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PRACTICE AND POLICY

Genetic diversity and IUCN Red List status

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Abstract

The International Union for Conservation of Nature (IUCN) Red List is an important and widely used tool for conservation assessment. The IUCN uses information about a species' range, population size, habitat quality and fragmentation levels, and trends in abundance to assess extinction risk. Genetic diversity is not considered, although it affects extinction risk. Declining populations are more strongly affected by genetic drift and higher rates of inbreeding, which can reduce the efficiency of selection, lead to fitness declines, and hinder species' capacities to adapt to environmental change. Given the importance of conserving genetic diversity, attempts have been made to find relationships between red-list status and genetic diversity. Yet, there is still no consensus on whether genetic diversity is captured by the current IUCN Red List categories in a way that is informative for conservation. To assess the predictive power of correlations between genetic diversity and IUCN Red List status in vertebrates, we synthesized previous work and reanalyzed data sets based on 3 types of genetic data: mitochondrial DNA, microsatellites, and whole genomes. Consistent with previous work, species with higher extinction risk status tended to have lower genetic diversity for all marker types, but these relationships were weak and varied across taxa. Regardless of marker type, genetic diversity did not accurately identify threatened species for any taxonomic group. Our results indicate that red-list status is not a useful metric for informing species-specific decisions about the protection of genetic diversity and that genetic data cannot be used to identify threat status in the absence of demographic data. Thus, there is a need to develop and assess metrics specifically designed to assess genetic diversity and inform conservation policy, including policies recently adopted by the UN's Convention on Biological Diversity Kunming-Montreal Global Biodiversity Framework.

KEYWORDS

conservation policy, data synthesis, genetic drift, heterozygosity, mitochondrial DNA, molecular markers, nuclear DNA, vertebrates

La diversidad genética y los estados de la Lista Roja de la UICN

Resumen: La Lista Roja de la Unión Internacional para la Conservación de la Naturaleza (UICN) es una importante herramienta de uso extendido para evaluar la conservación. La UICN utiliza datos sobre la distribución y tamaño poblacional de una especie, la calidad y niveles de fragmentación de su hábitat y sus tendencias de abundancia para valorar su riesgo de extinción. A pesar de que la diversidad genética afecta al riesgo de extinción, la UICN no la considera. La deriva génica y las tasas altas de endogamia afectan con mayor fuerza a las poblaciones en declinación, lo que puede reducir la eficiencia de la selección, derivar en la

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disminución de la aptitud y dificultar la capacidad de una especie de adaptarse ante el cambio ambiental. Se ha intentado encontrar la relación entre la diversidad genética y el estado en las listas rojas ya que su conservación es muy importante. Aun con lo anterior, no hay un consenso actual sobre si la diversidad genética está capturada en las categorías vigentes de la Lista Roja de la UICN de manera que sea informativa para la conservación. Para poder evaluar el poder predictivo de la correlación entre la diversidad genética y el estado en la Lista Roja de los vertebrados, sintetizamos trabajos previos y analizamos de nuevo los conjuntos de datos con base en tres tipos de información genética: ADN mitocondrial, microsatélites y genomas completos. Las especies con un estado de riesgo de extinción más alto fueron propensas a una diversidad genética más baja para todos los tipos de marcadores, aunque estas relaciones fueron débiles y variaron entre los taxones, lo cual es coherente con trabajos anteriores. Sin importar el tipo de marcador, la diversidad genética no fue un identificador certero de las especies amenazadas en ninguno de los grupos taxonómicos. Nuestros resultados indican que el estado de lista roja no es una medida útil para guiar las decisiones específicas por especie en relación con la protección de la diversidad genética. También indican que los datos genéticos no pueden usarse para identificar el estado de amenaza si no se tienen los datos demográficos. Por lo tanto, es necesario desarrollar y evaluar las medidas diseñadas específicamente para valorar la diversidad genética e informar las políticas de conservación, incluidas las que adoptó recientemente la ONU en el Convenio del Marco Mundial Kunming-Montreal de la Diversidad Biológica.

PALABRAS CLAVE

ADN mitocondrial, ADN nuclear, deriva génica, heterocigosidad, marcadores moleculares, políticas de conservación, síntesis de datos, vertebrados

INTRODUCTION

The International Union for Conservation of Nature (IUCN) Red List is a widely used criterion-based evaluation of species extinction risk and conservation status. The IUCN uses the best available data from across species ranges to evaluate demographic threats. Species are placed into 1 of several extinction risk categories based on species-wide risk assessments. These categories include the number of adult individuals (Criterion A); small range sizes, very high levels of population fragmentation, fluctuating populations, or few locations where species persist (Criterion B); small population size and declining populations (Criterion C); a very small number of individuals (Criterion D); or quantitative analysis of extinction risk, such as population viability analysis (Criterion E; IUCN, 2012).

Genetic diversity is not incorporated into IUCN Red List risk assessments. However, fragmented, small, and declining populations are susceptible to the erosion of genetic diversity due to increased levels of genetic drift and decreased gene flow. This means that red-list criteria might also be informative for species extinction risk due to the loss of genetic diversity. Low genetic diversity is associated with reduced population mean fitness and inbreeding—both can contribute to population declines. Together with other demographic processes, these genetic factors could increase extinction risk via an extinction vortex (Blomqvist et al., 2010; Frankham, 2005; Palomares et al., 2012).

The potential links between red-list status and genetic diversity have led to an ongoing conversation about how these metrics might inform each other. Risk statuses might be useful for assessing and guiding the protection of genetic diver-

sity by identifying species at risk of rapid genetic erosion (e.g., Canteri et al., 2021; Garner et al., 2020). Conversely, measures of genetic diversity might inform red-list assessments for data-deficient species (Brüniche-Olsen et al., 2021; Petit-Marty et al., 2021). Resolving these questions is important because genetic diversity has not been well integrated into global conservation policy (Hoban et al., 2020; Laikre, 2010), despite its importance for evolutionary potential and population persistence. However, genetic diversity conservation and its consequence, adaptive capacity, have recently received greater policy recognition by the UN's Convention on Biological Diversity (CBD), specifically the outcomes of COP15, including the adoption of the Kunming-Montreal Global Biodiversity Framework (<https://www.cbd.int/doc/c/e6d3/cd1d/daf663719a03902a9b116c34/cop-15-1-25-en.pdf>).

Determining whether red-list status and genetic diversity are related in a way that is useful for species assessments is timely for conservation policy given recent CBD post-2020 Global Biodiversity Framework talks (Hoban et al., 2023; Xu et al., 2021). Indeed, there were discussions of the utility of the IUCN Red List Index as a metric for a species' genetic health or genetic diversity conservation at the recent COP15 (S. Hoban & L. Laikre, personal communication). Several studies have addressed the question of whether the IUCN Red List, given its association with demography, is suitable for identifying species with low genetic diversity (Brüniche-Olsen et al., 2018, 2021; Canteri et al., 2021; Doyle et al., 2015; Garner et al., 2020; Li et al., 2016; Nabholz et al., 2008; Petit-Marty et al., 2021; Rivers et al., 2014; Willoughby et al., 2015) and whether genetic data can inform status assessments for data-deficient species (e.g., Brüniche-Olsen et al., 2021; Petit-Marty et al., 2021). Find-

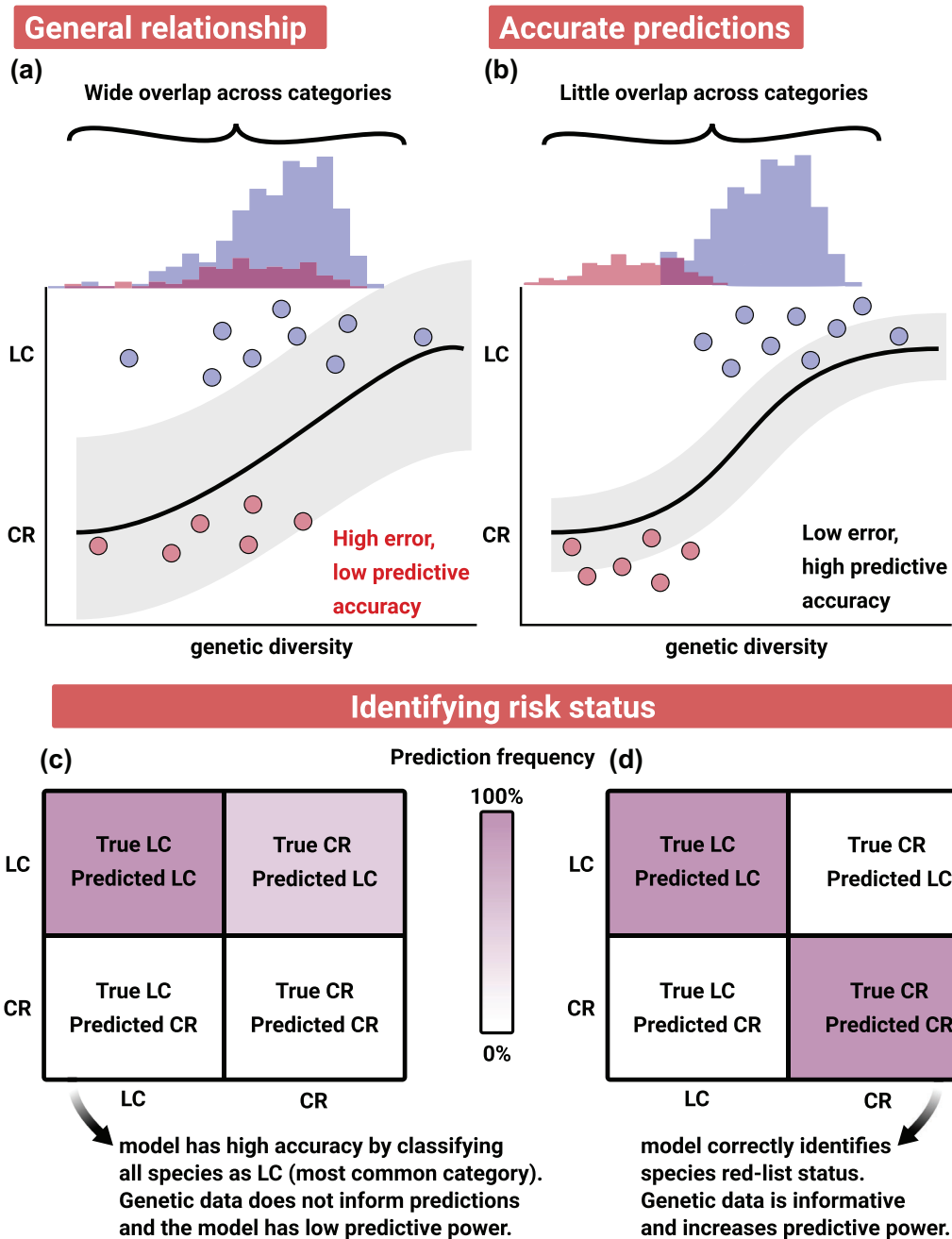


FIGURE 1 A toy comparison of scenarios where (a) genetic diversity is similar across extinction risk categories and (b) genetic diversity is higher in species at lower extinction risk. (a, c) A model can identify general relationships between genetic diversity and extinction risk category while making inaccurate predictions. (b, d) When genetic diversity more strongly differs across extinction risk categories, models can be used to capture trends and accurately predict species risk status (LC, least concern; CR, critically endangered).

ings that threatened species tend to have lower genetic diversity than nonthreatened species have led some authors to advocate the use of red-list threat status by policy makers as an indicator of species genetic diversity when genetic data are unavailable (Canteri et al., 2021) and to suggest use of genetic data as a tool for risk status assessment (Brüniche-Olsen et al., 2018, 2021; Petit-Marty et al., 2021). However, it is possible for statistical models to detect general correlations between quantities of interest while simultaneously having poor predictive performance (Figure 1). The relevance of red-list status as a proxy for intraspecific genetic diversity or vice versa hinges

on the strength of this relationship and model predictive accuracy. However, predictive accuracy in this context has not been explored.

If models of relationships between genetic diversity and red-list threat status can accurately predict threat status, then policy makers could use red-list status to assess or approximate genetic diversity levels in the absence of genetic data, which is still not available for most species. Additional metrics developed specifically for assessing genetic diversity status and trends would not be needed (Hoban et al., 2020, 2021; Laikre et al., 2020). Further, high predictive accuracy would mean that red-list status could

also be assessed with genetic data for data-deficient species if available. However, if the relationship between red-list status and genetic diversity is weak and has poor predictive accuracy, relying solely on red-list status would result in a lack of formal and sufficient protection for genetic diversity in natural populations, warranting the implementation of other indicators and proxies of genetic diversity (e.g., the recently adopted effective population size >500 indicator [i.e. headline indicator A.5 for Goal A and Target 4 of the Kunming-Montreal GBF] [CBD, 2022; Hoban et al., 2020]). To evaluate the extent to which species genetic diversity is predictive of red-list status, we reanalyzed 3 genetic data sets (2 previously used for this purpose) containing estimates of genetic diversity obtained from different markers (mitochondrial gene sequences, microsatellites, and whole-genome sequences [WGS]).

DATA AND ANALYSES

Our first data set was composed of estimates of mitochondrial DNA (mtDNA) *cytochrome b* diversity from 1036 bird species. This data set was compiled by Canteri et al. (2021), who used it to assess the relationship between red-list risk (threatened or not) and genetic diversity. Threatened species were those listed as vulnerable, endangered, and critically endangered. They concluded that red-list status captures species with low genetic diversity. Canteri et al. (2021) obtained *cytochrome b* sequences from GenBank, a genetic sequence database, and measured genetic diversity at the species level with nucleotide diversity for species with 5 sequences minimum (median = 11 sequences per species across the data set).

Our second data set consisted of genetic diversity estimates from WGS for 68 bird species from a data set compiled by Brüniche-Olsen et al. (2021) from 2 sequence databases, EMBL-EBI and NCBI. Genetic diversity was measured with genome-wide observed heterozygosity estimated from the site frequency spectrum for 1 sequence per species. With these data, Brüniche-Olsen et al. (2021) found that threatened species (endangered and critically endangered) had lower observed genomic heterozygosity than nonthreatened species.

Finally, our third data set was the MacroPopGen database (Lawrence et al., 2018, 2019). This database contains site-level estimates of genetic diversity from microsatellite markers for vertebrate species (terrestrial vertebrates and freshwater fish) across North and South America harvested from the literature. For this data set, we obtained red-list statuses of species with the rredlist package (Chamberlain, 2020), an R interface for the Red List Application Programming Interface. We were able to extract red-list statuses for 693 species (80 amphibians, 215 birds, 143 mammals, 120 reptiles, 134 ray-finned fishes, and 1 lamprey), excluding data-deficient species. The median number of sample locations per species was 4 (range: 1–226), and the median number of individuals sampled per species was 212 (2–37,088). The median number of sample locations in each vertebrate group was 8.5 (1–117) for amphibians, 1.5 (1–41) for birds, 7 (1–226) for fish, 4 (1–156) for mammals, and 8 (1–111) for reptiles. The median number of individuals sampled across all sites per species for each group was 304 (10–20,113) for amphibians, 132

(2–8518) for birds, 331 (5–37,088) for fish, 168 (6–8900) for mammals, and 284 (10–6400) for reptiles.

We chose gene diversity (reported as expected heterozygosity in MacroPopGen) as our metric of genetic diversity for microsatellites because it does not depend strongly on sample size (Charlesworth & Charlesworth, 2010). Gene diversity is the average probability that 2 randomly selected alleles in a population are different (Nei, 1973). We averaged gene diversity across sample sites to obtain a species-level measure of genetic diversity comparable to the genetic diversity estimates in the mtDNA and WGS data sets.

Although we tested these 3 marker types, biological differences among markers mean they are not all equally informative for conservation. Mitochondrial genomes are maternally inherited, behave as a single locus because they do not recombine, and have several protein-coding genes, meaning they do not evolve neutrally (Galtier et al., 2009). Mitochondrial DNA diversity is generally not correlated with genome-wide diversity or adaptive potential, 2 core targets of conservation genetics (Kardos et al., 2021). It is also not strongly related to population size (Bazin et al., 2006), a central component of IUCN Red List assessment. Mitochondrial markers have been strongly criticized as general tools for population genetics, phylogenetics, and conservation outside of specific contexts (Edwards & Bensch, 2009; Galtier et al., 2009; Paz-Vinas et al., 2021; Schmidt & Garroway, 2021a; Zink & Barrowclough, 2008).

In contrast, nuclear microsatellites and whole-genome data both capture genome-wide diversity. Although single genomes can characterize individual genetic diversity, they do not necessarily reflect population- or species-wide genetic diversity levels. Genetic diversity estimated from multiple individuals at ~10 microsatellite loci is well correlated (83%) with genome-wide diversity (Mittell et al., 2015). Among bird species in our analyses, only 5 species were present across all 3 data sets (54 species shared between mtDNA and microsatellite data sets; 20 between mtDNA and WGS; 9 between WGS and microsatellite). Microsatellite genetic diversity was not correlated with mtDNA genetic diversity for species in both data sets (Figure 2).

We modeled relationships between our measures of genetic diversity (nucleotide diversity for mtDNA data, observed genome-wide heterozygosity for WGS data, and gene diversity for microsatellite data) and red-list categories with the same 2 models fit to each data set. The first model type was an ordinal logistic regression implemented in R (R Core Team, 2021) with the polr function in the MASS package (Venables & Ripley, 2002). The dependent variable was threat status ordered by risk (LC, least concern; NT, near threatened; VU, vulnerable; EN, endangered; CR, critically endangered). Then, to more closely resemble previous work (Brüniche-Olsen et al., 2021; Canteri et al., 2021), we also tested how well genetic diversity classified broader binary red-list categories, threatened (comprised of CR, EN, and VU categories) versus nonthreatened (NT, LC), with binary logistic regressions. These models were standard logistic regressions: generalized linear models with a binomial error distribution fit with the glm function in R 4.1.1 (R Core Team, 2021). We assessed model predictive accuracy with confusion matrices generated with the caret package (Kuhn, 2021). All analyses were repeated for mtDNA, microsatellite, and WGS

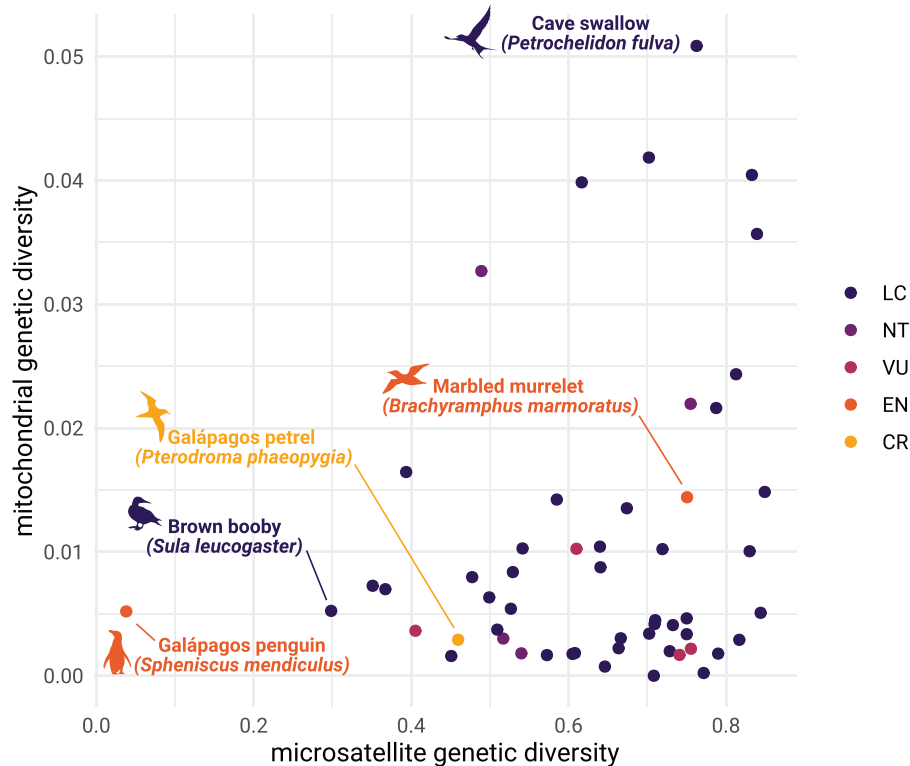


FIGURE 2 Relationship of mitochondrial genetic diversity (nucleotide diversity) to microsatellite diversity (gene diversity) in 54 bird species ($r = 0.22$; 95% CI: -0.05 to 0.46). Highlighted species show mismatches between mitochondrial genetic diversity, nuclear genetic diversity, and IUCN Red List conservation status (LC, least concern; NT, near threatened; VU, vulnerable; EN, endangered; CR, critically endangered). For example, the endangered Galápagos penguin has lower nuclear genetic diversity than other species in our data set, but mitochondrial diversity comparable to several other species, and the Marbled murrelet, also endangered, has relatively high mitochondrial and nuclear diversity.

diversity estimates separately. We were interested in whether genetic diversity predicted red-list status and whether red-list status was informative for species genetic diversity. A strong correlation between genetic diversity and red-list status would suggest that either may be used to inform the other. We focused on predicting red-list status from genetic diversity data.

Data and code to reproduce analyses are available on GitHub (https://github.com/chloewsch/GD_IUCN).

GENETIC DIVERSITY AND RED-LIST STATUS

Consistent with previous analyses (Brüniche-Olsen et al., 2021; Canteri et al., 2021; Li et al., 2016; Petit-Marty et al., 2021; Willoughby et al., 2015), red-list status was statistically related to genetic diversity across marker types and the examined taxa, except for fish (Table 1). Threat status tended to increase as genetic diversity decreased for all markers (Figure 3).

The predictive accuracy of our models ranged from 57% to 84% for specific red-list categories (ordinal regressions) and 63% to 90% for predicting whether species were threatened or nonthreatened (logistic regressions). However, confusion matrices showed that these levels of predictive accuracy were achieved by classifying nearly all species as LC or nonthreatened, the most common category (Appendix S1).

This result highlights that there was no strong tendency for markedly low genetic diversity to be associated with CR, EN, or VU species. The range of genetic diversity in LC species encapsulated genetic diversity across all other red-list categories for all markers and taxa (Figure 3), and LC was the most common status (84% of mtDNA data, 65% of microsatellite data, 69% of WGS data). This scenario of high model accuracy but low predictive power is known as the “accuracy paradox” (Fernandes et al., 2010). These results demonstrate that a species’ red-list status cannot be predicted from species-level genetic data and red-list status cannot be used as a surrogate for species’ risk of genetic erosion in the absence of genetic data. Thus, red-list status alone is not useful for informing decisions related to the conservation of genetic diversity of individual species.

LOW VERSUS DECLINING GENETIC DIVERSITY

That our models did not correctly identify threat status based on genetic diversity likely arose from the multiple reasons species can have low genetic diversity, and because the IUCN Red List was not developed to assess genetic diversity. Species that have undergone particularly significant declines in abundance or range extent and species with historically low abundance or small ranges are all expected to have low genetic diversity.

TABLE 1 Relationship between International Union for Conservation of Nature Red List categories and genetic diversity as measure with mtDNA, microsatellite, and whole-genome sequencing (WGS) data.^a

Data type and taxon	<i>n</i>	Accuracy	(95% CI) ^b	Beta	(SE) ^c
Ordinal regression, microsatellites					
Birds	215	0.66	(0.60–0.73)	−3.17	(0.89)
Mammals	143	0.64	(0.56–0.72)	−4.67	(1.13)
Amphibians	80	0.74	(0.67–0.83)	−2.99	(1.6)
Reptiles	120	0.57	(0.47–0.66)	−4.3	(1.38)
Fish	134	0.63	(0.55–0.72)	−0.63	(0.91)
Ordinal regression, mtDNA					
Birds	1048	0.84	(0.82–0.86)	−69.75	(11.95)
Ordinal regression, WGS					
Birds	68	0.69	(0.57–0.80)	−748.8	(232.9)
Logistic regression, microsatellites					
Birds		0.79	(0.73–0.84)	−3.09	(1.02)
Mammals		0.78	(0.71–0.85)	−6.06	(1.45)
Amphibians		0.81	(0.71–0.89)	−3.59	(1.81)
Reptiles		0.63	(0.53–0.71)	−3.26	(1.48)
Fish		0.68	(0.59–0.76)	−0.65	(0.98)
Logistic regression, mtDNA					
Birds		0.90	(0.88–0.92)	−124.29	(21.61)
Logistic regression, WGS					
Birds		0.79	(0.68–0.88)	−939.54	(338.82)

^aModel summaries for ordinal regressions (response variable is all 5 red-list categories ranked 1-LC, 2-NT, 3-VU, 4-EN, and 5-CR) and logistic regressions (binary response variable, threatened vs. nonthreatened).

^b95% confidence interval for model accuracy.

^cStandard error of beta coefficients.

In the early stages of population decline, genetic diversity loss can be difficult to detect because genetic drift erodes genetic diversity slowly across many generations, and relationships between the loss of diversity and range loss can be nonlinear (Landguth et al., 2010; Pflüger et al., 2019). Moreover, changes in nuclear genetic diversity following habitat disturbance are variable across taxa. For example, mammals generally lose diversity in highly urbanized areas, but at different rates depending on species (DiBattista, 2008; Habrich et al., 2021; Schmidt et al., 2020). Bird species either lose or gain genetic diversity in more urban areas (Schmidt et al., 2020), whereas changes in amphibian genetic diversity are more idiosyncratic depending on species and location (Schmidt & Garroway, 2021b). Variation in response to local and contemporary habitat changes can obscure the relationship between a species' genetic diversity and its red-list status over time.

There is also a more fundamental issue underlying analyses that relate average species genetic diversity to red-list status for the purposes of identifying species with concerning low levels of genetic diversity. Of central conservation importance for both abundance and genetic diversity is the extent of, or potential for, decline. Species have variable levels of genetic diversity at mutation–drift equilibrium that are associated with traits that affect census population size (Buffalo, 2021; Eo et al., 2011; Romiguier et al., 2014). Our results suggested that demographically stable species (LC) span a wide range of genetic diversity

(Figure 3). It is also well-known that low genetic diversity is not always indicative of conservation concern. Both Canteri et al. (2021) and Brüniche-Olsen et al. (2021) report that among those species with the lowest genetic diversity in their data, not all were listed as threatened. Species can persist with low contemporary genetic diversity, especially if long-term effective population sizes are also small and abundance is stable (e.g., Fraser et al., 2014; Reed, 2010).

Critically for conservation genetics, models comparing mean genetic diversity across species do not address whether rates of genetic erosion are increasing in threatened species. Instead, they address why genetic diversity differs across species with red-list criteria as explanatory variables. Weak relationships between red-list status and genetic diversity likely capture species-level characteristics associated with range size, life history, and historical population size (coalescent effective population size) that contribute to genetic diversity variation across species (Romiguier et al., 2014). To an extent, such factors can be, and often are, corrected for by including phylogenetic relatedness in models to account for historical genetic diversity correlations between related species. The remaining variation can be attributed to unique (not conserved) traits or population histories, contemporary genetic diversity change, and residual error. However, what low genetic diversity means is relative. In these types of comparative models, low is defined relative to other species, whereas conservation geneticists are primarily

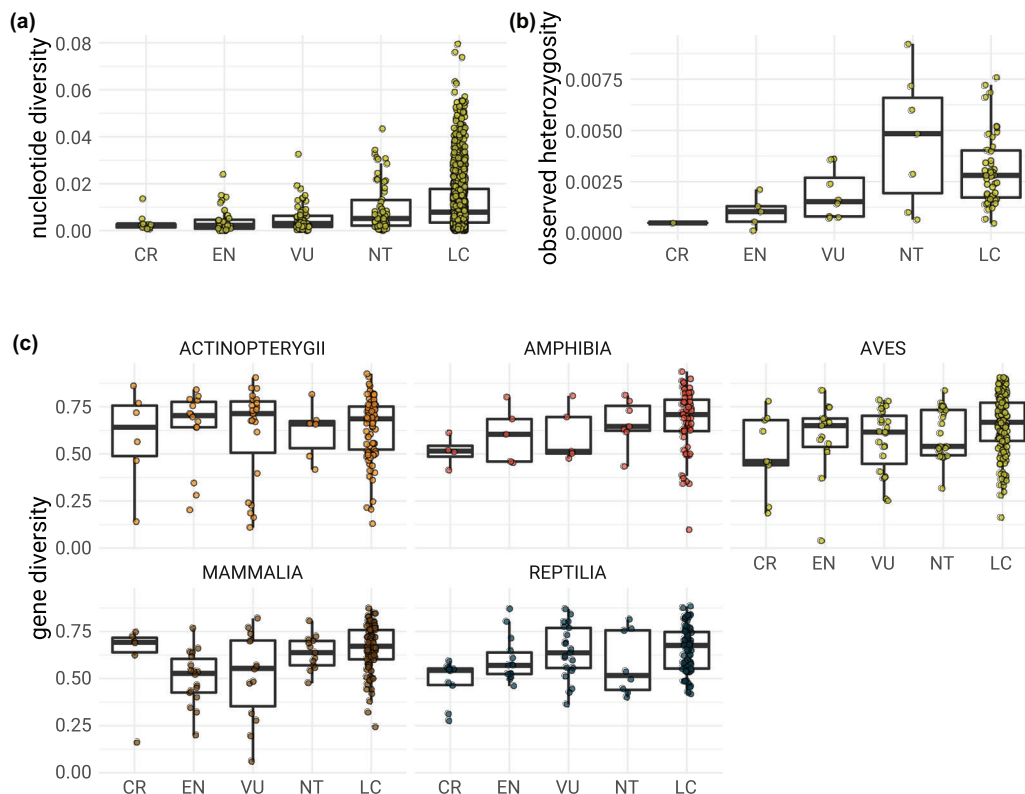


FIGURE 3 Relationship of (a) avian mitochondrial genetic diversity, (b) avian whole-genome genetic diversity, and (c) microsatellite genetic diversity of vertebrates to International Union for Conservation of Nature Red List categories (CR, critically endangered; EN, endangered; VU, vulnerable; NT, near threatened; LC, least concern).

concerned with low contemporary genetic diversity compared with past levels of genetic diversity in a species. Thus, questions about decline or risk of genetic erosion cannot be fully addressed when comparing genetic diversity snapshots across species. Because the nature and causes of genetic diversity loss are variable across genetic markers, populations, species, and species' ranges, interspecific comparisons of red-list rankings and average species genetic diversity are not particularly informative for identifying species at risk of genetic erosion.

Genetic diversity declines are ideally assessed with intraspecific data sampled over time, but unfortunately, this is difficult to do at scale (but see Leigh et al., 2019). To an extent, data limitations can be overcome by repurposing publicly available genetic data and substituting space for time to study environmental factors related to decline with data from multiple populations per species (Habrich et al., 2021; Schmidt & Garraway, 2021b; Schmidt et al., 2020). Alternative genetic metrics might be used that respond more quickly to abundance declines than heterozygosity or gene diversity, such as allelic richness or long runs of homozygosity, which can detect inbreeding before widespread losses of genetic diversity. However, red-list status is also unrelated to runs of homozygosity burden in mammals (Brüniche-Olsen et al., 2018).

Peart et al. (2020) presented an approach that does not require multiple estimates of genetic diversity within species, accounts for unique population histories, and avoids direct com-

parison of genetic diversity across species. Using genomic data and contemporary abundance data, they estimated the ratio of coalescent effective population size to census population size (N_e/N_c) for pinniped species. After controlling for species' population histories (i.e., regressing Tajima's D on N_e/N_c), the residual variation in N_e/N_c can be understood as the deviation in abundance from expectations based on effective population size, with positive residuals indicating recent abundance declines. For a given population size, species with low N_e/N_c will experience stronger effects of genetic drift, causing them to lose genetic diversity and fix deleterious alleles more quickly (Peart et al. 2020). This metric, which is focused on abundance, was related to red-list status of pinnipeds (Peart et al. 2020). Species with higher N_e/N_c residuals were more likely to be threatened. The lack of availability of genomic data may limit applications of this approach for the foreseeable future. Although its predictive accuracy is still uncertain, it appears promising. Below, we list other simpler ways genetic diversity can be incorporated in species risk assessments to improve its protection.

A WAY FORWARD

Red-list rankings are used extensively for conservation planning, often at the species or regional level. Defining conservation

status helps to prioritize actions for species at the highest risk levels (CR and EN) and identify at-risk regions or key biodiversity areas (Hoffmann et al., 2008). The red-list process of compiling information from experts also allows analysis of regional and global threats to species (Rodrigues et al., 2006). Change in the red-list index over time is a useful global indicator of biodiversity loss (Tittensor et al., 2014) (see Fraixedas et al. [2022] for critique of other aspects of the IUCN Red List). Given its focus on demographic change, it was important to test whether red-list status captured genetic diversity, which would remove the need to develop additional tools to assess genetic erosion and enable the use of genetic data to inform red-list assessment. We found that the IUCN Red List, on its own, did not reflect the genetic diversity patterns of individual species and thus is not reliable for informing policy aimed at conserving and recovering genetic diversity. Direct genetic diversity assessments, in combination with the use of well-verified proxies or indicators of genetic diversity (Hanson et al., 2017; Hoban et al., 2020, 2022) and other conservation tools, are needed to assess species' vulnerability to genetic erosion.

Moving forward, it is necessary to shift away from policy tools that were not designed to evaluate or protect genetic diversity when the goal is to conserve genetic diversity (Hoban et al., 2022). Nuclear genetic data are becoming available for increasing numbers of species (Leigh et al., 2021), enhancing the ability to look more deeply into genetic diversity status within and among populations of species (Hoban et al., 2022). As more genomes become fully sequenced, there are more proposals for assessing genetic erosion status using genome-level statistics (Bertorelle et al., 2022; Brüniche-Olsen et al., 2018; Peart et al., 2020; van Oosterhout, 2020, 2021). However, most species will lack genetic data for the foreseeable future. This highlights the need to develop and verify effective proxies that are directly connected to genetic diversity (Hoban et al., 2020, 2021). For example, proxies could include the proportion of populations with low effective size (which will slow genetic erosion) or the proportion of lost distinct populations (Hoban et al., 2020, 2021, 2022). Such proxies were recently adopted by the Convention on Biological Diversity COP15 decision for use by all countries in monitoring and reporting on genetic diversity conservation, even when genetic data are not available (i.e., as headline or complementary indicators for the Kunming-Montreal GBF [<https://www.cbd.int/doc/c/179e/aecb/592f67904bf07dca7d0971da/cop-15-l-26-en.pdf>]).

We also suggest that the current protocol for recording information for red-list assessment be modified to include genetic information for species when available. For example, a straightforward technical change to the submission system could additionally include information on genetic status, such as genetic diversity, inbreeding, hybridization, or any other genetic information that the community deems relevant for conservation (see Brüniche-Olsen et al., 2018; Garner et al., 2020; Thurfjell et al., 2022). Standardized fields could be used to record such data, as is currently done for number of populations, area of occupancy, extent of occurrence, population trend, habitat affiliation, and lists of known threats. Genetic status could be similarly incorporated into IUCN Green Status assessments (Stephenson et al., 2019). Standardized collection and

storage of these data would lead to a global database of species' genetic statuses and make IUCN Red List assessments a more multifaceted resource. In short, a vital and feasible first step is to start recording and storing measures of species genetic status during the red-list assessment process, even if this information is not immediately used to inform the red-list status, which would require approval of IUCN members.

The rapid collection and use of genetic, genomic, and proxy metrics in a coordinated way across species is essential to help the scientific community inform conservation decision-making. Producing and aggregating these data, however, requires considerable effort. Sequence data can be stored in centralized repositories (e.g., GenBank); however, similar programmatically accessible databases are not available for other genetic markers, most notably microsatellites, which remain in wide use. To ensure accessibility to researchers and practitioners, proxy data should be aggregated in centralized databases that can be expanded and updated over time to capture temporal trends, ideally as part of the IUCN Red List or Green Status. For all data types, improving metadata standards (minimally to include the location and date of sampling) is imperative (Leigh et al., 2021), and recent advances such as the GEOME database (Deck et al., 2017) are opening the door to more accessible, searchable, and reusable genetic data. The ongoing development of genetic indicators as well as a suite of agreed-upon genetic "essential biodiversity variables" (Andersson et al., 2022; Hoban et al., 2022), relatively simple metrics that can be comparable across species, means that policy makers can begin to move beyond the IUCN Red List to safeguard genetic diversity in all species.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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