Leveraging Large Scale, Open-Access Population Data to Calculate Genetic Indicators: A Continental Assessment of European Birds

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Abstract

The Kunming-Montreal Global Biodiversity Framework (KMGBF) committed countries worldwide to conserving and restoring genetic diversity. Yet, translating complex genetic data into actionable metrics remains formidable for most stakeholders, especially when DNA-based data are unavailable. Proxy metrics such as the KMGBF headline indicator (A.4) using effective population size (N_e) and the complementary indicator on maintained populations (PM) can be assessed without direct genetic data. By bypassing the need for direct genetic sampling, these indicators offer an accessible, broad-scale framework for monitoring population genetic health and guiding policy decisions.

This study provides a proof-of-concept for calculating genetic indicators for 187 bird species listed under Annex I of the EU Birds Directive. Using census and abundance data from Eionet (European Environment Information and Observation Network) and the European Breeding Bird Atlas, we developed a standardized pipeline for population delineation and indicator estimation, inferring N_e from census size (N_c) via different N_e/N_c ratios (0.1, 0.2, and 0.4). Results show that genetic indicator values for European birds are generally higher than those reported in multi-taxa studies, likely reflecting high avian dispersal. The proportion of $N_e \geq 500$ correlated strongly with EU IUCN Red List status, though some "Least Concern" species exhibited low values, highlighting cryptic genetic erosion. Additionally, long-distance migrants had higher effective population sizes than species with restricted occurrences. These overall results were consistent for all N_e/N_c ratios. By demonstrating that continental-scale genetic indicator assessments are feasible using open-access data, this study provides a scalable blueprint for countries to meet CBD reporting obligations, while offering policymakers a clear path to identify and prioritize species in need of genetic rescue. Specifically, species with low genetic viability should be prioritized for active management. Our findings underscore the importance of integrating ecological traits and dispersal dynamics into assessments of species' long-term evolutionary potential.

Keywords: Genetic Diversity, CBD, Effective Population Size, European Birds, Conservation Policy, Proxy Indicators.

1. INTRODUCTION

Genetic diversity enables both populations and species to adapt to changing conditions, while also supporting the resilience of ecosystems and the services they provide to people (Hoban, Bruford, et al., 2021; O'Brien et al., 2025). This importance is reflected in international commitments, such as the Convention on Biological Diversity (CBD), and the Sustainable Development Goals (O'Brien et al., 2025). The CBD's Kunming-Montreal Global Biodiversity Framework (KMGBF), established in late 2022, committed to the conservation of genetic diversity (Goal A, Target 4) and requires signatory countries to report on its state (CBD, 2022; da Silva et al., 2026).

Reporting on the status of genetic diversity effectively requires monitoring across different time points and numerous species. To achieve this without the high costs and time constraints associated with comprehensive DNA sequencing, several proxy-based genetic indicators have been proposed (Hoban et al., 2020; Laikre et al., 2020). Indicators are metrics that summarize the state of a system in a simplified manner to inform decision-making, often by distilling complex data into straightforward numbers through the use of thresholds or categories (Hoban et al., 2020). The KMGBF recognizes two specific genetic indicators: (1) the headline indicator (A.4) or the 'Proportion of populations with an effective size greater than 500' ($N_e \geq 500$) indicator, and (2) the 'Populations Maintained' (PM) indicator, which focuses on distinct or locally adapted populations to maintain among-population diversity, which focuses on maintaining sufficient population sizes to minimize long-term genetic erosion and preserve within-population diversity. Additionally, a third metric, the 'Genetic Monitoring' (GM) indicator, was defined (but not officially adopted) to evaluate the proportion of species subjected to sustained, long-term genetic tracking

designed to monitor population-level diversity over time (Hoban et al., 2020; Pearman et al., 2024). Parties to the CBD will assess and report on these indicators in their National Reports to be submitted in 2026 and 2029 (CBD, 2022). The recent draft Global review of collective progress in the implementation of the KMGBF showed that a number of countries reported on these indicators, while others are setting up the procedures, expertise and workflows to report genetic indicators in the future (Montereale Gavazzi, Giacomo et al., 2026).

Ultimately, these genetic indicators are intended for more than just CBD reporting; they can also be integrated into species management and policy decisions (Hoban, Bruford, et al., 2021; Hoban, da Silva, et al., 2024). They are valuable for targeting conservation frameworks toward species with the lowest genetic values, detecting significant population trends over time, and mobilizing public and political support for genetic biodiversity. These objectives align with the goals of other species assessment frameworks, such as the IUCN Red List, which evaluates extinction risk (IUCN, 2024) or, the IUCN Green Status, which assesses the recovery potential of species (IUCN, 2021). To be effective in these high-level policy frameworks, an indicator should be explainable without technical jargon. The genetic indicators adopted by the KMGBF translate complex concepts into intuitive, proxy-based metrics, serving as a 'first step' for non-geneticists to understand genetic threats. Specifically, they bypass the need for intensive, costly molecular analyses by leveraging readily available demographic data (e.g., census population sizes (N_c) and geographic distributions) and applying standardized scaling factors to approximate key evolutionary thresholds, such as the effective population size (N_e) and loss of populations (Hoban et al., 2020). Because N_e is typically much smaller than N_c, this approximation is achieved by applying N_e/N_c ratios that reflect the biological reality of the species' breeding system. As a result, metrics such as the Ne500 indicator are immediately relevant to the EU Habitats Directive via the concept of the Favorable Conservation Status (Directive 2009/147/EC, 2009). Furthermore, because genetic erosion ultimately drives population declines and extinction, these indicators could offer actionable data to inform species listing or delisting decisions under national and provincial endangered species legislation (Hoban et al., 2020).

Following the theoretical proposal of these indicators, it became necessary to demonstrate their practical application at a scale approximating that required for CBD National Reports. A large-scale pilot test in Sweden initially demonstrated data availability (Thurfjell et al., 2022). Subsequently, from 2022 to 2024, a collaboration across nine countries performed an assessment of the genetic indicators to demonstrate their feasibility (Mastretta-Yanes et al., 2024). This study showed that data were available from numerous sources and that collecting data and performing calculations is feasible with available resources, even in high-biodiversity developing countries. From a genetic biodiversity perspective, the study revealed that the Ne500 indicator was low (ranging from 0.08 to 0.42 among countries), the PM indicator was high (ranging from 0.45 to 0.95), and Genetic Monitoring ranged from 0 to 20 species among those evaluated. Crucially, the study found that even species with an IUCN status of 'Least Concern' could exhibit low indicator values (Mastretta-Yanes et al., 2024).

However, there are several limitations to these proof-of-concept studies. The primary limitation was that the choice of species was ad hoc; no single taxonomic group was studied in sufficient detail to test for factors that might influence indicator values within a group (e.g., migratory status or habitat type). Furthermore, there was no strategic selection of threatened and non-threatened species to allow for rigorous comparison. Finally, there was a lack of a single, unified data source for all species; data were gathered from various reputable, citable sources and expert input, similar to Red List assessments (see methodology described in Mastretta-Yanes et al., (2024). Additionally, because previous assessments were primarily conducted at a national level, it remains unclear how shifting to a continental or biological scale might influence the resulting indicator values.

In response to these constraints, the present study calculates genetic indicators for birds in Europe using a strategic choice of species and a standardized pipeline for data compilation, applying the same data sources across all targeted species. Furthermore, to account for the uncertainty inherent in proxy-based estimates, we evaluated the impact of different N_e/N_c ratios on the resulting indicator values. We chose birds as an emblematic group that captures public

and policy attention and for which extensive data are available through citizen science and formal monitoring. We focus on the EU as a Party to the CBD and because the EU provides protections for birds and maintains data in several accessible databases. Specifically, birds are protected under the Birds Directive (Directive 2009/147/EC, 2009) with birds of different threat statuses listed in the Directive's annexes. Additionally, Europe possesses long-term datasets of bird population census sizes and occurrence based on standardized monitoring, including the European Bird Breeding Atlas (EBBA; EBCC, 2022; Keller et al., 2020) and the European Environment Information and Observation Network (Eionet; European Environment Agency (EEA), 2020). By focusing on a single taxonomic group we can better test the influence of ecological and behavioral drivers, such as migration strategy and range size on indicator values. This focused approach also ensures greater accuracy for the indicator values within that group.

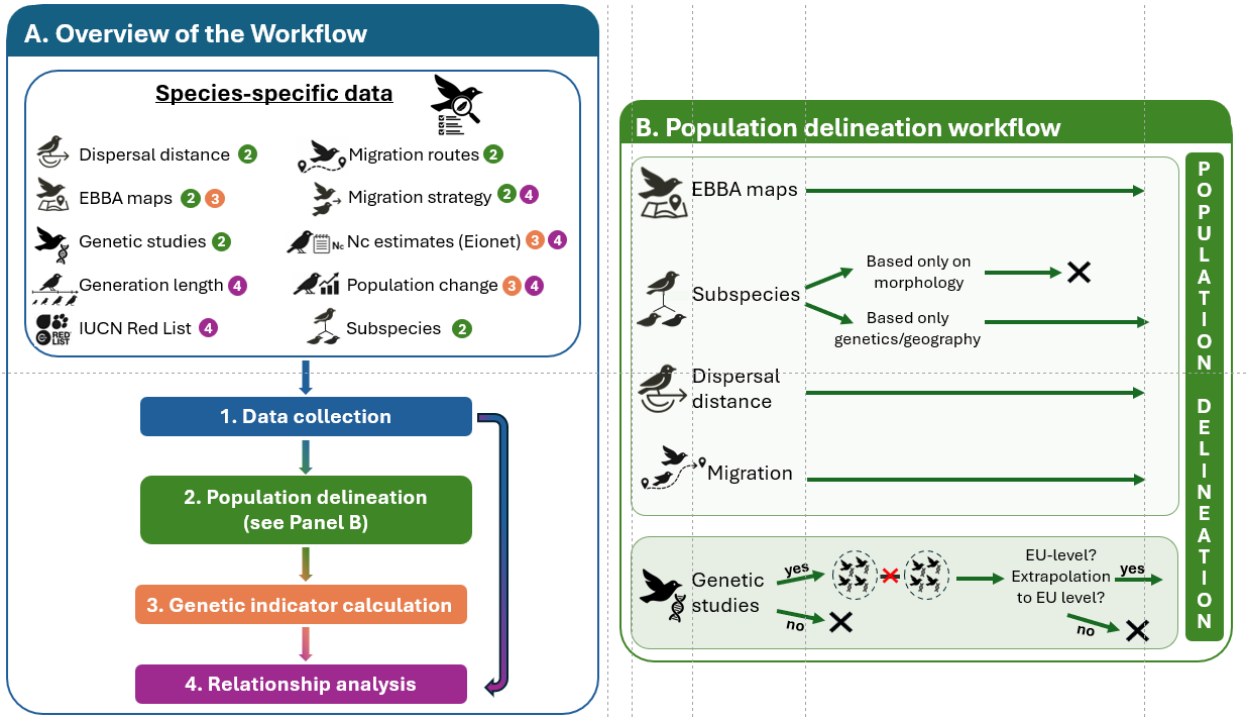
Our primary aim is to calculate genetic indicator values for bird species listed under Annex I of the Birds Directive in Europe, reflecting the highest level of legal protection. Our secondary aim is to determine the utility of existing data sources, such as the EBBA and Eionet, for calculating these genetic indicators. Third, we aim to test for relationships between the Ne500 indicator values and species-specific characteristics such as threat status (EU IUCN Red List categorization), range size (occurrence), migratory behavior and generation length. The selection of these variables was informed by established principles of conservation genetics, which demonstrate that specific life-history traits shape population dynamics and gene flow. For instance, migratory behavior often facilitates long-distance dispersal, potentially reducing population differentiation and buffering against the loss of genetic diversity in fragmented landscapes (e.g., Burg et al., 2006; de Freitas et al., 2022). Conversely, we expect range size to be a strong predictor of indicator values, as species with restricted distributions are more prone to genetic drift and founder effects (Frankham, 2005). Similarly, prior research indicated that Ne500 indicator values did not correlate closely with Red List categories (Mastretta-Yanes et al., 2024). Furthermore, generation length is included as it fundamentally scales the rate at which genetic diversity is lost over time (Frankham, 2005). By analyzing these variables, we can move

beyond a simple status report to understand the biological drivers that render certain avian taxa more genetically vulnerable than others. Ultimately, we evaluate our approach and discuss how our findings can shape future conservation policy frameworks and decisions.

2. METHODS

To determine genetic indicators for bird species listed under Annex I of the European Birds Directive, we first collected species-specific information such as distribution patterns, migratory status, dispersal distances and the recognition of subspecies and then collected genetic information on population differentiation (Section 2.1, Fig. 1A). These data informed the delineation of population boundaries (Section 2.2). Long- and short-term population change indices, derived from occurrence and abundance data, were then retrieved to evaluate temporal population dynamics (described in the Supporting Information 1.A). Subsequently, population census size estimates (N_c) were converted to effective population size estimates (N_e) via a range of N_e/N_c ratios. This process enabled the calculation of the KMGBF headline indicator (A.4) 'Ne500', the complementary 'populations maintained' indicator, and the unimplemented 'genetic monitoring indicator' (detailed in Section 2.3).

Subsequently we also explored how Ne500 indicator values correlate with species characteristics such as the EU IUCN Red List status, migratory status, number of populations delimited per species, occurrence (number of 50 km² squares where a species occurs according to EBBA2), population change indexes and generation length (section 2.4).



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191 ***Fig. 1 - Overview of the workflows used in this study. (A) General workflow showing the four main stages within***
192 ***this study: (1) collection of species-specific data, including dispersal distance, EBBA maps, genetic studies,***
193 ***generation length, migration routes and strategies, non-breeding census estimates, population change,***
194 ***subspecies information, and IUCN Red List assessments; (2) population delineation; (3) calculation of genetic***
195 ***indicators; and (4) relationship analysis. Colored numbers indicate for which step each of the species-specific***
196 ***data was used. (B) Population delineation workflow. Population boundaries were defined using multiple lines***
197 ***of evidence, including EBBA distribution maps, genetically and geographically supported subspecies,***
198 ***dispersal distances, migration patterns, and genetic studies. Subspecies classifications based solely on***
199 ***morphology were not considered. Where genetic data were available, population delineations were evaluated***
200 ***for consistency and, when necessary, extrapolated from regional to broader (EU-level) assessments. Arrows***
201 ***indicate information pathways used in delineation, whereas crosses indicate criteria that were excluded or not***
202 ***applied.***

203

204 2.1 Bird species and the collection of species-specific traits

205 The EU Birds Directive protects all wild bird species naturally occurring in the European Union
206 (EU) through hunting regulations, habitat conservation, and the mitigation of threats to bird
207 populations. Annex I specifically identifies species that are threatened with extinction, vulnerable

to habitat change, rare due to restricted distributions or small population sizes, or characterized by specialized habitat requirements. Consequently, EU member states must designate protected areas and implement targeted conservation measures for these species (Directive 2009/147/EC, 2009). We selected 187 bird species that are regularly native to the European Union (EU) and listed in Annex I of the EU Birds Directive, which includes species requiring special conservation measures because they are threatened, vulnerable, rare, or have specific habitat requirements (Directive 2009/147/EC, 2009). To focus on breeding populations, we excluded species classified as extinct after 1800 (Ex.), migratory passage or wintering only (M+W), and wintering only (W). Species lists were obtained from the European Commission's CIRCABC platform (version 1.3 https://circabc.europa.eu/ui/group/3f466d71-92a7-49eb-9c63-6cb0fadf29dc/library/f3bdeb3b-55c0-47a1-8482-e9a91b126b69/details). Although Annex I lists only specific subspecies for 14 species, we assessed the entire EU range of each species, treating the listed subspecies as geographically delimited populations (see Section 2.2). The complete species list is provided in Supporting Information 2, TableS1. For each of the 187 species, we compiled a standardized set of species-specific variables, including demographic, distributional, ecological, conservation, and genetic information required to calculate the genetic indicators and evaluate their ecological correlates. Variables included population size and trends, distribution, life-history and migratory traits, conservation status, and available population genetic information. Detailed descriptions of all variables and data sources are provided in Supporting Information 1.B, and an overview is presented in Table 1.

Table 1 - Summary table of species-specific traits used for population delineation, the computation of genetic indicators, and statistical analyses examining the relationships between these traits and the N_e ≥500 indicator value, along with their sources.

Species specific variables	Population delineation	Genetic indicator	Used as predictor variable in statistical tests of relationship with N_e500 indicator	Source
Estimates of N_c	no	N_e500	yes	Eionet (European Environment Agency (EEA), 2020)) and EBBA2 abundance maps (EBCC, 2022; Keller et al., 2020)
Occurrence	yes	PM	yes	EBBA2 occurrence maps, quantitative data as the number of 50-km squares in which the species was found to breed in Europe (EBCC, 2022; Keller et al., 2020)
Overall change in species' occurrence	no	PM	no	EBBA change maps; spatial data showing change in occurrence between two monitoring periods (EBCC, 2022; Keller et al., 2020)
Long-term population change	no	PM	yes	EBBA2; quantitative data, the reported numerical change in occupied grid squares which changed between EBBA1 and EBBA2, reported as a range of population change (EBCC, 2022; Keller et al., 2020)
Short-term population change	no	PM	yes	Calculated based on N_c estimates provided by Eionet (European Environment Agency (EEA), 2020)
Generation length	no	none	yes	Birdlife International Data Zone (BirdLife International, 2025)
Migratory status	yes	none	yes	Birdlife International Data Zone (BirdLife International, 2025)
Migration routes	yes	none	no	The Eurasian African Bird Migration Atlas (Spina et al., 2022; migrationatlas.org)
EU-level IUCN Red list assessment	no	none	yes	CIRCABC (Communication and Information Resource Centre for Administrations, Businesses and Citizens) (see details in Supporting Information1.B)
Subspecies	yes	none	no	Eionet (European Environment Agency (EEA), 2020), IOC World Bird List (https://www.worldbirdnames.org/new/classification/family-index-2), literature search

2.2 Population delineation workflow

Delineating populations is a critical first step for calculating genetic indicators, as these metrics are defined at the population level. In practice, most species are distributed as metapopulations (interconnected subpopulations) or as continuously distributed populations with spatial genetic structures where distance drives deviations from panmixia. The Ne500 indicator applies specifically to the metapopulation level (Waples, 2024), defined here as an entity within which allele frequencies exhibit long-term correlated evolution due to gene flow. Under an island model of gene flow (Wright, 1931), this occurs when the effective number of migrants per generation exceeds one, also known as the 'one migrant per generation' rule of thumb (Mills & Allendorf, 1996), which we refer to here as functional connectivity. While we frequently use the general term 'population,' we are factually referring to metapopulations as defined above. Where biological populations extended beyond the EU28 or Europe, delineations were made at the EU28 level, reflecting the reporting scope and conservation responsibility of the EU.

We rarely have direct information on landscape-level patterns of gene flow, so our assessment was largely based on indirect information. For each species, populations were delineated by synthesizing geographical distribution (EBBA occurrence maps), genetically supported subspecies, movement ecology (migratory behavior and dispersal), and available genetic structure studies (Fig. 1B; Table 1). Distribution maps provided the initial framework, while subspecies were retained only when supported by genetic or geographic evidence or when explicitly listed in Annex I. Movement ecology and genetic data were then used to evaluate functional connectivity and identify population boundaries. When genetic evidence was unavailable or inconclusive, delineation relied on ecological and biogeographic information to estimate connectivity.

In most cases, population delineation was derived from a synthesis of multiple data sources (Table 1). Furthermore, conservation priorities were integrated into the process: any subspecies explicitly listed in Annex I was automatically treated as a distinct population. Overall, this study

adopted a conservative approach to delineation, prioritizing simplicity over complex population structures that lacked definitive empirical support. To avoid the risk of over-splitting without strong evidence, we opted for a more inclusive grouping of individuals (examples are provided in Table 2). While we acknowledge that this approach may lead to a deliberate underestimation of the total number of distinct populations, it ensures a cautious application of the PM- and N_e500 indicators.

2.3 Genetic indicators

2.3.1 Genetic Monitoring (GM)

The genetic monitoring indicator (hereafter, GM indicator) tracks how many species and populations are monitored for genetic diversity using DNA-based methods, specifically as defined by (Hoban et al., 2020), it is a binary indicator for whether any genetic data exists for each species evaluated. We evaluated data availability by reviewing literature to see if genetic methods had been used to characterize species. This differs from the Genetic Monitoring Effort (GME) described by Pearman et al., (2024), as the GM indicator definition, and our approach, provides a snapshot of data rather than a measure of continuous monitoring. The GM indicator is binary: 1 indicates that at least one population of the species has been monitored using DNA-based methods, and 0 indicates that no such monitoring is known. We assessed this indicator through a literature review of population genetic studies. While we aimed for a comprehensive search, we acknowledge that some relevant studies may have been missed or published after the search was completed.

2.3.2 Populations Maintained (PM) indicator

The Populations Maintained (PM) indicator reflects the proportion of extant populations relative to the total number of known populations (extant and extinct) (Hoban et al., 2020). We calculated this indicator by comparing EBBA1 (1980s; Hagemeijer & Blair, 1997 and EBBA2 (2013–2017; (EBCC, 2022; Keller et al., 2020) distribution data. Using EBBA2 change maps and the

delineation criteria from Section 2.1.3, populations were classified as extinct if they were absent during the EBBA2 period and located outside the current dispersal range. Previously occupied areas within dispersal distance were assumed to remain extant. The resulting numbers of extant and extinct populations per species are provided in Table S1 (Supporting Information 2). PM-values range from 0 to 1, where 0 signifies complete population loss and 1 indicates full population maintenance (Mastretta-Yanes et al., 2024). Intermediate values occur when only a subset of populations persists. For species lacking baseline EBBA1 data, extinct populations could not be determined; consequently, the PM-indicator was not computed ('NA').

2.3.3 Ne500 indicator

The Ne500 indicator represents the proportion of populations within a species with an effective population size N_e of 500 or more, a threshold widely regarded as the minimum required to maintain long-term evolutionary potential and reduce extinction risk (Frankham, 2015; Franklin, 1980; Hoban et al., 2020). Because N_e cannot be directly measured from proxy data (non-genetic), estimating this indicator relies on census population sizes (N_c), from which N_e is inferred using predefined N_e/N_c ratios.

In this study, N_c estimates were primarily sourced from the Eionet Article 12 reporting database (Table 1), where data are reported at the species level and aggregated by country (European Environment Agency (EEA), 2020). Because this study focuses on delineated populations across the European Union rather than national boundaries, these raw estimates were processed to align with our defined population units. Consequently, country-level N_c values are not presented directly but served as the basis for deriving population-specific estimates.

Following population delineation (Section 2.2), N_c estimates were processed according to three scenarios: (1) for species represented by a single EU-wide population, the total EU-level N_c estimate from Eionet (European Environment Agency (EEA), 2020) was used directly; (2) for species comprising multiple populations distributed across different countries, but without subdivision within those countries, N_c was calculated by summing the relevant country-level

values from Eionet; and (3) for species with multiple distinct populations within a single country, where Eionet data lacked sufficient spatial resolution, abundance estimates from EBBA2 (EBCC, 2022; Keller et al., 2020) were used to derive population-specific N_c values. EBBA2 abundance is mapped using a 50 km² grid system, with values represented by six logarithmic classes ranging from 1 to 100,000 breeding pairs (EBCC, 2022; Keller et al., 2020). For populations delineated within countries, these abundance classes were extracted by assigning specific grid cells to each population. The reported minimum and maximum abundance classes were then converted into N_c estimates (number of individuals) to generate population-specific minimum and maximum values, from which the mean was calculated. Consequently, the final N_c estimates represent processed, standardized values aligned with delineated population units rather than raw data from Eionet or EBBA2.

To align with the standard census size (N_c) unit, which is the number of potentially breeding individuals (Waples & Feutry, 2022), we multiplied breeding pair counts, calling male, and breeding female proxies by two. Although mating systems and sex ratios may vary, these were not accounted for at the intra-species level. N_c values were then converted to N_e using an N_e/N_c ratio. While N_e/N_c ratios typically range from 0.1 to 0.3 (Hoban, Bruford, et al., 2021), broader estimates range from 0.09 in invertebrates to 0.48 in some birds (S. H. Clarke et al., 2024; Hoban, Paz-Vinas, et al., 2021, 2024). To account for this variance, we estimated Ne using three ratios: 0.1, 0.2, and 0.4. Based on the derived N_c estimates, we assigned a value of 0 to populations with $N_e<500$ and a value of 1 to those with $N_e\geq500$. These values were then used to determine the N_e500 indicator (the proportion of populations meeting the threshold) (Hoban, Paz-Vinas, et al., 2021). Calculations used N_c estimates from the most recent reporting periods (Eionet: 2013–2018; EBBA2: 2013–2017) for minimum, maximum, and mean values (Supporting Information 2, Table S3).

2.4 Statistical tests of relationship between genetic indicators and species-specific data

First, we analyzed the relationship between the GM-indicator and the EU IUCN Red List assessments using Fisher's exact tests, implemented via the fisher.test function in R, as both variables were considered categorical. Fisher's exact test is a statistical significance test used to determine if there is a non-random association between two categorical variables. We also performed bias-corrected Cramér's V (Bergsma, 2013) using the cramerV function from the rcompanion package version 2.5.2 (Mangiafico, 2026) to measure the effect size of the relationship. Cramér's V ranges from 0 to 1, where 0.1 shows a small effect, 0.3 a medium effect and 0.5 a large effect. All analyses were performed in R version 4.5.1 (R Core Team, 2025).

Secondly, we examined correlations between Ne500 indicator values based on the mean N_c estimates and species-specific traits (see Section 2.1), to assess how these factors influence the Ne500 indicator value. Predictor variables were classified as categorical (EU-level IUCN Red List status and migratory status) or continuous (number of populations, generation length, occurrence, long-term change index (LT-change) and short-term change index (ST-change) (both based on the mean N_c-estimates)). The relationships of those predictor variables and the values of the Ne500 indicator were analyzed using mixed-effects models. All models were fitted using the lmer function from the lme4 package (Bates et al., 2015), and significance of fixed effects was assessed using Satterthwaite's approximation for degrees of freedom (lmerTest package; Kuznetsova et al., 2017). All analyses and visualizations were conducted in R version 4.5.1 (R Core Team, 2025).

For categorical predictors, we fitted linear mixed-effects models (LMMs) with Ne500 indicator values inferred from mean N_c estimates as the response variable, using restricted maximum likelihood (REML). Fixed effects included each of the predictors of interest, the N_e/N_c ratio, and their interaction. Species identity was included as a random intercept to account for non-

independence of observations within species. Model assumptions were assessed visually using residual and normal Q-Q plots. Post-hoc pairwise comparisons between each class within categorical predictor variables were conducted using estimated marginal means (EMMs) with Tukey-adjusted p-values (emmeans package, v.2.0.1; Lenth et al., 2025). Point-range plots were then used to visualize the Ne500-EMMs using ggplot2 (Wickham, 2016). Distributions of Ne500 indicator values across categories were visualized using violin plots with overlapping boxplots generated with ggplot2 (Wickham, 2016), supplemented with individual data points using ggbeeswarm (v.0.7.3; Clarke et al., 2025).

For continuous predictors, we tested the added value of adding a quadratic component to the linear mixed model using the Akaike Information Criterion (AIC). Fixed and random effects were specified as above. When the inclusion of a quadratic term improved the model fit (based on ΔAIC), a quadratic model was selected; otherwise, linear models were used. All reported results and visualizations are based on the best-supported models. Model-based prediction plots were generated using the ggeffects package (Lüdecke, 2018) and visualized with ggplot2 (Wickham, 2016).

3. RESULTS

3.1 Bird species-specific data and population change indexes

For all 187 species, species-specific information was compiled in a comprehensive meta table (see Supporting Information 2, Table S1).

Based on the long-term change index (LT-change) provided by EBBA2, 39% (73/187) of the species exhibited an increasing trend, 24.6% (46/187) remained stable, and 19.3% (36/187) showed a decline. Long-term change data were unavailable for 17.1% (32/187) of the species. Regarding the short-term change index, which was here calculated based on N_c estimates over a six-year period, 24.6% (46/187) of species showed an increasing trend, while the majority of species (43.3%; 81/187) remained stable. 17.1% (33/187) of species exhibited a decline in

population trend and 15% (27/187) had no available short-term data. These results are visualized in the Fig. S1 (Supporting Information 1).

3.2 Population delineation

Six population delineation scenarios emerged from the synthesis of ecological characteristics (Fig. 1). Delineation was based either (1) solely on EBBA occurrence maps (48/187 species), or on a combination of sources: (2) EBBA maps, subspecies, and genetic studies (5/187); (3) EBBA maps and genetic studies (36/187); (4) EBBA maps and migration data (36/187); (5) EBBA maps, genetic studies, and migration (51/187); and (6) EBBA maps, subspecies, genetic studies, and migration (11/187). The specific scenario applied to each species is listed in Table S1 (Supporting Information 2). The number of populations per species ranged from 1 to 18 (median = 1; mean = 1.6), with 142 species defined as a single EU population. For the 45 species with more complex structures, delineation was driven by intra-reporting unit differentiation (e.g., between the Canary Islands, Madeira, and Azores; 12/187 species), Annex I subspecies listings, or known dispersal barriers. Subspecies classification was used for 17 species, while genetic data informed the delineation of 101 species. This workflow is illustrated through four examples in Table 2 and a comprehensive summary of data sources is provided in Table S1 (Supporting Information 2).

Table 2 –Proof-of-concept examples of the population delineation pipeline. This table details the transition from species-specific ecological background to final population assignment and references the corresponding spatial data in the Supporting Information 3 document for four different species: the Grey partridge (Perdix perdix), the Eurasian Spoonbill (Platalea leucorodia), the Peregrine falcon (Falco peregrinus) and the Red kite (Milvus milvus)

Species	Ecology & Dispersal	Population Delineation Logic	Resulting Populations	Map Reference (Supporting Information 3)	Primary Uncertainty
Grey Partridge (*Perdix perdix*)	Sedentary, hence limited dispersal (e.g., Buner et al., 2005; Putaala & Hissa, 1998); well-documented genetic structure (Bech et al., 2014; Karaiskou et al., 2025; Liukkonen-Anttila et al., 2002).	Separated Annex I subspecies and isolated populations (e.g., UK, Ireland, Nordic islands) from the EU mainland; further subdivision based on geographic barriers (mountains/straits) and dispersal distance.	1 EU mainland, 8 isolated, 2 *italica*, 3 *hispanensis* (14 populations)	p. 222	Underestimation of fine-scale structure, especially regarding subspecies not listed in Annex I (e.g., ssp. *perdix, sphagnetorum,* and *armoricana*).
Eurasian Spoonbill (*Platalea leucorodia*)	Migratory water bird; two distinct flyways with main wintering areas are located in northeastern and northwestern Africa (Lok et al., 2013; Pigniczki, 2017, 2022; Pigniczki et al., 2024); no population level genetic data available.	Based on migratory behavior and EU distribution aligned with known flyways (Eastern and Western flyway).	1 Eastern Europe 1 Western Europe (2 populations)	p. 234	Lack of genetic data may mask finer-scale subpopulations structure.
Peregrine Falcon (*Falco peregrinus*)	High dispersal; variable migration ranging from sedentary to long-distance strategies within the same breeding populations (Ganusevich et al., 2004; Sokolov et al., 2019); minimal genetic distinction (Wink, 2019).	Assumed broad continental connectivity due to high dispersal capacity (Bond et al., 2019; Curk et al., 2020; Drewitt et al., 2021); Canary Islands treated as a distinct population based on isolation dynamics (Ferrer et al., 2011; Sanz-Aguilar et al., 2015).	1 EU mainland, 1 Canary Islands (2 populations)	p. 125	Data limitations precluded subdivision of European mainland origins.
Red Kite (*Milvus milvus*)	Migratory; post near-extinction recovery in UK/Ireland through reintroduction programs since the 1990s (Heneberg et al., 2016; Orros & Fellowes, 2015); regional gene flow (Roques & Negro, 2005; Skujina, 2013).	Based on migratory/genetic data; isolated UK/Ireland and Mediterranean islands (EURING, 2022).	1 EU mainland, 1 Ireland/UK, 1 Italy, 1 Sardinia and Sicily, 1 Balearic Islands (5 populations)	p. 203	Grouping of sedentary, genetically distinct Iberian populations with the EU mainland population may underestimate regional structure (Roques & Negro, 2005).

413

3.3 Genetic indicators

3.3.1 Genetic monitoring (GM-indicator)

This study assessed 187 species. The literature search conducted for this study found that at least one population had been genetically evaluated for 101 species, representing 54% of the selected species (Supporting Information 2, Table S3).

3.3.2 Populations maintained (PM-indicator)

The PM-indicator was 1 for 86% of species (161/187), indicating no extinct populations based on EBBA change maps (Supporting Information 2, Table S3). Six species (3%) exhibited PM-values between 0.5 and 0.96, and 21 species (11%) were assigned 'NA' due to missing change maps (Fig. 2; Supporting Information 2, Table S1). The overall mean and median PM-values were 0.99 ± 0.004 and 1, respectively.

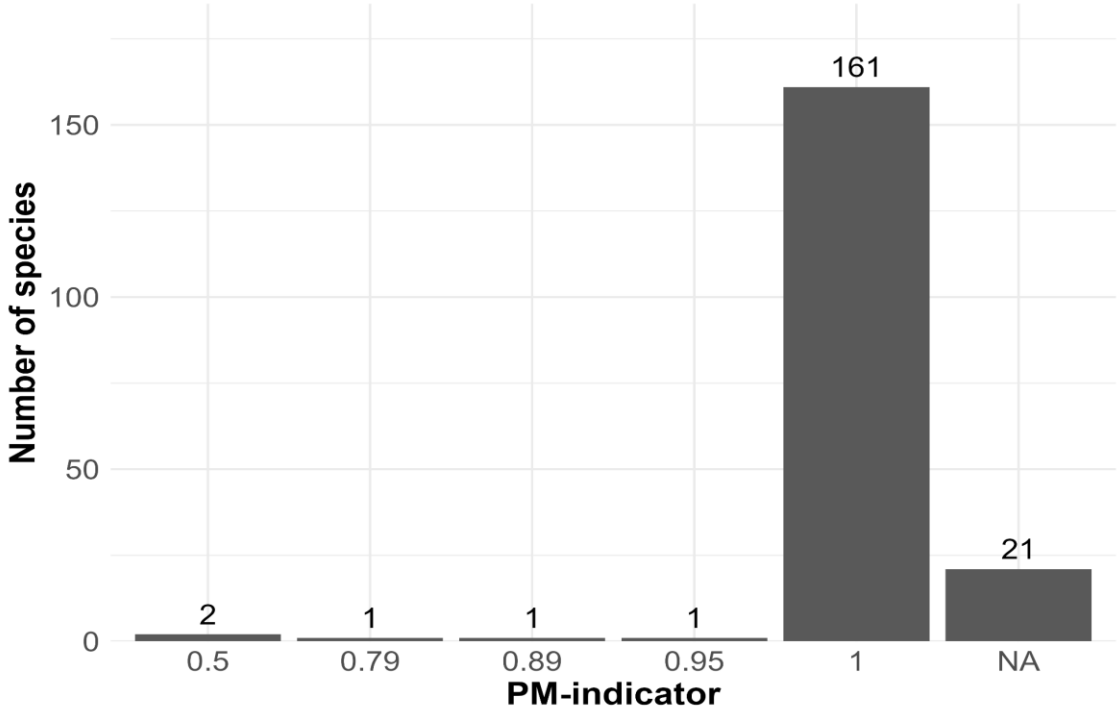


Fig. 2 - Barplot showing the distribution of PM-values for the analyzed species within this study. "NA" indicates the number of species for which no EBBA-change map was available, therefore the definition of extinct populations was not possible.

3.3.3 Ne500 indicator

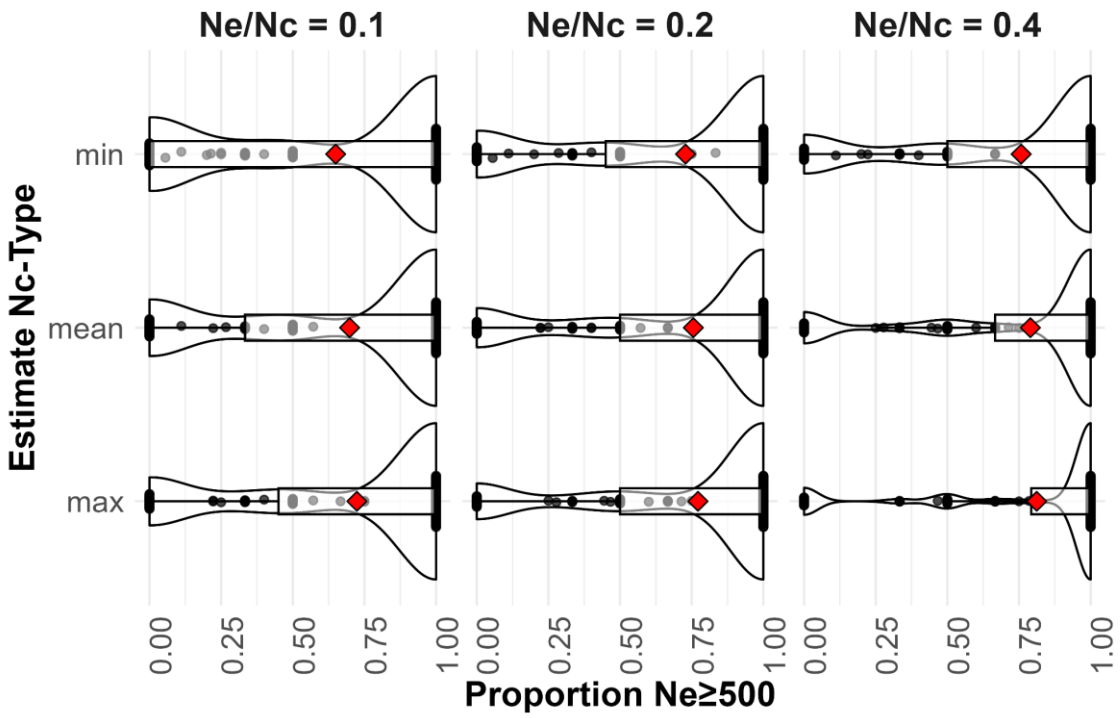
For 142 of the 187 species, the overall EU-level N_c estimate reported by Eionet (European Environment Agency (EEA), 2020) was used directly. For 21 species, the estimates required additional processing because their populations spanned multiple countries without internal subdivision; in these cases, country-level N_c values were aggregated based on the defined population units. For the remaining 24 species, where multiple distinct populations were delineated both across and within countries, Eionet data lacked sufficient spatial resolution. Consequently, N_c values for these species were derived from EBBA2 abundance maps (EBCC, 2022; Keller et al., 2020) by aggregating grid cells across six logarithmic abundance classes (1–100,000 breeding pairs). All N_c estimates (minimum, maximum, and mean) were then converted to N_e using three N_e/N_c ratios: 0.1, 0.2, and 0.4 (Supporting Information 2, Table S3).

Subsequently, the Ne500 indicator was calculated for each delineated population and species. The distribution of these values across all ratios and N_c estimate types (Fig. 3) indicates that most assessed species exhibited high $N_e \geq 500$ values, largely independent of the ratio applied (Supporting Information 2, Table S2).

A more detailed analysis showed that Ne500 indicator values shifted predictably with both the N_c estimate and the applied N_e/N_c ratio. Across all ratios (0.1, 0.2, and 0.4) and N_c estimate types (minimum, mean, and maximum), the median Ne500 indicator value was consistently 1. Increasing the N_e/N_c ratio resulted in progressively higher first quartile (Q1) values, from 0-0.45 at a ratio of 0.1, to 0.45-0.50 at 0.2, and 0.50-0.76 at 0.4, indicating that a greater proportion of simulations exceeded the $N_e \geq 500$ threshold. Mean Ne500 indicator values, based on mean N_c estimates, also increased with the applied ratio, slightly, from 0.698 ± 0.03 at a ratio of 0.1, to 0.756 ± 0.03 at 0.2, and 0.790 ± 0.03 at 0.4. The mean Ne500 values based on minimum and maximum N_c estimates are reported in Table S4 (Supporting Information 1). The total number of

453 species displaying a certain value for the Ne500 indicator based on mean N_c estimates, are
454 visualized in barplots found in Fig. S2 (Supporting Information 1).

455



456

457 ***Fig. 3: Violinplots and boxplots for the overall distribution of values for N_e500-indicator (proportion N_e ≥ 500)***
458 ***over the used N_e/N_c ratios (0.1,0.2, and 0.4), based on the minimum, mean and maximum Nc-estimates available***
459 ***for each species. The distribution density is visualized with the violins and within each violin, a dot***
460 ***corresponds to a species and its N_e500 value. The boxplot included in each violin visualizes how values are***
461 ***distributed and how the median value, the interquartile range and potential outliers lie. The mean N_e500***
462 ***indicator values per estimate and per ratio are indicated with a red diamond.***

463

464 3.4 Statistical tests of relationship between genetic indicators and
465 species-specific data

466 3.4.1 GM and Red List category

Fisher's exact tests showed there was a statistically significant association between GM and EU Red List category (Fisher's exact test; p = 0.0002), though the strength of this association was small to moderate (Cramér's V = 0.173).

3.4.2 Ne500 and species-specific data

The distribution of Ne500 indicator values for the categorical variables is presented in the corresponding sections below. An overview of the distribution of the Ne500 indicator values for the continuous variables (number of populations, generation length, occurrence, long-term change, and short-term change) is provided in Fig. S3 (Supporting Information 1). P-values from the linear mixed models examining the relationship between Ne500 and the continuous explanatory variables are reported in Table S6, Supporting Information 1.

3.4.2.1 EU Red List categories

The Ne500 indicator showed a strong linear relationship with the Red List category ($p = 1.72 \times 10^{-7}$), with the highest values found in the least threatened species (Fig. 4a). Distribution across IUCN categories is illustrated in Fig. 6. While the N_e/N_c ratio had a significant positive effect (p = 0.011 for 0.2; p = 0.002 for 0.4), no significant interaction between category and ratio was found. Pairwise comparisons revealed that the CR, EN, VU, and NT categories had significantly lower EMM Ne500-values values compared to the LC category (all $p \leq 0.004$) (Fig. 4a; Supporting Information 1, Table S5). At a ratio of 0.2, EMMs ranged from 0.17 ± 0.14 to 0.88 ± 0.03. Other ratios' EMMs with corresponding standard errors are provided in Table 3.

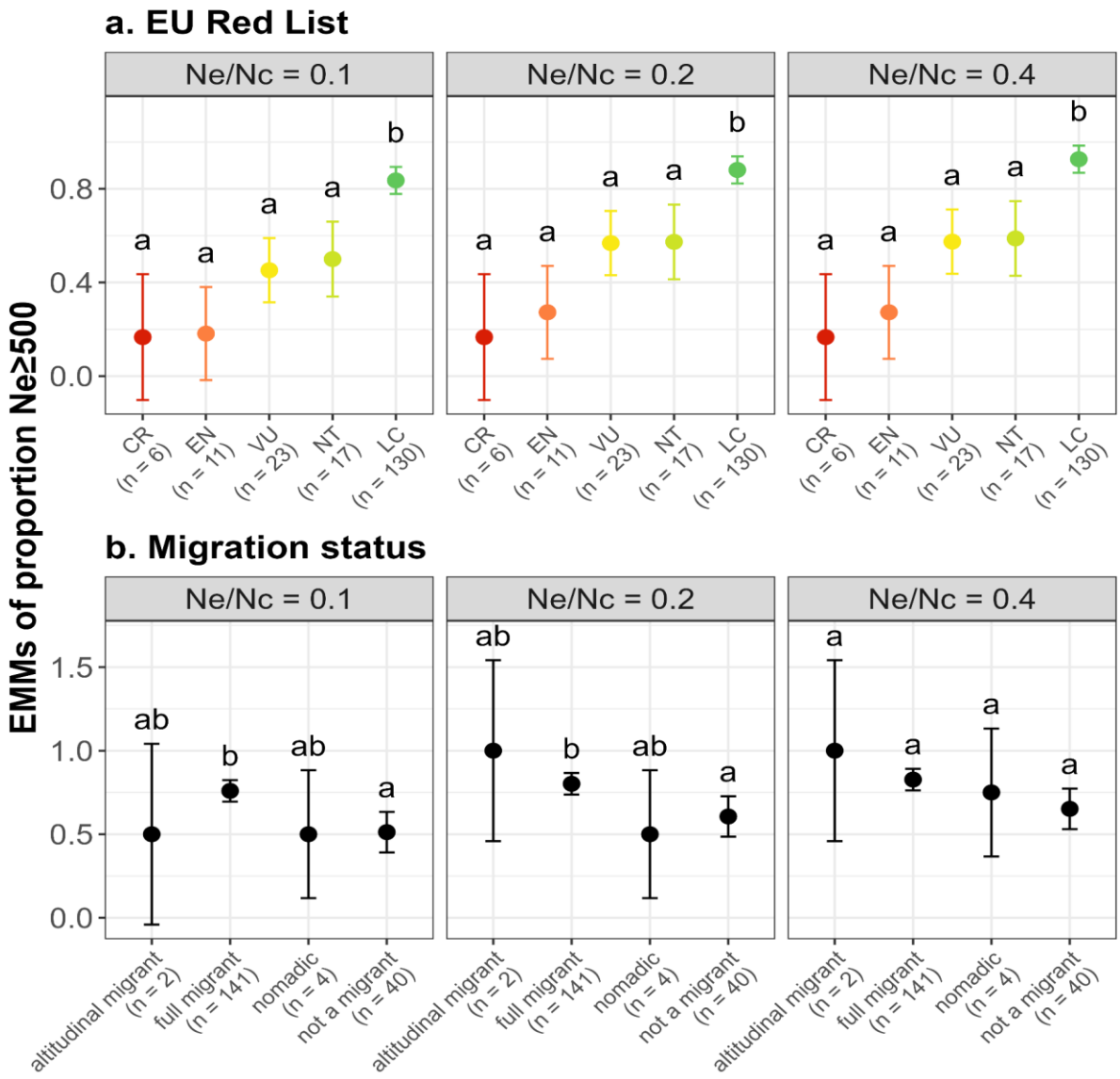


Fig. 4 - Faceted point–range plots showing estimated marginal means (EMMs) of proportion N_e≥500 (Ne500 indicator values) with 95% confidence intervals across categorical variables (EU Red List category and Migration status), by ratio. Groups that share a letter are not significantly different from each other, groups with different letters are significantly different from each other. Panel a displays EMMs of Ne500 indicator values for all EU Red List categories (CR = Critically Endangered, EN = Endangered, VU = vulnerable, NT = Nearly Threatened and LC = Least Concern). Each colour represents the different IUCN Red List categories correspondingly. Panel b displays EMMs of Ne500 indicator value for all defined categories of migration status.

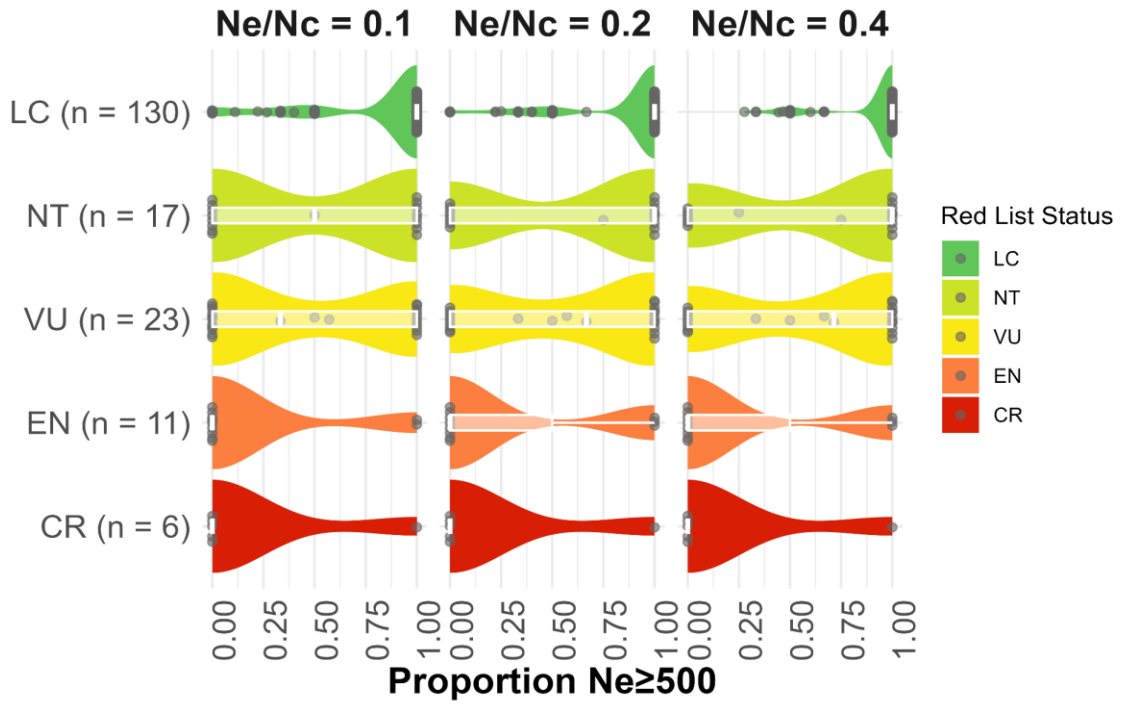


Fig. 5 - Violinplots and boxplots displaying the overall distribution of proportion N_e≥500 (Ne500 indicator values) across the different Red list categories (at the EU level; CR = Critically Endangered, EN = Endangered, VU = vulnerable, NT = Nearly Threatened and LC = Least Concern). Each colour represents the different IUCN Red List categories correspondingly. Width of the violin represents the density of data points at a specific N_e500 value.

Table 3 - Summary table presenting Ne500 indicator values and their relationship with categorical variables, EU-level IUCN Red List status and migratory status, based on linear mixed-effects models (LMMs). Reported are the mean Ne500 values (estimated marginal means (EMMs) ± standard error (SE)) for the three ratios (0.1, 0.2, 0.4), highlighting how N_e500 varies across conservation and migratory categories.

Species-specific data	Categorial variable	Sample size	Mean N_e500 values (N_e/N_c ratio 0.1)	Mean N_e500 values (N_e/N_c ratio 0.2	Mean N_e500 values (N_e/N_c ratio 0.4	SE
EU-level IUCN Red List criteria						
	CR	6	0.17	0.17	0.17	0.14
	EN	11	0.18	0.27	0.27	0.10
	VU	23	0.45	0.57	0.58	0.07
	NT	17	0.50	0.57	0.59	0.08
	LC	130	0.84	0.88	0.93	0.03
Migratory status	Altitudinal migrant	2	0.5	1	1	0.28
	Full migrant	141	0.75	0.80	0.82	0.03
	Nomadic	4	0.5	0.5	0.75	0.20
	Not a migrant	40	0.51	0.60	0.65	0.06

3.4.2.2 Ne500 and migratory status

A linear mixed model showed that the interaction between migratory status and the N_e/N_c ratio was significant for all categories ($p<0.01$ or $p<0.05$; Supporting Information 1, Table S5) except nomads at the 0.4 ratio ($p=0.16$; Supporting Information 1, Table S5). This suggests that the positive influence of the N_e/N_c ratio on the Ne500 indicator value was more pronounced in altitudinal migrants than in non-migrants, nomads, or full migrants. Consequently, although migratory status alone did not significantly affect the indicator, it modulated the effect of the N_e/N_c ratio. Fig. 6 shows the distribution of the Ne500 values (based on the mean N_c estimates) across migratory statuses.

For the lower ratios (0.1 and 0.2), full migrants had significantly higher EMMs of the Ne500 values than non-migrants ($p_{0.1} = 0.003$ and $p_{\mathbf{0.2}} = 0.027$, respectively). This difference was not significant at the 0.4 ratio ($p_{0.4} = 0.060$). EMMs with standard errors for all ratios are visualized in Fig. 4b and presented in Table 2.

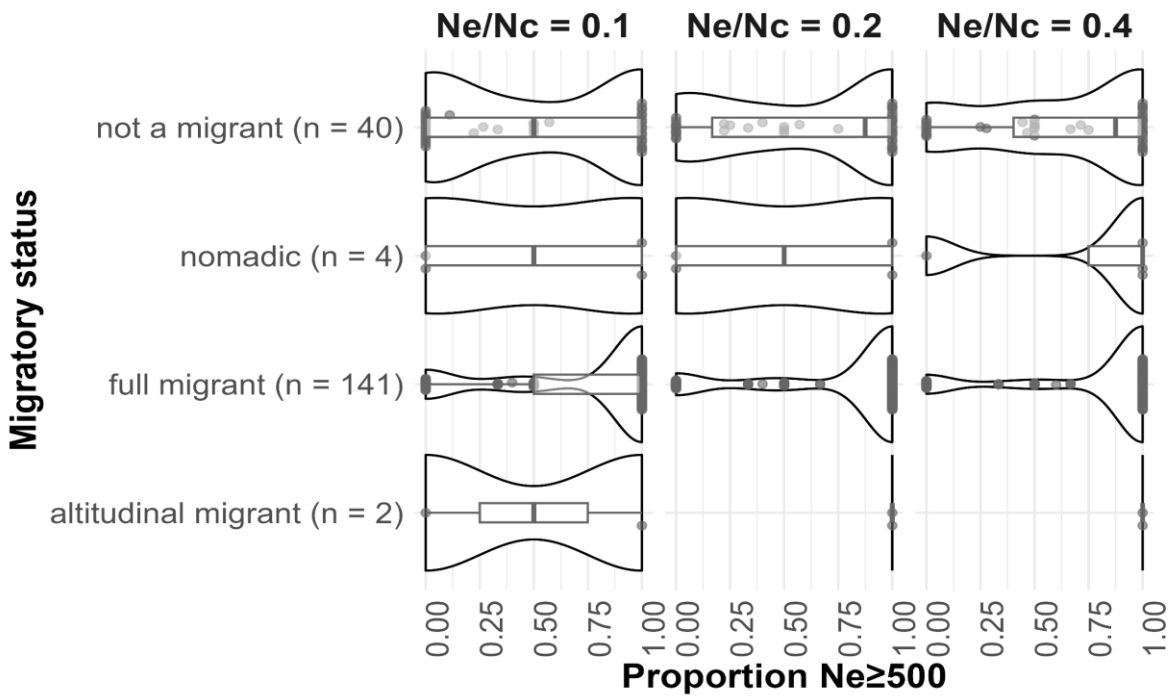


Fig. 6 - Violinplots and boxplots displaying the overall distribution in Ne500 values (proportion N_e≥500) across the different migratory status categories. Width of the violin represents the density of data points at a specific N_e500 value.

3.4.3 Ne500 and number of populations

For the correlation between the Ne500 value and the number of populations per species, a linear model was fitted (AIC_{lin} = 1.83). The number of populations was shown to significantly and negatively affect the N_e500-value (p=0.002), with values being lower when the number of populations increases (Fig. 7a). Applying different ratios (0.2 and 0.4) also had a significant effect (respectively: $p_{0.2}$ = 0.013 and $p_{0.4}$ = 0.0004), meaning both scenarios displayed higher values than the 0.1 N_e/N_c ratio. Interaction between the ratio and the number of populations was not significant for ratio 0.2 (p = 0.52) and ratio 0.4 (p = 0.1).

3.4.4 Ne500 and generation length

A linear model was preferred for the interaction between the Ne500 indicator value and generation length (AIC_{lin} = 12.42). The applied ratio had a significant positive effect (p = 0.02 for ratio 0.2 and p = 0.001 for ratio 0.4). In contrast, the effect of generation length was not significant (p = 0.16), although a slight negative trend was observed, indicating that longer generation lengths tend to be associated with lower Ne500 values (Fig. 7b).

3.4.5 Ne500 and occurrence

Based on AIC, a quadratic model was fitted for the relationship between the Ne500 indicator value and occurrence (AIC_{quad} = -8.01). Consistent with previous results, the N_e/N_c ratio had a significant effect on the N_e500 ($p_{0.2}$ = 2.51 x 10^{-5} and $p_{0.4}$ = 9.55 x 10^{-10}). Both the linear and quadratic components of occurrence had significant positive effects on Ne500 (p_{lin} = 1.75 x 10^{-7} and p_{quad} = 0.0001). The interaction between ratio 0.4 and the linear and quadratic terms of occurrence was also significant ($p_{0.4, lin}$ = 0.006 and $p_{0.4, quad}$ = 0.033) indicating that the effect of occurrence on Ne500 differs slightly at this ratio. Specifically, the linear increase is somewhat reduced and the curvature of the relationship is slightly altered for ratio 0.4. Overall, these results indicate that Ne500 increases with occurrence in a nonlinear (quadratic) manner, such that species occupying more sites tend to have higher Ne500 values, but the rate of increase slows at high occupancy levels (i.e., a curved relationship), with this pattern being modestly influenced by the N_e/N_c ratio (Fig. 7c).

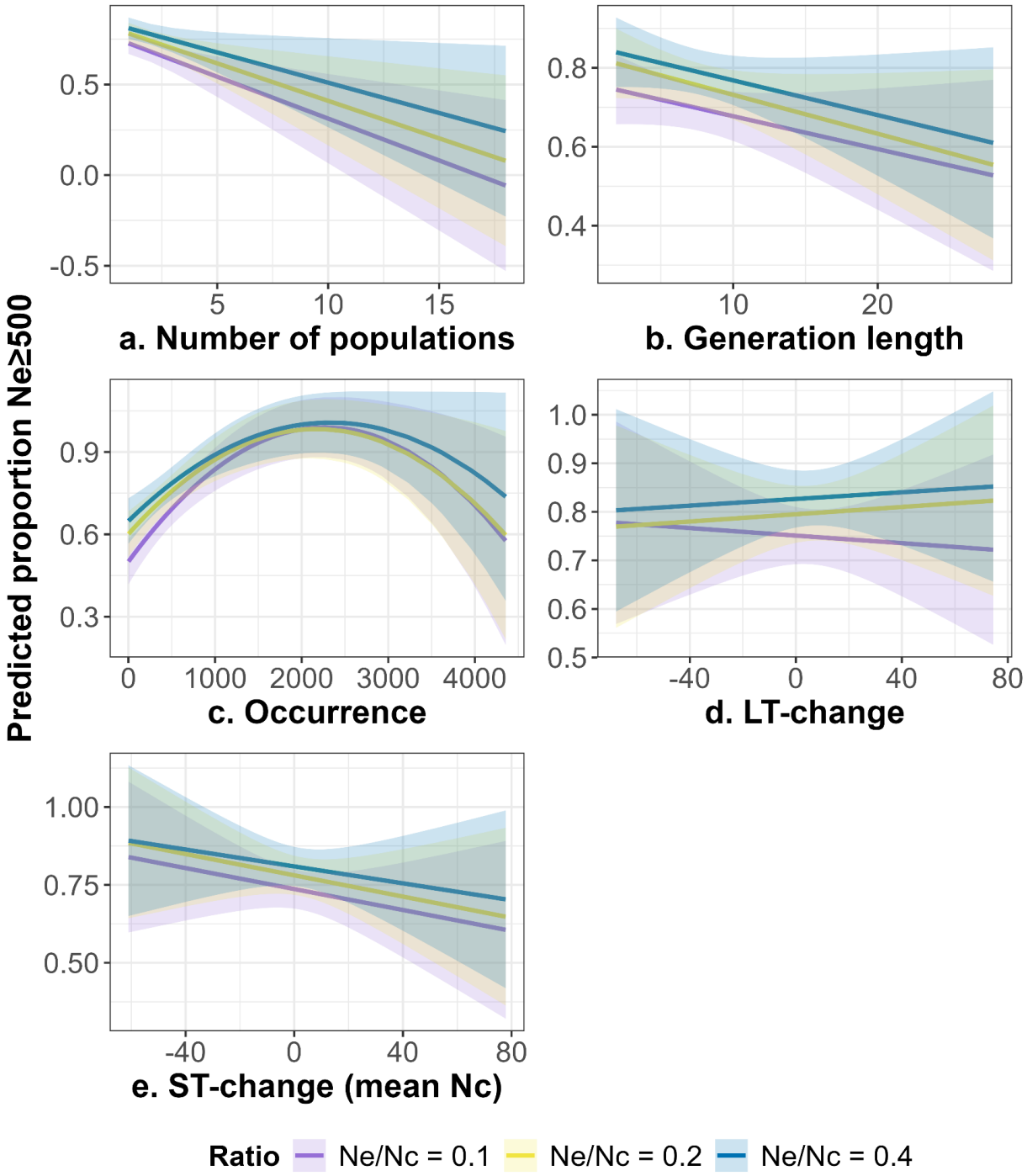
3.4.6 N_e500 and long-term change index (LT-change)

A linear model was chosen to assess the relationship between the long-term change index (LT-change provided by EBBA2) and the Ne500 indicator (ΔAIC > 2 in favour of the linear model), but no significant effect of LT-change on N_e500 values was detected (p = 0.78). In contrast, the N_e/N_c ratio had a significant effect on Ne500 ($p_{0.1}$ = 0.005, $p_{0.4}$ = 2.34 x 10^{-6}). Higher ratios (0.2

and 0.4) were associated with increased Ne500 values, but no interaction with LT-change was found, indicating that the ratio affected overall Ne500 levels without altering the relationship with LT-change (Fig. 7d).

3.4.7 Ne500 and short-term (ST) change index (based on mean N_c estimates)

The chosen model for correlation testing between Ne500 values and ST-change was in favor of the linear model (ΔAIC = -75.8). Short term change index (ST-change, based on mean Nc-estimates) had no significant effect on Ne500 values ($p = 0.37$). No interaction effect between ratio and ST-change was detected. Again, Ne500 values vary across scenarios (minimal positive effect ratio 0.2 = 4.41×10^{-2} and ratio 0.4 = 7.26×10^{-5} with $p_{0.2} = 0.008$ and $p_{0.4} = 1.58 \times 10^{-5}$), but is not explained by short-term change (Fig. 7e).



579

580 ***Fig. 7 - Plots showing the predicted Ne500 values for the different continuous variables based on the results***

581 ***of the LMM exploring the correlation between Ne500 and said continuous variables. The different colors***

582 ***indicate the three possible ratios.***

583

4. DISCUSSION

This study provides a first proof-of-concept for large-scale genetic indicator assessment on the European scale, and the first in depth application to a single taxonomic group, by repurposing extensive existing datasets collected over several decades. Together, these analyses offer a foundational blueprint for expanding such assessments across diverse lineages and geographic boundaries.

4.1 Continental Patterns and Taxon-Specific Mobility

Our findings indicate that genetic indicator values for bird species (on the EU-level) are generally higher than those reported in the first large-scale calculation of the genetic indicators across nine countries (Mastretta-Yanes et al., 2024). This discrepancy could stem from the difference in spatial scale. While country-level assessments reflect political boundaries, our continental-scale approach aligns more closely with the biological units of bird populations (e.g., accounting for migratory and transboundary behavior).

Furthermore, the relatively high values of both, the Ne500 (0.76 ± 0.03, based on N_e/N_c ratio of 0.2) and PM (PM = 0.99 ± 0.004) indicators likely reflect the inherent mobility of birds. High dispersal capacity allows many species to bypass barriers, maintaining connectivity across the European continent (e.g., Kociolek et al., 2011; Suárez et al., 2022; White, 2016). This suggests that genetic threats could be less pervasive in birds than in other vertebrates with limited dispersal capacities. However, birds are not immune to genetic erosion; indeed, despite birds being among the most comprehensively monitored taxonomic groups (Garnett & Geyle, 2018; Moussy et al., 2022), recent evidence suggests that *Aves* may experience higher rates of genetic diversity loss among several classes or organisms for which there is significant data (Shaw et al., 2025), highlighting that high current indicator values might not preclude rapid future decline.

While some uses of the term genetic monitoring (Pearman et al., 2024) focus on longitudinal DNA-based monitoring, the scope of the definition of the GM indicator (Hoban et al., 2020) and of our analysis was broader. The GM indicator, and our, objective was to determine the overall availability of population genetic data, some of which was utilized for population delineation. Our finding that 54% of the 187 assessed bird species possessed such data aligns with the established literature, confirming that birds remain a primary focus of taxonomic and genetic research (e.g., Wink, 2021). However, we note two main issues regarding our interpretation of the GM indicator. First, it likely underestimates total monitoring effort due to the exclusion of grey literature and non-English reports, as well as its narrow focus on genetic methods applied to species characterization (in contrast to the Genetic Monitoring Effort framework described by Pearman et al., (2024). Second, because the indicator is binary, it may overestimate spatial coverage of the monitoring, as a species receives a score of PM= 1 even if only a single population or region within its distribution was studied.

4.2 Ecological Drivers of Genetic Diversity

We evaluated several ecological factors to determine their influence on the Ne500 indicator. First, we observed a strong relationship between the indicator and European IUCN Red List status, which was more pronounced than in previous investigations (Mastretta-Yanes et al., 2024). While "Least Concern" (LC) and "Near Threatened" (NT) species (147 out of 187 studied species) generally exhibited higher indicator values, several exceptions existed. Specifically, 21% (31/147) of LC or NT species had a Ne500 value of 0.5 or below (considering mean N_c estimates and N_e/N_c = 0.2). E.g., species such as the Bonelli's Eagle (*Aquila fasciata*), the Eastern Imperial Eagle (*Aquila heliaca*), the Laurel Pigeon (*Columba junoniae*), and Ruddy Shelduck (*Tadorna ferruginea*) all had a Ne500 indicator value of 0 (see Supporting Information 2, Table S2). This

confirms that common or non-threatened species can still be at significant risk of losing genetic diversity.

Migration strategy also showed a significant relationship with the Ne500 indicator, with migratory species exhibiting significantly higher Ne500 values (when applying N_e/N_c ratios of 0.1 and 0.2) than non-migratory species. This aligns with the expectation that migratory behavior facilitates gene flow and reduces population differentiation (e.g., (Burg et al., 2006; de Freitas et al., 2022; Friesen et al., 2007) and thus the risk of population isolation. In contrast, the number of delineated populations had a significant negative effect on the indicator. This relationship is ecologically intuitive: as a species' distribution is divided into more sub-units, individual populations are increasingly likely to be smaller and suffer from restricted connectivity.

Interestingly, generation length did not significantly affect Ne500 indicator values. The slight negative trend observed in our study, though not significant, could provide a compelling insight: species under pressure and with inherently long generation lengths may be more genetically vulnerable because they face a higher probability of not reaching the age required to successfully contribute to the gene pool (Waples et al., 2013).

Finally, we examined the influence of species occurrence, which exhibited a quadratic relationship with the indicator. However, at the highest levels of occurrence, the Ne500 values reach a plateau, likely driven by the tendency for widespread species to be fragmented into smaller units by Europe's geography (e.g., peninsulas and islands). This scale-dependent interaction could be further influenced by migratory behavior; as mobile species can bypass physical barriers, while widespread sedentary species remain susceptible to geographically induced isolation (Hartfelder et al., 2020; White, 2016). This is exemplified by the Great Spotted Woodpecker (*Dendrocopos major*), a non-migratory species with one of the largest occurrences in our dataset (3,950 EBBA2-squares), yet it maintained a low Ne500 value of 0.33. Similarly, the non-migratory Hazel Grouse

(*Tetrastes bonasia*) showed a relatively low Ne500 value of 0.5 despite an occurrence of 1,678 squares (Supporting Information 2, Table S1).

Notably, a migratory strategy does not automatically guarantee widespread occurrence; for example, the migratory Zino's Petrel (*Pterodroma madeira*), Lesser White-fronted Goose (*Anser erythropus*), and Roseate Tern (*Sterna dougallii*) occupied only 1, 15, and 27 EBBA2 squares, respectively (refer to pages 247,15 and 260 in Supporting information 3). Furthermore, mean occurrence did not differ significantly between migratory (n = 138; occupation of 800 ± 80.3 squares) and non-migratory (n = 40; occupation of 791 ± 154 squares) species. Collectively, these results provide a finer-scale examination of the impact of species ranges than the assessment by Mastretta-Yanes et al., (2024), which focused solely on the binary distinction between large and restricted ranges.

Lastly, indices for both short-term and long-term population change had no significant relationship with the indicator. This suggests that Ne500 is not simply a reflection of whether a species is currently expanding or shrinking, but is instead driven by factors happening at the local scale and by ecological characteristics.

4.3 Methodological insights and Caveats

The indicator value depends to a degree on the N_e/N_c ratio, which has previously been noted as critical to determine (Frankham, 1995), particularly in the absence of direct genetic data (Mastretta-Yanes et al., 2024). Because the suggested default N_e/N_c ratio of 0.1 carries substantial uncertainty, this study accounted for ratio variability (e.g., Clarke et al., 2024; Hoban, Paz-Vinas, et al., 2021, 2024) by calculating bird-specific indicators across three values: 0.1, 0.2, and 0.4. Our results demonstrated that while higher ratios shifted a greater proportion of species toward higher indicator values, the mean changes only by a slight amount and the overall

distribution remained bimodal (Fig. 3), consistent with previous work (Mastretta-Yanes et al., 2024).

Biologically, relying on a generalized taxon-wide ratio across Aves is plausible, as birds share relatively similar reproductive life histories, typically producing few offspring relative to body size and exhibiting a narrow range of maximum lifetime reproductive investment (Charnov et al., 2007; Sibly et al., 2012). Because N_e/N_c ratios are largely a function of variance in lifetime reproductive success (Waples, 2024), values across bird species vary minimally and generally remain constrained within the 0.1 to 0.4 range (Hoban, Bruford, et al., 2021; Hoban, Paz-Vinas, et al., 2024).

As a result, a uniform taxon-specific ratio is sufficient for broad, high-level policy assessments. However, our findings indicate that the Ne500 indicator remains moderately sensitive to the exact N_e/N_c ratio and census size (N_c), making precise species-specific values essential for local management. This sensitivity is especially critical for species hovering near demographic tipping points. For instance, shifting the assumed ratio from 0.1 to 0.4 lowers the required N_c threshold from 5,000 to 1,250 individuals, a difference that can abruptly flip a population's indicator value from 0 to 1. Therefore, while generalized ratios serve macro-level trends, future applications should continue evaluating a spectrum of values when local conservation outcomes are at stake.

We observed a few instances of high sensitivity across various species in our dataset. For the Long-legged Buzzard (*Buteo rufinus*), which consists of a single European population, adjusting the ratio from 0.1 to 0.2 shifted the indicator value from 0 to 1 (Supporting Information 2, Table S2). In species with multiple delineated populations, the effect was step-wise but equally significant: the Ne500 indicator for Bolle's pigeon (*Columba bolii*; 4 populations delineated) ranged from 0, 0.25 to 0.5 across the three tested ratios, while the indicator value for the Red Kite (*Milvus milvus*; 5 populations delineated) increased from 0.4 to 0.6, when a 0.4 N_e/N_c ratio was

applied (Supporting Information 2, Table S2). These results demonstrate that the interaction between the chosen ratio, census size, and population delineation can fundamentally alter a species' assigned conservation status, highlighting why securing empirical, species-specific ratios is vital for reliable long-term monitoring and local conservation management. Moreover, it seems that for birds and other species with low fecundity, the N_e needed for long-term conservation exceeds 1000 (Pérez-Pereira et al., 2022).This effectively doubles the corresponding N_c threshold, largely offsetting the effect of assuming a higher N_e/N_c ratio. This higher N_e threshold (>1000) has also been advocated more generally (Frankham, 2015), reflecting the recognition that the traditional $N_e \geq 500$ criterion is a pragmatic rule of thumb rather than a biologically universal threshold for maintaining long-term evolutionary potential.

The population delineation workflow (Fig. 1b) developed in this study combined occurrence data, population estimates, and available genetic data to calculate indicator values. By prioritizing simplicity over complexity, we adopted a conservative approach to avoid over-splitting species without strong empirical evidence. While we acknowledge that this may result in an underestimation of the total number of distinct populations, it ensures a more robust and reproducible methodology. In practice, genetic data proved invaluable for complementing occurrence-based delineation. This was especially evident when range data alone were insufficient to define biologically meaningful populations; in such cases, our findings were further strengthened by consulting with experienced ornithologists. This highlights the critical importance of integrating expert knowledge as a complementary source of information to supplement large open-access databases.

We also acknowledge several caveats that may lead to an "optimistic" overestimation of genetic health (via high Ne500 indicator values). First, the reliance on data from 2013–2018 means our indicators may not reflect recent catastrophic declines. Since 2018, bird populations have faced substantial pressures, including habitat loss, climate change (e.g., Lees et al., 2022; Poll et al.,

2026), anthropogenic pressures (e.g., Rigal et al., 2023), and the emergence of highly pathogenic avian influenza. Recent studies have demonstrated measurable impacts of avian influenza on seabird populations in Europe (Falchieri et al., 2022; Knief et al., 2024; Macgregor et al., 2024), suggesting that some current population sizes may be lower than those reflected in the datasets used here. Additionally, landscape fragmentation may have been either under- or overestimated, as spatial data from before 2018 might not yet reflect recent population genetic shifts that influence the overall genetic structure. Consequently, the actual impact on gene flow between populations could be masked, as evidenced by recent genomic data showing extensive inbreeding even across seemingly continuous distributions in EBBA2 (e.g., Hazel Grouse, *Bonasia bonasia*; Song et al., 2024). For that, indicators will require regular re-assessment during future reporting cycles to remain accurate. Recent guidance suggests that populations should be monitored at least approximately every four years in order for indicator values to track the actual genetic status of species (Hébert et al., 2026). Consequently, the indicators calculated within this study could be underestimations in many cases. However, this challenge is also known within the Red List of species, with nearly a fifth of all Red List assessments already more than 10 years old (Rondinini et al., 2014).

Second, and beyond these spatial and temporal constraints, the quality and accuracy of the N_c estimates themselves vary. Population estimates derived from EBBA2 (EBCC, 2022; Keller et al., 2020) and Eionet (European Environment Agency (EEA), 2020) differ substantially in scale and methodology, ranging from logarithmic abundance classes to direct counts of breeding pairs or individuals. This variability is compounded by differences in monitoring between Member States, which may lead to the under- or overestimation of population sizes. Furthermore, using calling males and breeding females as proxies for breeding pairs may introduce bias, as a calling male does not necessarily guarantee a breeding event. Finally, this analysis omitted two key

reproductive factors known to modulate N_e variations in species-specific breeding strategies and potential biased sex ratios within populations (e.g., Frankham, 1995).

4.4 Policy Implications and Future Directions

The adoption of the Kunming-Montreal Global Biodiversity Framework (KMGBF) has transitioned the monitoring of genetic diversity from a scientific preference to a mandatory international commitment for all CBD signatory parties (CBD, 2022). We here illustrate that the European Union has the potential to use existing data and methods to report on the status of genetic diversity. By repurposing existing census and occurrence data, we provide a scalable blueprint that can be transitioned from a proof-of-concept to a standardized reporting mechanism for EU Member States. Moving forward, our workflow could be expanded to other groups (e.g., mammals, pollinators, or freshwater fish) by leveraging similar open-access databases like European Mammals on Maps Atlas (EMMA) and the New Atlas of Amphibians and Reptiles in Europe (NA2RE). To improve future assessments, we recommend the development of a repeatable analysis pipeline and clearer guidance on sampling depth required to robustly estimate N_e.

Identifying species of concern is an ongoing priority in conservation, and our results demonstrate that the Ne500 indicator is a powerful tool for this purpose. Species with low indicator values, regardless of their census size, should be prioritized for conservation and genetic studies, as they may be suffering from cryptic genetic erosion that undermines their long-term viability. For example, White-rumped Swift (*Apus caffer)*, Common loon (*Gavia immer)* or Great grey owl (*Strix nebulosa)*; all species with Ne500 value = 0 (based on mean N_c estimates and a N_e/N_c ratio 0.2) and for which GM turned out to be 0. In our dataset we also note that about 1 in 5 LC and NT species had low Ne500 indicator values, emphasizing that genetic losses can happen in common species. For these species, our results justify an immediate shift in conservation priority, moving them from passive monitoring to active genetic sampling and management. By identifying such

gaps, this framework allows policymakers to allocate limited conservation funding toward the species with the highest genetic risk.

Given the critical role of genetic diversity in maintaining population viability, evaluating the genetic structure of threatened taxa is fundamental to effective conservation planning (e.g., Frankham, 2010; Hoban, Bruford, et al., 2021; Laikre et al., 2009). To refine this process, the development of a repeatable, transparent analysis pipeline, coupled with clearer guidance on the sampling depth required to robustly estimate N_e will be essential. Such improvements will transform genetic indicators from a mere reporting exercise into a cornerstone of adaptive biodiversity management.

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