     |       |       |     |     |     |     |     |     |     |
| Intercept             | 0.557 ± 0.154 | 3.618 | 0.000 | 0.596 ± 0.154 | 3.860 | 0.000 | 0.073 ± 0.138 | 0.533 | 0.594 |
| High                  | - - - - - - - - - - - - - - - - - - - - |
| Medium                | 0.010 ± 0.036 | 0.292 | 0.770 | -0.001 ± 0.036 | -0.015 | 0.988 | -0.046 ± 0.032 | -1.421 | 0.156 |
| Low                   | -0.008 ± 0.035 | -0.245 | 0.807 | -0.007 ± 0.035 | -0.193 | 0.847 | 0.002 ± 0.031 | 0.089 | 0.928 |
| Not occurring in forests | 0.062 ± 0.036 | 1.716 | 0.087 | 0.072 ± 0.036 | 1.976 | 0.049 | -0.001 ± 0.032 | -0.049 | 0.960 |
| Habitat type          |       |       |     |     |     |     |     |     |     |
| Intercept             | 0.632 ± 0.150 | 4.227 | 0.000 | 0.685 ± 0.148 | 4.620 | 0.000 | 0.083 ± 0.135 | 0.611 | 0.541 |
| Terrestrial           | -0.080 ± 0.020 | -3.846 | 0.000 | -0.097 ± 0.020 | -4.889 | 0.000 | -0.034 ± 0.018 | -1.862 | 0.063 |
| Not restricted to the terrestrial environment | - - - - - - - - - - - - - - - - - - - - |
in the population–level patterns of diversity. Neither did we find significant differences between the mean genetic diversity values of *Bubo bubo*; populations that are declining in many parts of its range in Europe (Tucker and Heath, 1994) despite being categorized as LC in the European Red List. In general, studies evaluating the genetic diversity of European raptors are being encouraged as a strategy for the conservation of these birds (e.g., Martínez-Cruz, 2011).

Czech populations of *Tetrao urogallus* showed larger values of *H*$_o$ and *H*$_e$ than the Spanish populations. The distribution of this species extends across most of Europe, but its distribution in the Iberian Peninsula is restricted to northern Spain. Unlike other populations living in pure– or mixed–conifer forests, the local *Tetrao urogallus cantabricus* only inhabits purely deciduous forests, and this specificity has put the population at risk (Storch et al., 2006). A study examining the genetic differentiation between this and other European populations showed that the birds from Cantabria form a clade with low genetic variability that differs from all other populations (Rodríguez-Muñoz et al., 2007).

We also found differences between the average *H*$_o$ and *H*$_e$ values obtained for a Spanish population and an Austrian population of *Cyanistes caeruleus*, with the largest heterozygosity found in the Spanish population. This species is widely distributed throughout Europe and is native to both of the surveyed countries, but studies by Kvist et al. (1999, 2004), who analysed mitochondrial DNA sequences, proposed that regions in Europe were recolonized by this species from two different Pleistocene refugia after the last ice age through a colonization route from the Balkans to central and northern Europe as well as a route from the Iberian peninsula to the north and east. The differences we found between the mean genetic diversity values for the species in Spain and Austria can be explained by the possible isolation of the populations in Pleistocene refugia, which would allow different degrees of change in the populations.

For *Nipponia nippon*, we found similar mean genetic diversity values between a Japanese and a Chinese population. The historical distribution of this species included the Russian Far East, China, and Japan, but it is now extinct throughout most of its range (IUCN category EN). Drastic reductions in populations of *Nipponia nippon* were caused by deforestation of nesting habitat, over–hunting and loss of wetlands as well as use of agrochemicals in rice fields, especially during the 1950s, which reduced the abundance and diversity of its preys (Li et al., 2009; Changqing, 2010). Overall, the observed genetic diversity was low in both populations, and the inbreeding coefficients were positive and high, reflecting the degree of risk to the populations of this species.

Genetic diversity, ecological attributes and conservation status

As expected, the non–independence of sister clades in ecological attributes and conservation status (i.e., related species tend to have more similar ecological attributes than expected and therefore also conservation status) add a significant effect to the patterns of genetic diversity observed for birds. When the phylogenetic signal was taken into account, the pGLS confirmed that conservation status is reflected in the levels of genetic diversity sampled in birds; the lower the heterozygosity values the higher the risk of extinction. Consistently, the lowest averages of *H*$_o$ and *H*$_e$ were observed in birds of the EW category. Birds classified as threatened, possibly occurring with small and fragmented populations, tended to have lower heterozygosity. The risk of extinction is reportedly higher for small populations (e.g., Mace et al., 2008; Frankham, 2015) because they are more susceptible to genetic drift with accumulation of deleterious recessive alleles due to inbreeding (Hedrick and García–Dorado, 2016), and loss of locally adapted traits (Frankham, 1995).

Non–migratory species showed the lowest levels of *H*$_o$ and *H*$_e$, confirming our hypothesis. The dispersal ability through flight routes contributes significantly to the increase of gene flow in migratory species (Losos et al., 2013) and consequently decreases the population structure in this group of birds. Paradis et al. (1998) reported that migratory bird species disperse more than resident birds. Dispersal is a fundamental component of metapopulations, gene flow, and genetic structure (Neigel and Avise, 1993), and is dependent on phylogeny (Paradis et al., 1998). However, our results lead us to question whether the greater diversity observed in migratory species is not simply a sampling bias, since the dispersion of these species facilitates their sampling. Gilroy et al. (2016), however, observed that populations of migratory birds showed higher intra–population variability (migratory diversity) and considered that they tended to decline less because they are more resistant to environmental changes.

When we analysed the isolated effect of each variable, we found the lowest significant mean values of *H*$_o$ occurred in bird species that naturally occur in forests and are therefore highly dependent on forest ecosystems. This result evidences the importance of forests as places of shelter and breeding for birds (e.g., LaManna and Martin, 2016; Seilwood et al., 2017; Giubbina et al., 2018), so that species that have no access to food or reproductive resources in these environments may experience negative effects. These results are important at a time when many of the major forest ecosystems worldwide —especially in the neotropics—are experiencing severe disturbances (Hansen et al., 2013) which directly affect bird species (e.g., Pereira et al., 2014). Ram et al. (2017) showed that forest birds have more positive tendencies than non–forest birds in face of climatic changes, suggesting that these species are positively affected by factors other than climate. Alternatively, loss of diversity in non–forest birds can perhaps be explained by high exposure to predation and hunting in such environments. Features such as landscape composition influence predation patterns at finer scales (e.g., Thompson et al., 2002; Stephens et al., 2003; Chiavacci et al., 2018). For example, the abundance of some common nest predators (e.g., *Procyon lotor*) tends to be higher in more intensive agricultural landscapes (Chalfoun et al., 2002).
The categories and criteria developed by the IUCN have been important in designing conservation plans and strategies (Miller et al., 2007), but current efforts have been focused on species and on the global conservation plan. However, conservation actions should be implemented at the population level as extinction rates are estimated to be three to eight times higher than extinction rates of species (Hughes et al., 1997), and it is at this level that substantial losses of genetic diversity occur (Garner et al., 2006). Many bird populations have been identified as threatened (e.g., Alves et al., 2010; Van De Pol et al., 2010; Fernandes–Ferreira et al., 2012; Dunham and Grand, 2017; Yong et al., 2018), which implies the risk to further decrease the heterozygosity values reported for species outside of the LC category and expose their populations to risk of local extinction (Garcia and Marini, 2006). However, since both population size and geographical range are two of the key criteria used by the IUCN to assign threat status, and as both are directly linked to heterozygosity, several studies assessing conservation priorities have excluded species with small populations and/or populations with narrow geographical ranges (Fisher et al., 2003; Jones et al., 2003). Therefore, it is important to include genetic diversity of populations when determining global conservation actions.

The lowest mean $H_O$ and $H_E$ values were observed in Otidiformes, Accipitridae, Gaviiformes and Ciconiiformes, which supports the hypothesis that the solitary behaviour of species of Otidiformes (previously included in Gruiformes but currently considered a proper order) and aspects of their reproductive behaviour, including monogamy and nesting at ground level, might be affecting their genetic diversity as species with complex social systems are more vulnerable to...
the effects of low population densities (Brito, 2009). For example, breeding pairs show low reproductive success unless a minimum number of helpers are present to aid in nest defence against predators and food provisioning for chicks (Brito et al., 2004). Conversely, the genetic patterns of Accipitriformes (traditionally included in the order Falconiformes but currently elevated to a proper order, Hackett et al., 2008) have been strongly affected by interspecific hybridization and anthropogenic disturbances (e.g., Poulakakis et al., 2008; Nam and Lee, 2009; Váli et al., 2010). Falconiformes species are mostly birds of prey with naturally low abundances, so given the lack of mating partners these species tend to hybridize, promoting population declines that put them under threat (Randler, 2006). Additionally, species with a high degree of habitat specialization and small clutch sizes are strongly associated with small population sizes, limited geographical ranges and, thus, higher extinction risk (Krüger and Radford, 2008). Ferrer and Negro (2004) have demonstrated that large predators, such as eagles and lynxes, highly specialised in certain prey species, and with small populations, are permanently threatened with extinction. Furthermore, birds in the orders Gaviiformes and Ciconiiformes have been affected by changes in land use and degradation of freshwater systems because of their high dependence on aquatic habitats (Arzel et al., 2015), vulnerability to pathogens (Silva et al., 2010), and exposure to pollutants derived from aquatic contamination (Fontenelle, 2006). There are strong examples in the literature suggesting that populations of many Ciconiiformes have undergone genetic bottlenecks as evidenced by the loss of genetic diversity and an increase in deleterious mutations (Li et al., 2014) due to inbreeding, climate change, habitat loss, hunting and environmental pollution, especially by agrochemicals (e.g., Zhang et al., 2004; Mifio et al., 2009).

Significant correlations were observed between the number of loci used and the estimates of $H_o$ and $H_e$. Although the relationships were negative, they nevertheless suggest that low microsatellite locus sample sizes may bias diversity estimates. Small numbers of loci can be used only when evaluating a large number of individuals and when the mean heterozygosity of the population is high (Nei, 1978). Thus, given the number of individuals sampled, the studies we evaluated apparently failed to follow the basic requirements for the estimation of genetic diversity (i.e., they used small numbers of loci despite the mean heterozygosity values being high). However, the number of alleles per locus seems to be a good indicator of accuracy when assessing genetic distances with microsatellite markers. Kalinowski (2002) showed that good results can be achieved using few loci with several alleles or many loci with few alleles.

In recent centuries bird species have been deteriorating in status and becoming extinct at a rate that may be 2–3 orders of magnitude higher than in pre–human times (Brooke et al., 2008). Relating genetic diversity estimates with IUCN Red List categories represents an attempt to understand the circumstances under which a bird species becomes extinct, since it is possible to link these figures to high rates of inbreeding or reduced effective population size and gene flow. Brooke et al. (2008) showed that conservation actions have benefited species on the verge of extinction, but are less directed or have less effect on moderately endangered species. We are aware that the IUCN has specific guidelines to address genetic issues in reintroductions and translocations of species (IUCN/SSC, 2013), but as the status of birds has worsened worldwide with populations declining faster than ever, especially those of the Pacific marine species (BirdLife, 2013), studies on genetic diversity of bird populations should be promoted to identify populations at risk.

**Conclusion**

Studies including bird genetic diversity data obtained using microsatellite markers increased significantly between 2013 and 2014, reflecting the popularization of this technique during this period. However, most of these studies were conducted on Passeriformes and/or taxa belonging to the least concern (LC) IUCN category, suggesting that sampling effort is an obstacle to the application of molecular techniques to study less abundant and/or threatened species.

Our findings show that ecological attributes of bird species such as migratory habit, forest dependence and habitat type have a significant effect on genetic diversity parameters.

More importantly, we corroborate our hypothesis that bird species classified under the most threatened IUCN categories (i.e. EW) have lower values of genetic diversity especially for $H_o$ and $H_e$, whereas species classified under LC have higher values. This indicates that populations with high genetic diversity have a larger effective population size and therefore a lower extinction risk.

From the perspective of conservation genetics, we believe that genetic diversity data should be incorporated and support current criteria for the IUCN Red List to generate a more complex and realistic picture of the conservation status of avian species.

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**References**

Abouheif, E., 1999. A method for testing the assumption of phylogenetic independence in comparative data. *Evolutionary Ecology Research*, 1: 895–909.

Allendorf, F. W., Luikart, G., Aitken, S. N., 2012. *Conservation and the genetics of populations*, 2nd
animal biodiversity and conservation 42.2 (2019) 331

Alves, R. R. da N., Nogueira, E. E. G., Araujo, H. F. P., Brooks, S. E., 2010. Bird–keeping in the caatinga, NE brazil. Human ecology, 38: 147–156.

Arzel, C., Ronká, M., Tolvanen, H., Aarás, N., Kamp–pinnen, M., Vihervaara, P., 2015. Species diversity, abundance and brood numbers of breeding waterbirds in relation to habitat properties in an agricultural watershed. Annales zoologici Fennici, 52: 17–32.

Babar, M. E., Nadeem, A., Hussain, T., Wajid, A., Shah, S. A., Iqbal, A., Sarfaraz, Z., Akram, M., 2012. Microsatellite marker based genetic diversity among four varieties of Pakistani aseel chicken. Pakistan veterinary journal, 32: 237–241.

Bailie, J. E. M., Hilton–Taylor, C., Stuart, S. N. (Eds.), 2004. IUCN Red List of threatened species. A global species assessment. IUCN–SSC.

Ballesteros–Mejia, L., Lima, N. E., Lima–Ribeiro, M. S., Collevatti, R. G., 2016. Pollination mode and mating system explain patterns in genetic differentiation in Neotropical plants. Plos one, 11: e0158660.

Barker, F. K., Cibois, A., Schikler, P., Feinstein, J., Cracraft, J., 2009. Phylogeny and diversification of the largest avian radiation. Proceedings of the National academy of sciences, 106: 11040–11045.

Bennett, P. M., Owens, I. P. F., 2002. Evolutionary ecology of birds: life histories, mating systems, and extinction. Oxford university press, Oxford, United Kingdom.

Bennun, L., Regan, E. C., Bird, J., van Bochove, J–W., Katariva, V., 2004. Reproduction cooperativa: ajudar ou não ajudar, eis a questão.

Bijlsma, R., Loeschcke, V., 2012. Genetic erosion impedes adaptive responses to stressful environments. Evolutionary Applications, 5: 117–129.

BirdLife International, 2013. State of the world’s birds – indicators for our changing world. British library–in–publication data.

Bolker, B. M., Brooks, M. E., Clark, C. J., Geange, S. W., Poulsen, J. R., Stevens, M. H. H., White, J. S., 2009. Generalized linear mixed models: a practical guide for ecology and evolution. Trends in ecology & evolution, 24: 127–135.

Brito, D., Rocha, F. S., Oliveira, L. C., Carvalho, F. M. V., 2004. Reprodução cooperativa: ajudar ou não ajudar, eis a questão. Brios, 12: 11–24.

Brito, D., 2009. Análise de viabilidade de populações: uma ferramenta para a conservação da biodiversidade no Brasil. Oecologia brasiliensis, 13: 452–469.

Brooke, M. L., Butchart, S. H. M., Garnett, S. T., Crowley, G. M., Mantilla–Beniers, N. B., Stattersfield, A. J., 2008. Rates of movement of threatened bird species between IUCN red list categories and toward extinction. Conservation biology, 22: 417–427.

Chalfoun, A. D., Thompson III, F. R., Ratnaswamy, M. J., 2002. Nest predators and fragmentation: a review and meta–analysis. Conservation biology, 16: 306–318.

Changqing, D., 2010. Crested ibis. Chinese birds, 1: 156–162.

Chiavacci, S. J., Benson, T. J., Ward, M. P., 2018. Linking landscape composition to predator–specific nest predation requires examining multiple landscape scales. Journal of applied ecology, 55: 2082–2092.

Contina, A., Alcantara, J. L., Bridge, E. S., Ross, J. D., Oakley, W. F., Kelly, J. F., Ruegg, K. C., 2018. Genetic structure of the painted bunting and its implications for conservation of migratory populations. Ibis, 161(2): 372–386, https://doi.org/10.1111/ibi.12641

Coster, S. S., Welsh, A. B., Costanzo, G., Harding, S. R., Anderson, J. T., Katzner, T. E., 2019. Gene flow connects coastal populations of a habitat specialist, the clapper rail rallus crepitans. Ibis, 161(1): 66–78, https://doi.org/10.1111/ibi.12599

Dawson, D. A., Hanotte, O., Greig, C., Stewart, I. R. K., Burke, T., 2000. Polymorphic microsatellites in the blue tit parus caeruleus and their cross–species utility in 20 songbird families. Molecular ecology, 9: 1941–1944.

Dawson, D. A., Horsburgh, G. J., Küpper, C., Stewart, I. R. K., Ball, A. D., Durrant, K. L., Hansson, B., Bacon, I., Bird, S., Klein, Á., Krupa, A. P., Lee, J.–W., Martin–Gálvez, D., Simeoni, M., Smith, G., Spurgin, L. G., Burke, T., 2010. New methods to identify conserved microsatellite loci and develop primer sets of high cross–species utility – as demonstrated for birds. Molecular ecology resources, 10: 475–494.

Do, T. H., Krott, M., Juergues, N., Böcher, M., 2018. Red lists in conservation science–policy interfaces: A case study from Vietnam. Biological conservation, 226: 101–110.

Double, M. C., Dawson, D., Burke, T., Cockburn, A., 1997. Finding the fathers in the least faithful bird: a microsatellite–based genotyping system for the superb fairy–wren Malurus cyaneus. Molecular Ecology, 6: 691–693.

Drummond, A. J., Suchard, M. A., Xie, D., Rambaut, A., 2012. Bayesian phylogenetics with BEAUti and the BEAST 1.7. Molecular biology and evolution, 29: 1969–1973.

Dunham, K., Grand, J. B., 2017. Evaluating models of population process in a threatened population of steller's eiders: a retrospective approach. Ecosphere, 8: e01720.

Ercison, P. G., Klopfstein, S., Irestedt, M., Nguyen, J. M., Nylander, J. A., 2014. Dating the diversification of the major lineages of passeriformes (aves). BMC evolutionary biology, 14: 8.

European Red List, 2015. European red list of birds, the iucn red list of threatened species. Luxembourg:Office for official publications of the European.

Evans, S. R., Sheldon, B. C., 2008. Interspecific patterns of genetic diversity in birds: correlations with extinction risk. Conservation biology, 22:
Felsenstein, J., 1985. Phylogenies and the comparative method. *The American Naturalist*, 125: 1–15.

Fernandes–Ferreira, H., Mendonça, S. V., Albano, C., Ferreira, F. S., Alves, R. R. N., 2012. Hunting, use and conservation of birds in Northeast Brazil. *Biodiversity and Conservation*, 21: 221–244.

Fisher, D. O., Blomberg, S. P., Owens, I. P. F., 2003. Molecular markers identify super specialists paying a price. *Conservation Biology*, 18: 344–349.

Fraser, R. W., Greenwood, J. J. D., Jarvis, P. J., 2002. A new and comprehensive database of evolutionary relationships among birds. *Journal of Avian Biology*, 33: 2610–2618.

Frankham, R., 1995. Conservation genetics. *Annual Review of Genetics*, 29: 305–327.

Frankham, R., 2015. Genetic rescue of small inbred populations: meta-analysis reveals large and consistent benefits of gene flow. *Molecular Ecology*, 24: 2610–2618.

Frankham, R., Briscoe, D. A., Ballou, J. D., 2002. Introduction to population genetics, 2nd Edition Cambridge University Press, Cambridge, UK.

Furness, R. W., Greenwood, J. J. D., Jarvis, P. J., 1993. Can birds be used to monitor the environment? In: *Birds as Monitors of Environmental Change*: 1–41 (R. W. Furness, J. J. D. Greenwood). Springer Netherlands, Dordrecht.

Garcia, F. I., Marini, M. Â., 2006. Estudo comparativo entre as listas global, nacional e estaduais de aves ameaçadas no Brasil. *Natureza e Conservação*, 4: 24–49.

Garland, T., Harvey, P. H., Ives, A. R., 1992. Procedures for the analysis of comparative data using phylogenetically independent contrasts. *Systematic Biology*, 41: 18–32.

Garner, A., Rachlow, J. L., Hicks, J. F., 2005. Patterns of genetic diversity and its loss in mammalian populations. *Conservation Biology*, 19: 1215–1221.

Gilroy, J. J., Gill, J. A., Butchart, S. H. M., Jones, V. R., Franco, A. M. A., 2016. Migratory diversity predicts population declines in birds. *Ecology Letters*, 19: 308–317.

Giubbina, M. F., Martensen, A. C., Ribeiro, M. C., 2018. Sugarcane and Eucalyptus plantation equally limit the movement of two forest-dependent understory bird species. *Austral Ecology*, 43: 527–533.

Griffith, S. C., Dawson, D. A., Jensen, H., Ockendon, N., Greig, C., Neumann, K., Burke, T., 2007. Fourteen polymorphic microsatellite loci characterized in the house sparrow *Passer domesticus* (Passeridae, Aves). *Molecular Ecology Notes*, 7: 333–336.

Griffith, S. C., Stewart, I. R. K., Dawson, D. A., Owens, I. P. F., Burke, T., 1999. Contrasting levels of extrapair paternity in mainland and island populations of the house sparrow (*Passer domesticus*): is there an ‘island effect’? *Biological Journal of Linnean Society*, 68: 303–316.

Guizard, S., Piégu, B., Arensburger, P., Guillou, F., Bigot, Y., 2016. Deep landscape update of dispersed and tandem repeats in the genome model of the red jungle fowl, *Gallus gallus*, using a series of de novo investigating tools. *BMC Genomics*, 17: 659.

Hackett, S. J., Kimball, R. T., Reddy, S., Bowler, R. C. K., Braun, E. L., Braun, M. J., Chojnowski, J. L., Cox, W. A., Han, K.–L., Harshman, J., Huddleston, C. J., Marks, B. D., Miglia, K. J., Moore, W. S., Sheldon, F. H., Steadman, D. W., Witt, C. C., Yuri, T., 2008. A Phylogenomic Study of Birds Reveals Their Evolutionary History. *Science*, 320: 1763–1768.

Hadfield, J. D., 2010. MCMC methods for multiresponse generalized linear mixed models: the MCMCglmm R package. *Journal of Statistical Software*, 33: 1–22.

Hansen, M. C., Potapov, P. V., Moore, R., Hansen, M., Turubanova, S. A., Tyukavina, A., Thau, D., Stehman, S. V., Goetz, S. J., Loveland, T. R., Kommareddy, A., Egorov, A., Chini, L., Justice, C. O., Townshend, J. R. G., 2013. High-resolution global maps of 21st–century forest cover change. *Science*, 342: 850–853.

Hansen, M. M., Olivier, I., Waller, D. M., Nielsen, E. E., 2012. Monitoring adaptive genetic responses to environmental change. *Molecular Ecology*, 21: 1311–1329.

Harrop, A. H. J., Collinson, J. M., Dudley, S. P., Kehoe, C., 2013. The British List: A checklist of birds of britain (8th edition). *Ibis*, 155: 635–676.

Harvey, P. H., Pagel, M. D., 1991. *The comparative method in evolutionary biology*. Oxford University Press, Oxford, United Kingdom.

Haworth, E. S., Cunningham, M. J., Calf Tjorve, K. M., 2018. Population diversity and relatedness in Sugarbirds (*Promeropidae: Promerops spp.*). *PeerJ*, 6: e5000.

Hedrick, P. W., Garcia–Dorado, A., 2016. Understanding inbreeding depression, purging, and genetic rescue. *Trends in Ecology & Evolution*, 31: 940–952.

Herrera–Dueñas, Pineda, J., Antonio, M. T., Aguirre, J. I., 2014. Oxidative stress of House Sparrow as bioindicator of urban pollution. *Ecological Indicators*, 42: 6–9.

Houston, W. A., Aspden, W. J., Elder, R., Black, R. L., 2018. Restricted gene flow in the endangered Capeicorn Yellow Chat *Epthianura crocea macgregori*: consequences for conservation management. *Bird Conservation International*, 28: 116–125.

Hughes, J. B., Daily, G. C., Ehrlich, P. R., 1997. Population Diversity: Its Extent and Extinction. *Science*, 278: 689–692.

Isakkson, M., Tegelstrom, H., 2002. Characterization of polymorphic microsatellite markers in a captive population of the eagle owl (*Bubo bubo*) used for supportive breeding. *Molecular Ecology Notes*, 2: 91–93.

IUCN, 2001. *IUCN Red List Categories and Criteria: Version 3.1*. IUCN Species Survival Commission. IUCN, Gland, Switzerland and Cambridge, U.K.
and other conservation translocations. Version 1.0. Gland, Switzerland: IUCN Species Survival Commission.

IUCN Standards and Petitions Subcommittee, 2015. Guidelines for Using the IUCN Red List Categories and Criteria. Version 11. Prepared by the Standards and Petitions Subcommittee, http://www.iucnredlist.org/documents/RedListGuidelines.pdf [Accessed on 10 December 2015].

Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K., Mooers, A. O., 2012. The global diversity of birds in space and time. Nature, 491: 444–448.

Ji, Y. J., Liu, Y. D., Ding, C. Q., Zhang, D. X., 2004. Eight polymorphic microsatellite loci for the critically endangered crested ibis, Nipponia nippon (Ciconiiformes: Threskiornithidae). Molecular Ecology Notes, 4: 615–617.

Jin, J., Ele, R., Gong, H., Wang, W., 2018. Role of risk preferences in explaining the public’s willingness to pay for marine turtle conservation in China. Ocean & Coastal Management, 160: 52–57.

Jombart, T., Balloux, F., Dray, S., 2010. adephylo: New tools for investigating the phylogenetic signal in biological traits. Bioinformatics, 26: 1907–1909.

Jones, K. E., Purvis, A., Gittleman, J. L., 2003. Biological correlates of extinction risk in bats. The American Naturalist, 161: 601–614.

Kalinowski, S. T., 2002. How many alleles per locus should be used to estimate genetic distances? Heredity, 88: 62–65.

Kangas, V.–M., Carrillo, J., Debray, P., Kivist, L., 2018. Bottlenecks, remoteness, admixture shape genetic variation in island populations of Atlantic and Mediterranean common kestrels (Falco tinnunculus). Journal of Avian Biology, 49: e01768.

Kennedy, J. D., Borregaard, M. K., Janssøn, K. A., Holt, B., Fjeldså, J., Rahbek, C., 2017. Does the glacial history and colonization of Europe influence the diversification and accumulation of clade rich bird species. Evolutionary Ecology, 25: 3833–3844.

Krüger, O., Radford, A. N., 2008. Doomed to die? Predicting extinction risk in the true hawks Accipitrinae. Animal Conservation, 11: 83–91.

Kvist, L., Ruokonen, M., Lumme, J., Orell, M., 1999. Different population structures in northern and southern populations of the European blue tit (Parus caeruleus). Journal of Evolutionary Biology, 12: 798–805.

Kvist, L., Viiri, K., Dias, P.C., Rytkonen, S., Orell, M., 2004. Glacial history and colonization of Europe by the blue tit Parus caeruleus. Journal of Avian Biology, 35: 352–359.

LaManna, J. A., Martin, T. E., 2016. Logging impacts on avian species richness and composition differ across latitudes and foraging and breeding habitat preferences. Biological Reviews of the Cambridge Philosophical Society, 92: 1657–1674.

Lamoreux, J., Akçakaya, H. R., Bennett, L., Collar, N. J., Bolteni, L., Brackett, D., Brautgam, A., Brooks, T. M., da Fonseca G. A. B., Mittermeier, R. A., Rylands, A. B., Gårdenfors, U., Hilton–Taylor, C., Mace, G., Stein, B. A., Stuart, S., 2003. Value of the IUCN Red List. Trends in Ecology & Evolution, 18: 214–215.

Lee, C.–R., Mitchell–Olds, T., 2011. Quantifying effects of environmental and geographical factors on patterns of genetic differentiation. Molecular Ecology, 20: 4631–4642.

Li, S., Li, B., Cheng, C., Xiong, Z., Liu, Q., Lai, J., Carey, H. V, Zhang, Q., Zheng, H., Wei, S., Zhang, H., Chang, L., Liu, S., Zhang, S., Yu, B., Zeng, X., Hou, Y., Nie, W., Guo, Y., Chen, T., Han, J., Wang, J., Wang, J., Chen, C., Liu, J., Stambrook, P. J., Xu, M., Zhang, G., Gilbert, M. T. P., Yang, H., Jarvis, E. D., Yu, J., Yan, J., 2014. Genomic signatures of near–extinction and rebirth of the crested ibis and other endangered bird species. Genome Biology, 15: 1–16.

Li, X., Tian, H., Li, D., 2009. Why the crested ibis declined in the middle twentieth century. Biodiversity and Conservation, 18: 2165–2172.

Limborg, M. T., Helyar, S. J., De Bruyn, M., Taylor, M. I., Nielsen, E. E., Ogden, R., Carvalho, G. R., Bekkavold, D., 2012. Environmental selection on transcriptome–derived SNPs in a high gene flow marine fish, the Atlantic herring (Clupea harengus). Molecular Ecology, 21: 3686–3703.

Losos, J. B., Baum, D. A., Futuyma, D. J., Hoekstra, H. E, Lenski, R. E., Moore, A. J., Peichel, C. L., Schluter, D., Whithlock, M. C., 2013. The princeton guide to evolution. Princeton University Press, New Jersey, USA.

Lyu, D., Wu, H., Hu, Y., Wang, W., 2018. Inbreeding evaluation using microsatellite and its effect on growth traits in turbot, Scophthalmus maximus. Aquaculture Research, 49: 1176–1181.

Mace, G. M., Collar, N. J., Gaston, K. J., Hilton–Taylor, C., Akçakaya, H. R., Leader–Williams, N., Milner–Gulland, E. J., Stuart, S. N., 2008. Quantification of extinction risk: IUCN’s system for classifying threatened species. Conservation Biology, 22: 1424–1442.

Martinez–Cruz, B., David, V. A., Godoy, J. A., Negro, J. J., O’Brien, S. J., Johnson, W. E., 2002. Eighteen polymorphic microsatellite markers for the highly endangered Spanish imperial eagle (Aquila adalberti) and related species. Molecular Ecology Notes, 2: 323–326.

Martinez–Cruz, B., 2011. Conservation genetics of Iberian Raptors. Animal Biodiversity and Conservation, 34: 341–353.

Martins, E. P., Hansen, T. F., 1997. Phylogenies and the comparative method: a general approach to incorporating phylogenetic information in to analysis of interspecific data. The American Naturalist, 149: 646–667 (erratum in The American Naturalist, 153: 448).

McCormack, J. E., Harvey, M. G., Faircloth, B. C., Crawford, N. G., Glenn, T. C., Brumfield, R. T.,
2013. A Phylogeny of Birds Based on Over 1,500 Loci Collected by Target Enrichment and High–Throughput Sequencing. Plos One, 8: e54848.

Miller, R. M., Rodriguez, J. P., Aniskowicz–Fowler, T., Bambaradeniya, C., Boles, R., Eaton, M. A., Gardenfors, U., Keller, V., Molur, S., Walker, S., Pollock, C., 2007. National threatened species listing cases: 2004–06 criteria and regional guidelines: Current status and future perspectives. Conservation Biology, 21: 684–696.

Miño, C. I., Sawyer, G. M., Benjamin, R. C., Del Lama, S. N., 2009. Parentage and relatedness in captive and natural populations of the Roseate Spoonbill (Aves: Ciconiiformes) based on microsatellite data. Journal of Experimental Zoology Part A Ecological Genetics and Physiology, 311A: 453–464.

Moura, R. F., Dawson, D. A., Nogueira, D. M., 2017. The use of microsatellite markers in Neotropical studies of wild birds: a literature review. Anais da Academia Brasileira de Ciências, 89: 145–154.

Moussy, C., Arlettaz, R., Copete, J. L., Dale, S., Dombrovski, V., Elts, J., Lorrillière, R., Marja, R., Pasquet, E., Piha, M., Seinola, T., Selstam, G., Jiquet, F., 2018. The genetic structure of the European breeding populations of a declining farmland bird, the ortolan bunting (Emberiza hortulana), reveals conservation priorities. Conservation Genetics, https://doi.org/10.1007/s10592–018–1064–9

Munday, P. L., Warner, R. R., Monro, K., Pandolfi, J. M., Marshall, D. J., 2013. Predicting evolutionary responses to climate change in the sea. Ecology Letters, 16: 1488–1500.

Nam, D.–H., Lee, D.–P., 2009. Abnormal lead exposure in globally threatened Cinereous vultures (Aegypius monachus) wintering in South Korea. Ecotoxicology, 18: 225–229.

Nei, M., 1978. Estimation of average heterozygosity and genotype distance from a small number of individuals. Genetics, 89: 583–590.

Neigel, J. E., Avisé, J. C., 1993. Application of a random walk to geographic distributions of animal mitochondrial DNA variation. Genetics, 135, 1209–1220.

Neumann, K., Wetton, J. H., 1996. Highly polymorphic microsatellites in the house sparrow Passer domesticus. Molecular Ecology, 5: 307–309.

Olano–Marín, J., Dawson, D. A., Girg, A., Hansson, B., Ljungqvist, M., Kempenaers, B., Mueller, J. C., 2010. A genome–wide set of 106 microsatellite markers for the blue tit (Cyanistes caeruleus). Molecular Ecology Resources, 10: 516–532.

Orme, D., 2013. The caper package: comparative analysis of phylogenetics and evolution in R. R package, version 5.

Otter, K., Ratcliffe, L., Michaud, D., Boag, P. T., 1998. Do female black–capped chickadees prefer high–ranking males as extra–pair partners? Behavioral Ecology and Sociobiology, 43: 25–36.

Padoa–Schioppa, E., Baietto, M., Massa, R., Bottoni, L., 2006. Bird communities as bioindicators: The focal species concept in agricultural landscapes. Ecological Indicators, 6: 83–93.

Paradis, E., Baillie, S. R., Sutherland, W. J., Gregory, R. D., 1998. Patterns of natal and breeding dispersal in birds. Journal of Animal Ecology, 67: 518–536.

Paradis, E., Claude, J., Strimmer, K., 2004. APE: analyses of phylogenetics and evolution in R language. Bioinformatics, 20: 289–290.

Pavoine, S., Ollier, S., Pontier, D., Chessel, D., 2008. Testing for phylogenetic signal in phenotypic traits: New matrices of phylogenetic proximities. Theoretical Population Biology, 73: 79–91

Pereira, G. A., Dantas, S. M., Silveira, L. F., Roda, S. A., Abano, C., Sonntag, F. A., Leal, S., Periquito, M. A., Malacco, G. B., Lees, A. C., 2014. Status of the globally threatened forest birds of northeast Brazil. Papéis Avulsos de Zoologia, 54: 177–194.

Piekarski, A., Greene, E., Anthony, N. B., Bottje, W., Dridi, S., 2015. Crossopt between autochog and obesity: potential use of avian model. Advances In Food Technology and Nutritional Sciences – Open Journal, 1: 32–37.

Poulakakis, N., Anthouli, A., Mantziou, G., Parmakelis, A., Skartsi, T., Vasilakis, D., Elorriaga, J., De La Puente, J., Gavashelishvili, A., Ghasabayan, M., Katzner, T., McGrady, M., Batbayar, N., Fuller, M., Natsagdorj, T., 2008. Population structure, diversity, and phylogeography in the near–threatened Eurasian black vultures Aegypius monachus (Falconiformes; Accipitridae) in Europe: Insights from microsatellite and mitochondrial DNA variation. Biological Journal of the Linnean Society, 95: 859–872.

Piertney, S. B., Höglund, J., 2001. Polymorphic microsatellite DNA markers in black grouse (Tetrao tetrix). Molecular Ecology Notes, 1: 303–304.

R Core Team. R: A language and environmental for statistical computing. R Foundation for Statistical Computing, Vienna, Austria, http://www.R–project.org/2018

Rabaud, S., Coreau, A., Merlet, L., 2018. Red lists of threatened species – Indicators with the potential to act as strategic circuit breakers between science and policy. Environmental Science and Policy.

Rajkumar, U., Gupta, B. R., Reddy, A. R., 2008. Genomic heterogeneity of chicken populations in India. Asian–Australasian Journal of Animal Science, 21: 1710–1720.

Ram, D., Axelsson, A.–L., Green, M., Smith, H. G., Lindström, Å., 2017. What drives current population trends in forest birds – forest quantity, quality or climate? A large–scale analysis from northern Europe. For. Ecol. Manage., 385: 177–188.

Randler, C., 2006. Behavioural and ecological correlates of natural hybridization in birds. Ibis, 148: 459–467.

Razgour, O., Taggart, J. B., Manel, S., Just, J., Ibáñez, C., Rebelo, H., Alberdi, A., Jones, G., Park., K., 2018. An integrated framework to identify wildlife populations under threat from climate change. Molecular Ecology Resources, 18: 18–31.

Richardson, D. S., Jury, F. L., Dawson, D. A., Salgueiro, P., Komdeur, J., Burke, T., 2000. Fifty Seychelles warbler (Acrocephalus sechellensis) microsatellite loci polymorphic in Sylvidae species and their cross–species amplification in other passerine birds. Molecular Ecology, 9: 2225–2230.
Rodríguez–Muñoz, R., Mirol, P. M., Segelbacher, G., Fernández, A., Tregenza, T., 2007. Genetic differentiation of an endangered capercaillie (Tetrao urogallus) population at the Southern edge of the species range. Conservation Genetics, 8: 659–670.

Rodríguez, J. P., Ashenfelter, G., Rojas–Suárez, F., García Fernández, J. J., Suárez, L., Dobson, A. P., 2000. Local data are vital to worldwide conservation. Nature, 403: 241–241.

Segelbacher, G., Paxton, R. J., Steinbrück, G., Trontelj, P., Storch, I., 2000. Characterization of microsatellites in capercaillie Tetrao urogallus (AVES). Molecular Ecology, 9: 1934–1935.

Selwood, K. E., McGeoch, M. A., Clarke, R. H., 2017. High-productivity vegetation is important for lessening bird declines during prolonged drought. Proceedings of the National Academy of Sciences, 25: 24084–24092.

Slate, J., Hale, M. C., Birkhead, T. R., 2007. Simple sequence repeats in zebra finch (Taeniopygia guttata) expressed sequence tags: a new resource for evolutionary genetic studies of passerines. BMC Genomics, 8: 52.

Souto, H. N., de Campos Júnior, E. O., Campos, C. F., Morelli, S., 2018. Biomonitoring birds: the use of a micronuclei test as a tool to assess environmental pollutants on coffee farms in southeast Brazil. Environmental Science and Pollution Research, 25: 24084–24092.

Spielman, D., Brook, B. W., Frankham, R., 2004. Most species are not driven to extinction before genetic factors impact them. Proceedings of the National Academy of Sciences, 101: 15261–15264.

Stephens, S. E., Koons, D. N., Rotella, J. J., Willey, D. W., 2003. Effects of habitat fragmentation on avian nesting success: a review of the evidence at multiple spatial scales. Biological Conservation, 115: 101–110.

Stoianovic, D., Olah, G., Webb, M., Peakall, R., Heinsohn, R., 2018. Genetic evidence confirms severe extinction risk for critically endangered swift parrots: implications for conservation management. Animal Conservation, 21: 313–323.

Storch, I., Bafuelos, M. J., Fernández–Gil, A., Obeso, J. R., Quevedo, M., Rodríguez–Muñoz, R., 2006. Subspecies Cantabrian capercaillie Tetrao urogallus cantabricus endangered according to IUCN criteria. Journal of Ornithology, 147: 653–655.

Tautz, D., Renz, M., 1984. Simple sequences are ubiquitous repetitive components of eukaryotic genomes. Nucleic Acids Research, 12: 4127–4138.

Thompson III, F. R., Donovan, T. M., DeGraff, R. M., Faaborg, J., Robinson, S. K., 2002. A multi-scale perspective of the effects of forest fragmentation on birds in eastern forests. Studies in Avian Biology, 25: 8–19.

Tisdell, C., Nantha, H. S., Wilson, C., 2007. Endangerment and likeability of wildlife species: How important are they for payments proposed for conservation? Ecological Economics, 60: 627–633.

Tucker, C. M., Cadotte, M. W., Carvalho, S. B., Davies, T. J., Ferrier, S., Fritz, S. A., Grenver, R., Helmus, M. R., Jin, L. S., Mooers, A. O., Pavoine, S., Purschke, O., Redding, D. W., Rosauer, D. F., Winter, M., Mazel, F., 2017. A guide to phylogenetic metrics for conservation, community ecology and macroecology. Biological Reviews of the Cambridge Philosophical Society, 92: 698–715.

Tucker, G. M., Heath, M. F., 1994. Birds in Europe. Their conservation status, 1st edition. BirdLife International, Cambridge.

Wraith, J., Pickering, C., 2018. Quantifying anthropogenic threats to orchids using the IUCN Red List. Ambio, 47: 307–317.

Väli, Ü., Dombrovski, V., Treinys, R, Bergmanis, U., Daróczí, S. J., Dravecky, M., Ivanovsk, V., Lontkowski, J., Maciorowski, G., Meyburg, B.–U., Mizer, T., Zeitz, R., Ellegrén, H., 2010. Widespread hybridization between the Greater Spotted Eagle Aquila clanga and the Lesser Spotted Eagle Aquila pomarina (Aves: Accipitriformes) in Europe. Biological Journal of the Linnean Society, 100: 725–736.

Van De Pol, M., Ens, B. J., Heg, D., Brouwer, L., Krol, J., Maier, M., Exo, K.–M., Oosterbeek, K., Lok, T., Eising, C. M., Koffijberg, K., 2010. Do changes in the frequency, magnitude and timing of extreme climatic events threaten the population viability of coastal birds? Journal of Applied Ecology, 47: 720–730.

Yong, D. L., Lim, K. S., Lim, K. C., Tan, T., 2018. Significance of the globally threatened Straw–headed Bulbul Pycnonotus zeylanicus populations in Singapore: a last straw for the species? Bird Conservation International, 28: 133–144.

Zanetti, E., De Marchi, M., Abbad, M., Cassandro, M., 2011. Variation of genetic diversity over time in local Italian chicken breeds undergoing in situ conservation. Poultry Science, 90: 2195–2201.

Zhang, B., Fang, S.–G., Xi, Y.–M., 2004. Low genetic diversity in the Endangered Crested Ibis Nipponia nippon and implications for conservation. Bird Conservation International, 14: 183–190.

Zollinger, S. A., Podos, J., Nemeth, E., Goller, F., Brumm, H., 2012. On the relationship between, and measurement of, amplitude and frequency in birdsong. Animal Behavior, 84: e1–e9.
### Supplementary material

Table 1s. Species found in published papers, with the respective IUCN categories and taxonomic classification regarding order and family.

Tabla 1s. Especies encontradas en artículos publicados, con las respectivas categorías de la UICN y la clasificación taxonómica con respecto al orden y la familia.

| Species                     | IUCN | Order             | Family             |
|-----------------------------|------|-------------------|--------------------|
| Acanthisitta chloris        | LC   | Passeriformes     | Acanthisittidae    |
| Accipiter gentils           | LC   | Falconiformes     | Accipitridae       |
| Aceros leucocephalus        | NT   | Coraciiformes     | Bucerotidae        |
| Aceros waldeni              | CR   | Coraciiformes     | Bucerotidae        |
| Acrocephalus arundinaceus   | LC   | Passeriformes     | Sylviidae          |
| Acrocephalus familiaris     | CR   | Passeriformes     | Sylviidae          |
| Acrocephalus paludicola     | VU   | Passeriformes     | Sylviidae          |
| Acrocephalus schoenobaenus  | LC   | Passeriformes     | Sylviidae          |
| Acrocephalus scirpaceus     | LC   | Passeriformes     | Sylviidae          |
| Acrocephalus sechellensis   | VU   | Passeriformes     | Sylviidae          |
| Aegithalos caudatus         | LC   | Passeriformes     | Aegithalidae       |
| Aegithalos concinnus        | LC   | Passeriformes     | Aegithalidae       |
| Aegithalos glaucogularis    | LC   | Passeriformes     | Aegithalidae       |
| Aerodramus fuciphagus       | LC   | Apodiformes       | Apodidae           |
| Aethia cristatella          | LC   | Charadriiformes   | Alcidae            |
| Aethia psittacula           | LC   | Charadriiformes   | Alcidae            |
| Aethia pusilla              | LC   | Charadriiformes   | Alcidae            |
| Aethia pygmaea              | LC   | Charadriiformes   | Alcidae            |
| Agelaius phoeniceus         | LC   | Passeriformes     | Icteridae          |
| Agelaius xanthomus          | EN   | Passeriformes     | Icteridae          |
| Alectoris rufa              | LC   | Galiformes        | Phasianidae        |
| Alectrurus risora           | VU   | Passeriformes     | Tyrannidae         |
| Alectura lathami            | LC   | Galiformes        | Megapodiidae       |
| Alle alle                   | LC   | Charadriiformes   | Alcidae            |
| Alophoixus pallidus         | LC   | Passeriformes     | Pycnonotidae       |
| Amazona aestiva             | LC   | Psittaciformes    | Psittacidae        |
| Amazona leucocephala        | NT   | Psittaciformes    | Psittacidae        |
| Amazona vittata             | CR   | Psittaciformes    | Psittacidae        |
| Ammodramus caudactus        | VU   | Passeriformes     | Emberizidae        |
| Anas laysanensis            | CR   | Anseriformes      | Anatidae           |
| Anas platyrhynchos          | LC   | Anseriformes      | Anatidae           |
| Anas superciliosa           | LC   | Anseriformes      | Anatidae           |
| Anodorhynchus hyacinthinus   | EN   | Psittaciformes    | Psittacidae        |
| Anodorhynchus leari         | EN   | Psittaciformes    | Psittacidae        |
| Anthobaphes violacea        | LC   | Passeriformes     | Nectariniidae       |
| Anthornis melanura          | LC   | Passeriformes     | Meliphagidae       |
| Aphrastura spinicauda       | LC   | Passeriformes     | Furnariidae        |
| Species                        | IUCN | Order             | Family          |
|-------------------------------|------|-------------------|-----------------|
| Aquila audax                  | LC   | Accipitriformes   | Accipitridae    |
| Aquila chrysaetos             | LC   | Falconiformes     | Accipitridae    |
| Aquila fasciatus              | LC   | Falconiformes     | Accipitridae    |
| Ara ararauna                  | LC   | Psittaciformes    | Psittacidae     |
| Ara chloropterus              | LC   | Psittaciformes    | Psittacidae     |
| Ara macao                     | LC   | Psittaciformes    | Psittacidae     |
| Arborophila rufiplectus       | EN   | Galliformes       | Phasianidae     |
| Ardea herodias                | LC   | Ciconiformes      | Ardeidae        |
| Armon torquatus               | LC   | Passeriformes     | Emberizidae     |
| Athenes cunicularia           | LC   | Strigiformes      | Strigidae       |
| Atlapetes latinuchus          | LC   | Passeriformes     | Emberizidae     |
| Atlapetes pallidiceps         | EN   | Passeriformes     | Emberizidae     |
| Attagornis clamosus           | EN   | Passeriformes     | Atrichornithidae|
| Balearia regulorum            | EN   | Gruiformes        | Gruidae         |
| Bartramia longicauda          | LC   | Charadriiformes   | Scolopacidae    |
| Biziura lobata                | LC   | Anseriformes      | Anatidae        |
| Branta bernica                | LC   | Anseriformes      | Anatidae        |
| Branta canadensis             | LC   | Anseriformes      | Anatidae        |
| Buarremon torquatus           | LC   | Passeriformes     | Emberizidae     |
| Bubo blakistoni               | EN   | Strigiformes      | Strigidae       |
| Bubo bubo                     | LC   | Strigiformes      | Strigidae       |
| Bucanetes githagineus         | LC   | Passeriformes     | Fringillidae     |
| Bucerahala islandica          | LC   | Anseriformes      | Anatidae        |
| Bucorvus leadbeateri          | VU   | Coraciiformes     | Bucorvidae      |
| Burhinus oedicnemus           | LC   | Charadriiformes   | Burhinidae      |
| Buteo buteo                   | LC   | Falconiformes     | Accipitridae    |
| Buteo ridgwayi                | CR   | Falconiformes     | Accipitridae    |
| Calidris alba                 | LC   | Charadriiformes   | Scolopacidae    |
| Calidris philocnemis          | LC   | Charadriiformes   | Scolopacidae    |
| Calidris temminckii           | LC   | Charadriiformes   | Scolopacidae    |
| Callipepla squamata           | LC   | Galliformes       | Odontophoridae  |
| Calyptorhynchus banksii       | LC   | Psittaciformes    | Psittacidae     |
| Calyptorhynchus baudini       | EN   | Psittaciformes    | Psittacidae     |
| Calyptorhynchus latrostris    | EN   | Psittaciformes    | Psittacidae     |
| Campylopeperus curvipennis    | LC   | Caprimulgiformes  | Trochilidae     |
| Campylorhynchus brunneicapillu| LC   | Passeriformes     | Trogodytidae    |
| Carpodacus mexicanus          | LC   | Passeriformes     | Fringillidae    |
| Catharus ustulatus            | LC   | Passeriformes     | Turdidae        |
| Centrocercus urophasianus     | NT   | Galliformes       | Phasianidae     |
| Cerorhina monocerata          | LC   | Charadriiformes   | Alidae          |
Table 1s. (Cont.).

| Species                        | IUCN | Order                      | Family          |
|--------------------------------|------|----------------------------|-----------------|
| *Chalcites basalis*            | LC   | Cuculiformes               | Cuculidae       |
| *Chalcites lucidus*            | LC   | Cuculiformes               | Cuculidae       |
| *Chalcites minutillus*         | LC   | Cuculiformes               | Cuculidae       |
| *Chamaea fasciata*             | LC   | Passeriformes              | Timaliidae      |
| *Charadrius marginatus*        | LC   | Charadriiformes            | Charadriidae    |
| *Charadrius pecuarius*         | LC   | Charadriiformes            | Charadriidae    |
| *Charadrius thoracicus*        | VU   | Charadriiformes            | Charadriidae    |
| *Chersophilus duponti*         | NT   | Passeriformes              | Alaudidae       |
| *Chiropygia caudata*           | LC   | Passeriformes              | Pipridae        |
| *Chlamydotis macqueenii*       | VU   | Otidiformes                | Otidae          |
| *Chlidonias hybrida*           | LC   | Charadriiformes            | Laridae         |
| *Chlondestes grammacus*        | LC   | Passeriformes              | Emberizidae     |
| *Ciconia ciconia*              | LC   | Ciconiiformes              | Ciconiidae      |
| *Cinclis cinclus*              | LC   | Passeriformes              | Cinclidae       |
| *Cinnyris stuhmanni*           | LC   | Passeriformes              | Nectariniidae   |
| *Circus pygargus*              | LC   | Accipitriformes            | Accipitridae    |
| *Colaptes auratus*             | LC   | Piciformes                 | Picidae         |
| *Colinus virginianus*          | NT   | Galliformes                | Odontophoridae  |
| *Columba janthina nitens*      | NT   | Columbiformes              | Columbidae      |
| *Columba livia*                | LC   | Columbiformes              | Columbidae      |
| *Coracias garrulus*            | NT   | Coraciiformes              | Coraciidae      |
| *Coracina newtoni*             | CR   | Passeriformes              | Campephagidae   |
| *Corapipo altera*              | LC   | Passeriformes              | Pipridae        |
| *Corvus brachyrhynchos*        | LC   | Passeriformes              | Corvidae        |
| *Corvus corone*                | LC   | Passeriformes              | Corvidae        |
| *Corvus monedulae*             | LC   | Passeriformes              | Corvidae        |
| *Coturnix japonica*            | NT   | Galliformes                | Phasianidae     |
| *Crax globulosa*               | EN   | Galliformes                | Cracidae        |
| *Crossopis auritum*            | LC   | Galliformes                | Phasianidae     |
| *Culicivora caudacuta*         | VU   | Passeriformes              | Tyrannidae      |
| *Cyanistes caeruleus*          | LC   | Passeriformes              | Paridae         |
| *Cyanocitta stelleri*          | LC   | Passeriformes              | Corvidae        |
| *Cyanopsitta spixii*           | CR   | Psittaciformes             | Psittacidae     |
| *Cygns atratus*                | LC   | Anseriformes               | Anatidae        |
| *Cygns buccinator*             | LC   | Anseriformes               | Anatidae        |
| *Cyphorhinus phaeoccephalus*   | LC   | Passeriformes              | Troglodytidae   |
| *Dasyornis brachypterus*       | EN   | Passeriformes              | Dasyornithidae  |
| *Dendroicnica turdina*         | LC   | Passeriformes              | Dendrocolaptidae|
| *Dendroica chrysoparia*        | EN   | Passeriformes              | Parulidae       |
| *Dinornis robustus*            | EX   | Dinornithiformes           | Dinornithidae   |
| Species                          | IUCN | Order                          | Family                  |
|---------------------------------|------|--------------------------------|-------------------------|
| *Diomedea exulans*              | VU   | Procellariiformes              | Diomedeidae             |
| *Dromaius novaehollandiae*      | LC   | Struthioniformes               | Dromaiidae              |
| *Drymodes brunneopygia*         | LC   | Passeriformes                  | Sylviiidae              |
| *Ecclectus roratus*             | LC   | Psittaciciformes               | Psitticidae             |
| *Egretta eulophotes*            | VU   | Pelecaniformes                 | Ardeidae                |
| *Egretta rufescens*             | NT   | Ciconiformes                  | Ardeidae                |
| *Elaenia ruficeps*              | LC   | Passeriformes                  | Tyrannidae              |
| *Emberiza cia*                  | LC   | Passeriformes                  | Emberizidae             |
| *Emberiza citrinella*           | LC   | Passeriformes                  | Emberizidae             |
| *Emberiza schoeniclus*          | LC   | Passeriformes                  | Emberizidae             |
| *Emeus crassus*                 | EX   | Struthioniformes               | Dinornithidae           |
| *Empidonax traillii*            | LC   | Passeriformes                  | Tyrannidae              |
| *Ephthianura albifrons*         | LC   | Passeriformes                  | Meliphagidae            |
| *Eudocimus ruber*               | LC   | Ciconiformes                  | Threskiornithidae       |
| *Eudyptes chrysolophus*         | VU   | Sphenisciformes                | Spheniscidae            |
| *Eudyptula minor*               | LC   | Sphenisciformes                | Spheniscidae            |
| *Eulidia yarrellii*             | EN   | Apodiformes                   | Trochilidae             |
| *Euryapteryx curtus*            | EX   | Dinornithiformes               | Emeidae                 |
| *Falco deiroleucus*             | NT   | Falconiformes                 | Falconidae              |
| *Falco naumannii*               | LC   | Falconiformes                 | Falconidae              |
| *Falco peregrinus*              | LC   | Falconiformes                 | Falconidae              |
| *Falco sparverius*              | LC   | Falconiformes                 | Falconidae              |
| *Falco tinnunculus*             | LC   | Falconiformes                 | Falconidae              |
| *Ficedula hypoleuca*            | LC   | Passeriformes                  | Muscicapidae            |
| *Ficedula parva*                | LC   | Passeriformes                  | Muscicapidae            |
| *Francolinus francescinus*      | LC   | Galliformes                   | Phasianidae             |
| *Fringilla teydea*              | NT   | Passeriformes                 | Fringillidae            |
| *Fulica alai*                   | VU   | Gruiformes                    | Rallidae                |
| *Galerida cristata*             | LC   | Passeriformes                 | Alaudidae               |
| *Galerida theklae*              | LC   | Passeriformes                 | Alaudidae               |
| *Gallinula chloropus*           | LC   | Gruiformes                    | Rallidae                |
| *Gallinula galeata sandvicensis*| LC   | Gruiformes                    | Rallidae                |
| *Gallus gallus*                 | LC   | Galliformes                   | Phasianidae             |
| *Garrulax elliotii*             | LC   | Passeriformes                 | Timaliidae              |
| *Gavia immer*                   | LC   | Gaviiformes                   | Gaviidae                |
| *Geospiza magnirostris*         | LC   | Passeriformes                 | Emberizidae             |
| *Geothlypis beldingi*           | EN   | Passeriformes                 | Parulidae               |
| *Grus carunculatus*             | VU   | Gruiformes                    | Gruidae                 |
| *Grus japonensis*               | EN   | Gruiformes                    | Gruidae                 |
| *Grus leucogeranus*             | CR   | Gruiformes                    | Gruidae                 |
| Species                          | IUCN | Order              | Family       |
|----------------------------------|------|--------------------|--------------|
| *Grus paradisea*                 | VU   | Gruiformes         | Gruidae      |
| *Guira guira*                    | LC   | Cuculiformes       | Cuculidae    |
| *Gyps bengalensis*               | CR   | Accipitriformes    | Accipitridae |
| *Gyps indicus*                   | CR   | Accipitriformes    | Accipitridae |
| *Gyps tenuirostris*              | CR   | Accipitriformes    | Accipitridae |
| *Haliaeetus albicilla*           | LC   | Falconiformes      | Accipitridae |
| *Haliaeetus vociferoides*        | CR   | Falconiformes      | Accipitridae |
| *Harpia harpyja*                 | NT   | Accipitriformes    | Accipitridae |
| *Henicorhina leucophrys*         | LC   | Coraciiformes      | Bucerotidae  |
| *Heteralocha acutirostris*       | EX   | Passeriformes      | Callaeidae   |
| *Himantopus leucocephalus*       | LC   | Charadriiformes    | Recurvirostridae |
| *Himantopus novaehollandiae*     | CR   | Charadriiformes    | Recurvirostridae |
| *Hippolais icterina*             | LC   | Passeriformes      | Sylviae      |
| *Hippolais polyglotta*           | LC   | Passeriformes      | Sylviae      |
| *Hirundo rustica*                | LC   | Passeriformes      | Hirundinidae |
| *Lagonosticta sanguinodorsalis*  | LC   | Passeriformes      | Estrildidae  |
| *Lagopus muta pyrenaica*         | LC   | Galliformes        | Phasianidae  |
| *Laniarius atrocinus*            | LC   | Passeriformes      | Malaconotidae |
| *Larus marinus*                  | LC   | Charadriiformes    | Laridae      |
| *Larus saundersi*                | VU   | Charadriiformes    | Laridae      |
| *Larus smithsonianus*            | LC   | Charadriiformes    | Laridae      |
| *Leptoptilos crumenifer*         | LC   | Ciconiformes       | Ciconiidae   |
| *Limothlypis swainsonii*         | LC   | Passeriformes      | Parulidae    |
| *Liocichla steeri*               | LC   | Passeriformes      | Timaliidae   |
| *Lonchura cantans*               | LC   | Passeriformes      | Estrildidae  |
| *Malurus coronatus*              | LC   | Passeriformes      | Maluridae    |
| *Meleagris gallopavo*            | LC   | Galliformes        | Phasianidae  |
| *Melospiza melodia*              | LC   | Passeriformes      | Emberizidae  |
| *Merops ornatus*                 | LC   | Coraciiformes      | Meropidae    |
| *Mimus parvulus*                 | LC   | Passeriformes      | Mimidae      |
| *Modulatrix stictigula*          | LC   | Passeriformes      | Muscicapidae |
| *Mohoua ochrocephala*            | EN   | Passeriformes      | Acanthizidae |
| *Morphnus guianensis*            | NT   | Accipitriformes    | Accipitridae |
| *Mycteria americana*             | LC   | Ciconiformes       | Ciconiidae   |
| *Neothraupis fasciata*           | NT   | Passeriformes      | Thraupidae   |
| *Nestor notabilis*               | VU   | Psittaciformes     | Strigopidae  |
| *Ninox connivens*                | LC   | Strigiformes       | Strigidae    |
| *Ninox novaeseelandiae*          | LC   | Strigiformes       | Strigidae    |
| *Ninox strenua*                  | LC   | Strigiformes       | Strigidae    |
| *Nipponia nippon*                | EN   | Ciconiformes       | Threskiornithidae |
Table 1s. (Cont.)

| Species                              | IUCN | Order                          | Family                      |
|--------------------------------------|------|--------------------------------|-----------------------------|
| Nisaetus nipalensis                  | LC   | Falconiformes                  | Accipitridae                |
| Notiomystis cincta                   | VU   | Passeriformes                  | Meliphagidae                |
| Nucifraga columbiana                 | LC   | Passeriformes                  | Corvidae                    |
| Numida meleagris                     | LC   | Galliformes                    | Numididae                   |
| Nycticorax nycticorax                | LC   | Ciconiiformes                  | Ardeidae                    |
| Oceanodroma leucocephala             | LC   | Procellariiformes              | Hydrobatidae                |
| Orthonyx temminckii                  | LC   | Passeriformes                  | Orthonychidae               |
| Otis tarda                           | VU   | Gruiformes                     | Otidae                      |
| Oxyura jamaicensis                   | LC   | Anseriformes                   | Anatidae                    |
| Oxyura leucocephala                  | EN   | Anseriformes                   | Anatidae                    |
| Pachycephala pectoralis              | LC   | Passeriformes                  | Pachycephalidae             |
| Pachyornis elephasitos               | EX   | Struthioniformes               | Dinomithidae                |
| Paradoxornis heudei                  | NT   | Passeriformes                  | Timaliidae                  |
| Pandion haliaetus                    | LC   | Accipitriformes                | Pandionidae                 |
| Paradoxornis heudei                  | NT   | Passeriformes                  | Timaliidae                  |
| Parus caeruleus                      | LC   | Passeriformes                  | Paridae                     |
| Parus major                          | LC   | Passeriformes                  | Paridae                     |
| Passer domesticus                    | LC   | Passeriformes                  | Passeridae                  |
| Passer montanus                      | LC   | Passeriformes                  | Passeridae                  |
| Pauxi mitu                           | EW   | Galliformes                    | Cracidae                    |
| Pauxi tuberosa                       | LC   | Galliformes                    | Cracidae                    |
| Pelecanus onocrotalus                | LC   | Pelecaniformes                 | Pelecanidae                 |
| Penelopides affinis                  | LC   | Coraciiformes                  | Bucerotidae                 |
| Penelopides manillae                 | LC   | Coraciiformes                  | Bucerotidae                 |
| Penelopides panini                   | EN   | Coraciiformes                  | Bucerotidae                 |
| Perisoreus infaustus                 | LC   | Passeriformes                  | Corvidae                    |
| Petrochelidon fulva                  | LC   | Passeriformes                  | Hirundinidae                |
| Petroica australis                   | LC   | Passeriformes                  | Petroicidae                 |
| Petroica goodenovii                  | LC   | Passeriformes                  | Petroicidae                 |
| Peucaea aestivali                    | NT   | Passeriformes                  | Emberizidae                 |
| Phalacrococarx aristotelis           | LC   | Suliformes                     | Phalacrocoracidae           |
| Phalacrococarx atriceps              | LC   | Suliformes                     | Phalacrocoracidae           |
| Phalacrocorax fuscescen              | LC   | Pelecaniformes                 | Phalacrocoracidae           |
| Philesturnus carunculatus            | NT   | Passeriformes                  | Callaeatidae                |
| Philesturnus rufusater               | NT   | Passeriformes                  | Callaeatidae                |
| Philomachus pugnax                   | LC   | Charadriformes                 | Scolopacidae                |
| Phoebastria albatrus                 | VU   | Procellariiformes              | Diomedeidae                 |
| Phoebastria immutabilis              | NT   | Procellariiformes              | Diomedeidae                 |
| Phoebastria nigripes                 | NT   | Procellariiformes              | Diomedeidae                 |
| Phoeniconias minor                   | NT   | Phoenicopteriformes            | Phoenicopteridae            |
### Table 1s. (Cont.)

| Species                        | IUCN | Order             | Family              |
|--------------------------------|------|------------------|---------------------|
| Phyllastrephus flavostriatus   | LC   | Passeriformes     | Pycnonotidae        |
| Ptiloscyopus ijimae             | VU   | Passeriformes     | Sylviidae           |
| Picoides tridactylus            | LC   | Piciformes        | Picidae             |
| Pipilo crissalis                | LC   | Passeriformes     | Emberizidae         |
| Platalea ajaja                  | LC   | Ciconiformes      | Threskiornithidae   |
| Plegadis chihi                  | LC   | Ciconiformes      | Threskiornithidae   |
| Pluvialis dominica              | LC   | Charadriiformes   | Charadriidae        |
| Podargus strigoides             | LC   | Caprimulgiformes  | Podargidae          |
| Podiceps griseogena             | LC   | Podicipediformes  | Podicipedidae       |
| Poecile hudsonicus              | LC   | Passeriformes     | Paridae             |
| Poephila cincta                 | LC   | Passeriformes     | Estrildidae         |
| Poicephalus robustus            | LC   | Psittaciformes    | Psittacidae         |
| Pomarea dimidiata               | VU   | Passeriformes     | Monarchidae         |
| Pomatostomus temporalis         | LC   | Passeriformes     | Pomatortomidae      |
| Procnias tricarunculata         | VU   | Passeriformes     | Cotingidae          |
| Prunella modularis              | LC   | Passeriformes     | Prunellidae         |
| Pseudonestor xanthophrys        | CR   | Passeriformes     | Fringillidae        |
| Psittacula eques                | EN   | Psittaciformes    | Psittacidae         |
| Puffinus carneipes              | LC   | Procellariiformes | Procellariidae      |
| Pygnotho дальensis              | LC   | Passeriformes     | Pycnonotidae        |
| Pygoscelis antarctica           | LC   | Sphenisciformes   | Spheniscidae        |
| Pyrrhocorax pyrrhocorax         | LC   | Passeriformes     | Corvidae            |
| Rallus elegans                  | NT   | Gruiformes        | Rallidae            |
| Ramphocelus bresilius           | LC   | Passeriformes     | Thraupidae          |
| Rhynchotus rufescens            | LC   | Tinamiformes      | Tinamidae           |
| Saxicola torquatus              | LC   | Passeriformes     | Muscicapidae        |
| Serinus rufibrunneus            | LC   | Passeriformes     | Fringillidae        |
| Setophaga striata               | LC   | Passeriformes     | Parulidae           |
| Spizella wortheni               | EN   | Passeriformes     | Emberizidae         |
| Sttipitrus malachurus           | LC   | Passeriformes     | Maluridae           |
| Streptopelia camelus            | LC   | Struthioniformes  | Struthionidae       |
| Sturnus unicolor                | LC   | Passeriformes     | Sturnidae           |
| Sylvia conspicillata            | LC   | Passeriformes     | Sylviidae           |
| Tachycineta albilinea           | LC   | Passeriformes     | Hirundinidae        |
| Tachycineta bicolor             | LC   | Passeriformes     | Hirundinidae        |
| Tachycineta leucorrhoa          | LC   | Passeriformes     | Hirundinidae        |
| Taeniopygia guttata             | LC   | Passeriformes     | Estrildidae         |
| Tarsiger cyanurus               | LC   | Passeriformes     | Muscicapidae        |
| Telespiza cantans               | VU   | Passeriformes     | Fringillidae        |
| Terpsiphone mutata              | LC   | Passeriformes     | Monarchidae         |
Table 1s. (Cont.).

| Species                     | IUCN | Order        | Family         |
|-----------------------------|------|--------------|----------------|
| *Terpsiphone corvina*       | CR   | Passeriformes| Monarchidae    |
| *Tetrao tetrix*             | LC   | Galliformes  | Phasianidae    |
| *Tetrao urogallus*          | LC   | Galliformes  | Phasianidae    |
| *Thamnophilus cryptoleucus* | NT   | Passeriformes| Thamnophilidae |
| *Thaumastura cora*          | LC   | Apodiformes  | Trochilidae    |
| *Turdus merula*             | LC   | Passeriformes| Turdidae       |
| *Tyto alba*                 | LC   | Strigiformes | Tytonidae      |
| *Upupa epops*               | LC   | Coraciiformes| Upupidae       |
| *Uria aalge*                | LC   | Charadriiformes| Aicidae        |
| *Uria lomvia*               | LC   | Charadriiformes| Aicidae        |
| *Urosphena squameiceps*     | LC   | Passeriformes| Sylviiidae     |
| *Xenicus gilviventris*      | VU   | Passeriformes| Acanthisittidae|
| *Zenaida aarta*             | LC   | Columbiformes| Columbidae     |
| *Zosterops abyssicus*       | LC   | Passeriformes| Zosteropidae   |
| *Zosterops borbonicus*      | LC   | Passeriformes| Zosteropidae   |
| *Zosterops lateralis*       | LC   | Passeriformes| Zosteropidae   |
| *Zosterops polioastra*      | LC   | Passeriformes| Zosteropidae   |
| *Zosterops senegalensis*    | LC   | Passeriformes| Zosteropidae   |
| *Zosterops vaughani*        | LC   | Passeriformes| Zosteropidae   |
| *Zosterops virens*          | LC   | Passeriformes| Zosteropidae   |