Sparse genetic data limit biodiversity assessments in protected areas globally

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Global conservation targets include protecting genetic diversity within species. Yet few studies have assessed whether protected areas (PAs) include genetically diverse populations across species globally. A first step is understanding the availability of population genetic data that could be used in these assessments. We surveyed georeferenced population-level nuclear (as opposed to mitochondrial or plastid-based) genetic data across continents and marine biomes (36,354 populations, 2809 species) and found substantial geographic and taxonomic gaps. Most data were concentrated in Europe and North America, with major gaps in Africa and Asia. For most taxonomic groups, data were available for <1% of described species. Globally, 52.08% of the total areal extent of PAs lacked genetically sampled populations. These gaps in data availability highlight the need for targeted genetic data collection, harmonization, and sharing to improve genetic diversity monitoring and conservation planning. Combined with proxy-based genetic indicators, such data are needed to inform PA assessments, bolster area-based conservation initiatives like 30 × 30, and support achievement of global genetic conservation targets.

Front Ecol Environ 2025; e2867, doi:10.1002/fee.2867

Genetic variation within populations (hereafter, "genetic variation") underlies population health, adaptive potential, species persistence, and ecosystem resilience (Hoban *et al.* 2023). Yet, estimates suggest that global genetic diversity has declined by 5.4–6.5% (Leigh *et al.* 2019) to >10% (Exposito-Alonso *et al.* 2022) on average since the Industrial Revolution. Despite constituting the most fundamental level of biodiversity, genetic variation has largely been excluded from global conservation initiatives (Hoban *et al.* 2023) and assessments of protected area (PA) design and effectiveness (Andrello *et al.* 2022; Nielsen *et al.* 2023; but see Figuerola-Ferrando *et al.* 2023). The recent Kunming-Montreal Global Biodiversity Framework (GBF; CBD 2022) under the Convention on Biological Diversity (CBD) established explicit goals and targets for maintaining and restoring genetic variation in wild species. Goal A aims to maintain genetic diversity within populations of all species by 2050, while Target 4 aims at halting species extinction, protecting genetic diversity, and managing human–wildlife conflicts by 2030 (CBD 2022). The GBF also includes a goal to increase the area protected globally to 30% by 2030 (the 30 × 30 initiative [Target 3]; CBD 2022), offering opportunities to integrate genetic variation into area-based conservation. Determining the baseline status of genetic variation in PAs and beyond can help measure progress toward these GBF protection commitments. A primary step toward informing genetic monitoring in PAs is assessing the availability of population-level nuclear genetic data worldwide. These genetic data can quantify this most fundamental level of biodiversity and can be used to inform progress toward global genetic conservation commitments and area-based conservation initiatives like 30 × 30.

Protected areas are a cornerstone of biodiversity conservation efforts (Maxwell *et al.* 2020). By preserving or connecting populations, PAs can help safeguard genetic variation (Andrello *et al.* 2022; Nielsen *et al.* 2023). Ideally, assessments of genetic variation within PAs would be based on empirical genetic data collected across many populations

In a nutshell:

- We assessed the coverage of population-level nuclear genetic data available within and outside of protected areas (PAs) globally (36,354 populations, 2809 species)
- Overall, genetic data were sparse; spatial and taxonomic gaps in data availability could limit their use in global PAs and conservation assessments
- Incorporating proxy-based genetic indicators that do not require genetic data could help address gaps in the short term
- Meanwhile, efforts to collect, harmonize, and share genetic data could focus on regions with limited data availability to facilitate the integration of empirical genetic information into PA design and performance assessments, enhancing conservation of genetic variation

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and species both within and outside of PAs (Figuerola-Ferrando *et al.* 2023). In recent decades, the growth of nuclear intraspecific genetic data has enabled the creation of "macrogenetic" databases, which compile genetic data across taxonomic groups over expansive spatial (regional to global) and/or temporal scales to facilitate the study of large-scale patterns in and drivers of genetic variation (Blanchet *et al.* 2017; Leigh *et al.* 2021). These data could also be used to inform PA design and evaluate its effectiveness. However, the spatial and taxonomic distribution of available population-level nuclear genetic data remains unknown, as each macrogenetic database has its own taxonomic and spatial scope and as no single meta-database has compiled these databases.

We estimated the global availability of population-level nuclear genetic data across continents and marine biomes by combining seven macrogenetic databases and examining the spatial distribution of the ~2 million genotyped individuals, 36,354 populations, and 2809 species included in these databases. We then examined the density of genetically sampled populations across taxonomic groups and within PAs. Our results highlight data gaps that, if addressed, could improve global genetic diversity assessments.

Methods

Building a meta-database of available genetic data

To assess the availability of population-level nuclear genetic data globally, we built a meta-database of genetic data previously compiled in large macrogenetic databases (Appendix S1: Table S1; *Supplementary data 1.xlsx* at https://doi.org/10.6084/m9.figshare.28639895.v1). Macrogenetic databases contain not only summaries of genetic variation from publications and genetic data repositories (eg Dryad and the International Nucleotide Sequence Database Collaboration [INSDC]) but also associated contextual metadata (eg geographic coordinates; Leigh *et al.* 2021). While certain previous macrogenetic studies focused on data from mitochondrial DNA (mtDNA) (eg Miraldo *et al.* 2016), here we included macrogenetic databases only with multi-locus population-level nuclear genetic data: that is, microsatellites, amplified fragment length polymorphisms (AFLPs), and single nucleotide polymorphisms (SNPs). This distinction is important, given that nuclear genotypic data are the most appropriate for tracking whole-genome and fine-scale evolutionary processes, especially over contemporary timeframes (Sunnucks 2000; Kardos *et al.* 2021), and given the many limitations of single-locus organelle-based DNA (eg mtDNA) data (Schmidt and Garroway 2021a; Leigh *et al.* 2021; Paz-Vinas *et al.* 2021).

We identified seven macrogenetic databases—namely, Beninde *et al.* (2022), Clark and Pinsky (2024), Crandall *et al.* (2023), De Kort *et al.* (2021), Karachaliou *et al.* (2025), Lawrence *et al.* (2019), and a database including data from Schmidt *et al.* (2020, 2023a) and Schmidt and Garroway (2021b, 2022) (Appendix S1: Table S1)—compiled at the population scale for multiple species. These databases varied in both spatial scale and taxonomic coverage (Appendix S1: Figure S1 and Table S1). Four of the databases were global in scope; one was global for mammals but focused on the US/Canada for birds, amphibians, and reptiles; one focused on the Americas; and one was specific to California (US) and its surrounding waters (Appendix S1: Table S1). Two were exclusive to marine fishes and one was exclusive to vertebrates (Appendix S1: Table S1). Four used only microsatellite data, one used both microsatellite and AFLP data, one compiled georeferenced accessions in the INSDC's Sequence Read Archive, and one, Beninde *et al.* (2022), included microsatellite, SNPs, allozymes, and mitochondrial data (the lattermost data being excluded from our analysis) (Appendix S1: Table S1). Details on each database's compilation are provided in Appendix S1: Table S1 and in their original publications. Although differences in search methods, taxonomic scales, marker types, and focal taxonomic groups may introduce some biases, this represents the most comprehensive compilation of nuclear genetic data published at the time of our analysis. For each dataset within each database, we extracted information on the species, its higher-level taxonomy, geographic coordinates of sampling locations for groups of genotyped individuals ("local" populations following De Kort *et al.* [2021]; hereafter, "populations"), sample sizes per population (when available), and other study-related metadata (eg first author, author list, or DOI of the original study, when available). We used these metadata to identify and remove duplicate entries across macrogenetic databases manually through cross-filtering methods. Because databases differed in the procedures used to georeference and delimit populations, we retained the version of the data that included the highest number of georeferenced populations when removing duplicate records. This was the most conservative approach, as manually assessing which database version best represented true biological populations was infeasible. Removing duplicated data (13.97%) reduced the original combined meta-database of 38,278 populations to 36,354 unique (nonduplicated) populations for final analyses. Finally, we assigned each species to their higher taxonomic groupings and identified whether its broad-scale habitat was marine, terrestrial (including freshwater habitats), or diadromous.

Building a dataset of protected areas

The World Database on Protected Areas (WDPA) (UNEP-WCMC and IUCN 2022) is the most comprehensive global database of PAs. We used the *wdpar* package (v1.3.8; Hanson 2022) in R (v4.2.2) to download and clean this global PA dataset (www.protectedplanet.net; downloaded 23 Nov 2022) following the procedures outlined by Butchart *et al.* (2015) and Runge *et al.* (2015). We removed areas with "proposed" or unknown status, excluded United Nations

Educational, Scientific, and Cultural Organization (UNESCO) Biosphere reserves, buffered PAs represented as point localities to circular areas using their reported spatial extent (Visconti *et al.* 2013), and repaired invalid geometries. To address overlapping areas in the WDPA, we transformed and flattened them into a raster with 1-km^2 grid cells for global area calculations.

Assessing taxonomic and spatial extent of available genetic data

We assessed spatial and taxonomic gaps in data availability among species and taxonomic groups by comparing our meta-database with the refined PAs database. We used ArcGIS 10.7 tools (ESRI) to assess how many populations were sampled inside and outside of PAs, noting species' taxonomic group (details below) and habitat type. When using spatial selection and join procedures to identify PAs containing genetically sampled populations, we considered a 1-km buffer around population coordinates to account for coordinate uncertainty in georeferencing procedures, as one kilometer corresponds to the median coordinate uncertainty estimated for all INSDC Biosamples from the Crandall *et al.* (2023) metadata database. To estimate geographic coverage, we summed the areal extent of PAs that contained at least one genetically sampled population and divided it by the total areal extent of PAs within continents and marine realms (Appendix S1: Table S2). We present aggregated area assessments based on total area protected (in square kilometers) rather than by number of PAs, because there is substantial geographic overlap among PAs in the WDPA, and their sizes vary considerably.

To assess the density of genetic data, we aggregated populations using an optimized hotspots analysis of point counts within a global hexagonal grid relying on default parameters in ArcGIS Pro (v3.1.1) and calculated the proportion of points inside PAs per hexagonal cell (cell size ~8000 km^2). Final layers were projected into a Robinson projection for visualization. We tested for spatial association among the number of genetically sampled populations within and outside of PAs using Lee's *L*, which characterizes both the degree of correlation and the similarity of spatial clustering (Lee 2001). We used a *K* of eight nearest neighbors with a bisquare local weighting scheme and square root transformation, and we then assessed significance using 999 permutations. Finally, we extracted the total number of described species per taxonomic group from the Catalogue of Life web portal (www.catalogueoflife.org, accessed 2 Jul 2023) to estimate taxonomic coverage relative to the meta-database.

Results and discussion

The global coverage of genetically sampled populations was sparse and spatially clustered. Data coverage was rich in Europe and North America, together harboring 72.17% of all genotyped terrestrial populations (55.79% when considering only data from databases with a global focus), while data coverage was comparatively sparse across much of Africa and parts of Asia, with the exception of South Korea and Japan (Figure 1; Appendix S1: Table S2). Oceania was also generally data-rich, although notable geographic disparities remained; for example, New Guinea and central Australia were data-poor as compared to New Zealand and Australia's coastal regions. Of all compiled genetically sampled populations, 65.51% were extracted from the global macrogenetic databases and included a broad range of taxonomic groups across the Animalia, Plantae, Chromista, and Fungi kingdoms, suggesting that spatial data gaps for these groups should not be driven by limits in the scope of these databases (Appendix S1: Figure S1 and Table S1).

We further identified major taxonomic gaps. Genetic data were available for <1% of the total described species in many major taxonomic groups, with large variation among groups (Figure 2). For instance, only 0.014% of the nearly one million described species of Insecta had genetically sampled populations, whereas 6.383% of the over 6000 described species of Mammalia were genetically sampled at the population level. Notably, even the most genetic data-rich taxonomic groups (Pinophyta, Petromyzontida, Mammalia, Aves) were represented by ≤10.25% of their described species (Figure 2). Terrestrial plants, mammals, birds, herptiles, mollusks, and marine fishes were particularly well-represented globally, although coverage of most terrestrial vertebrates was more extensive in North America due to the focused scope of some databases in this region and on this taxonomic group (Appendix S1: Table S1).

Thirty-nine percent of genetically sampled populations (Figures 1 and 2) were within PAs, and all major taxonomic groups had >16.67% of their populations sampled within PAs (Figure 2). Polypodiophyta, Ctenophora, and Phaeophyta had more than 70% of their genetic data collected within PAs. Protected areas could be a focus for the collection of genetic data from some taxa for multiple reasons: for instance, PAs may have a high likelihood of containing target populations for conservation, offer better access to wild or less-disturbed areas for conducting genetic-based studies, or facilitate operating long-term research projects. However, results from Lee's *L* test suggest that, at least in certain parts of the world, these high concentrations of data within PAs appear to be a function of spatially clustered sampling rather than a particular focus on PAs. Globally, genetic data availability within and outside of PAs was significantly positively correlated (Lee's $L = 0.2205$, $P \leq 0.002$, Pearson's $R = 0.319$). This varied spatially across the planet, with significantly positively correlated sampling (high data availability both inside and outside of PAs) concentrated in North America and Europe, and regions of significant negative correlations (high data availability within PAs but low data availability outside of PAs) apparent throughout Europe,

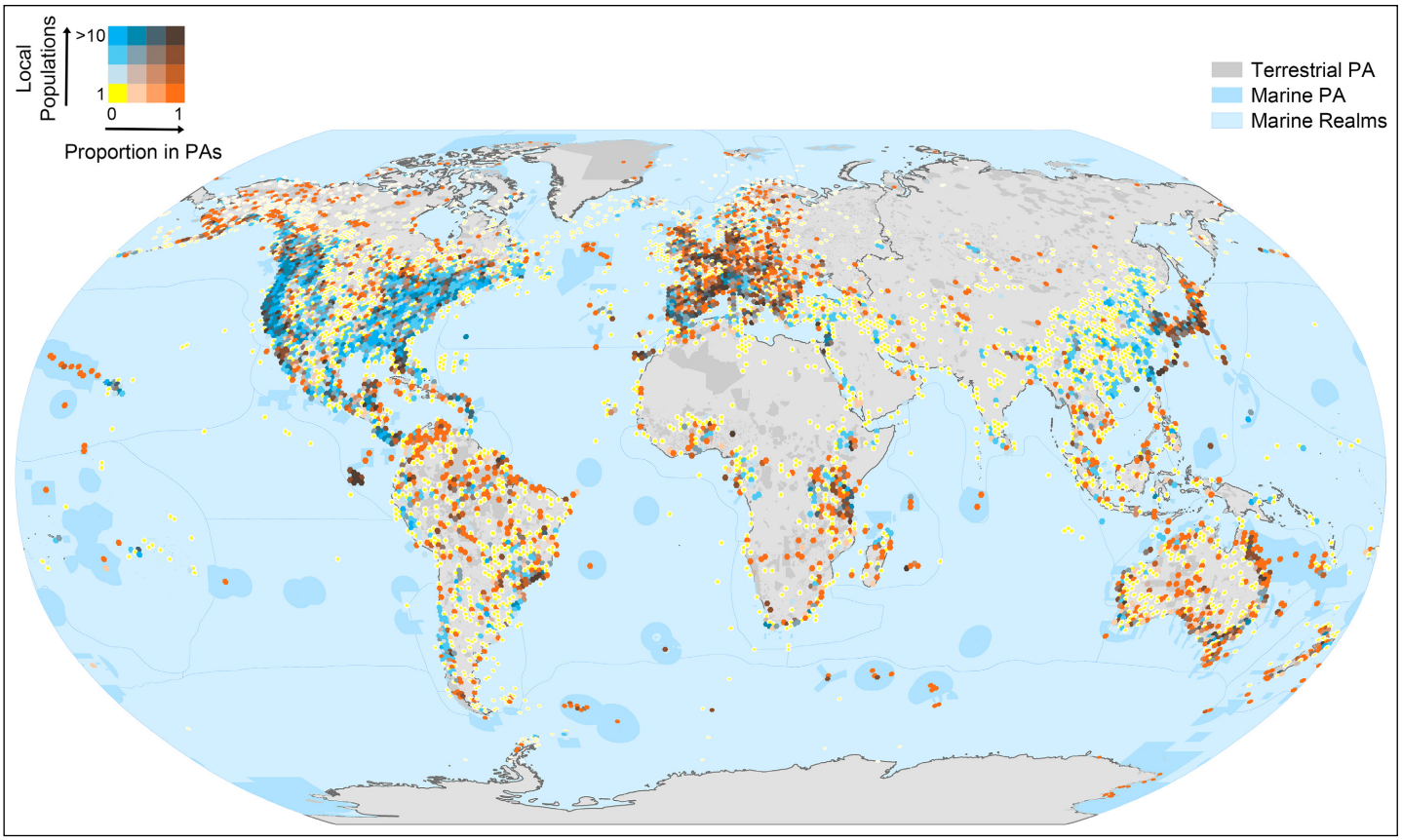

Figure 1. Global map of available population-level nuclear genetic data within and outside marine and terrestrial protected areas (PAs). In the top-left key, the vertical color-scale (yellow to blue) represents the number of local populations with available genetic data within 8000-km^2 hexagons, while the horizontal color-scale (yellow to orange) represents the proportion of local populations within the hexagon inside a PA. Yellow hexagons have just one local population that is outside of a PA, whereas dark brown hexagons have >10 local populations all within PAs. Marine realms defined by Costello *et al.* (2017); terrestrial and marine PAs defined using the World Database on Protected Areas (www.protectedplanet.net; accessed 23 Nov 2022).

Japan, and Australia, as well as in several marine realms (Appendix S1: Figure S2).

Generally, however, genetic data availability within PAs was sparse. Overall, 52.08% of the total area protected globally (67.31% terrestrial, 41% marine) had no sampled populations (Figure 1; mean number of populations per PA with genetic data = 2.57, median = 1; maximum = 278). Notably, only 12.83% and 16.48% of the total area protected in Africa and Asia, respectively, had ≥1 sampled population in our meta-database (Figure 1; Appendix S1: Table S2), and over 90% of the total area protected in the Southeast Pacific, Chile, New Zealand, and "Arctic Seas" (collectively, the Arctic Ocean, Barents Sea, Beaufort Sea, Chukchi Sea, Greenland Sea, Kara Sea, Laptev Sea, and White Sea) marine realms (classifications following Costello *et al.* [2017]; Figure 1) had no populations sampled (Figure 1; Appendix S1: Table S2). Indeed, even some of the largest PAs had no or only limited available data (eg Rapa Nui Island, Chile; Kermadec Islands, New Zealand; Marae Moana, Cook Islands; Figure 1; *Supplementary data 2.xlsx* at https://doi.org/10.6084/m9.figshare.28639898.v1).

Where genetic sampling in PAs occurred, typically there were few sampled populations. Although just under half of surveyed PAs contained genetic data from at least one population, notably fewer PAs had data from ≥5 populations (24.17%) or ≥10 populations (15.24%) (Appendix S1: Table S2). There were a few exceptions, however; several PAs harbored larger numbers of genetically sampled populations, which could be used to assess the efficacy of these PAs for conserving genetic variation. Data-rich PAs include the Channel Islands National Park in the US (135 populations, 30 species) as well as the World Heritage Sites of the Galápagos Islands in Ecuador (278 populations, 47 species) and the Great Barrier Reef in Australia (81 populations, 23 species) (Figure 1; *Supplementary data 2.xlsx* at https://doi.org/10.6084/m9.figshare.28639898.v1).

Our results show that the global distribution of available population-level nuclear genetic data is sparse and uneven, highlighting the need for further collection of genetic data worldwide but especially in data-limited areas. Filling taxonomic and spatial gaps could be particularly relevant for conservation, as patterns of genetic variation may be neither similar

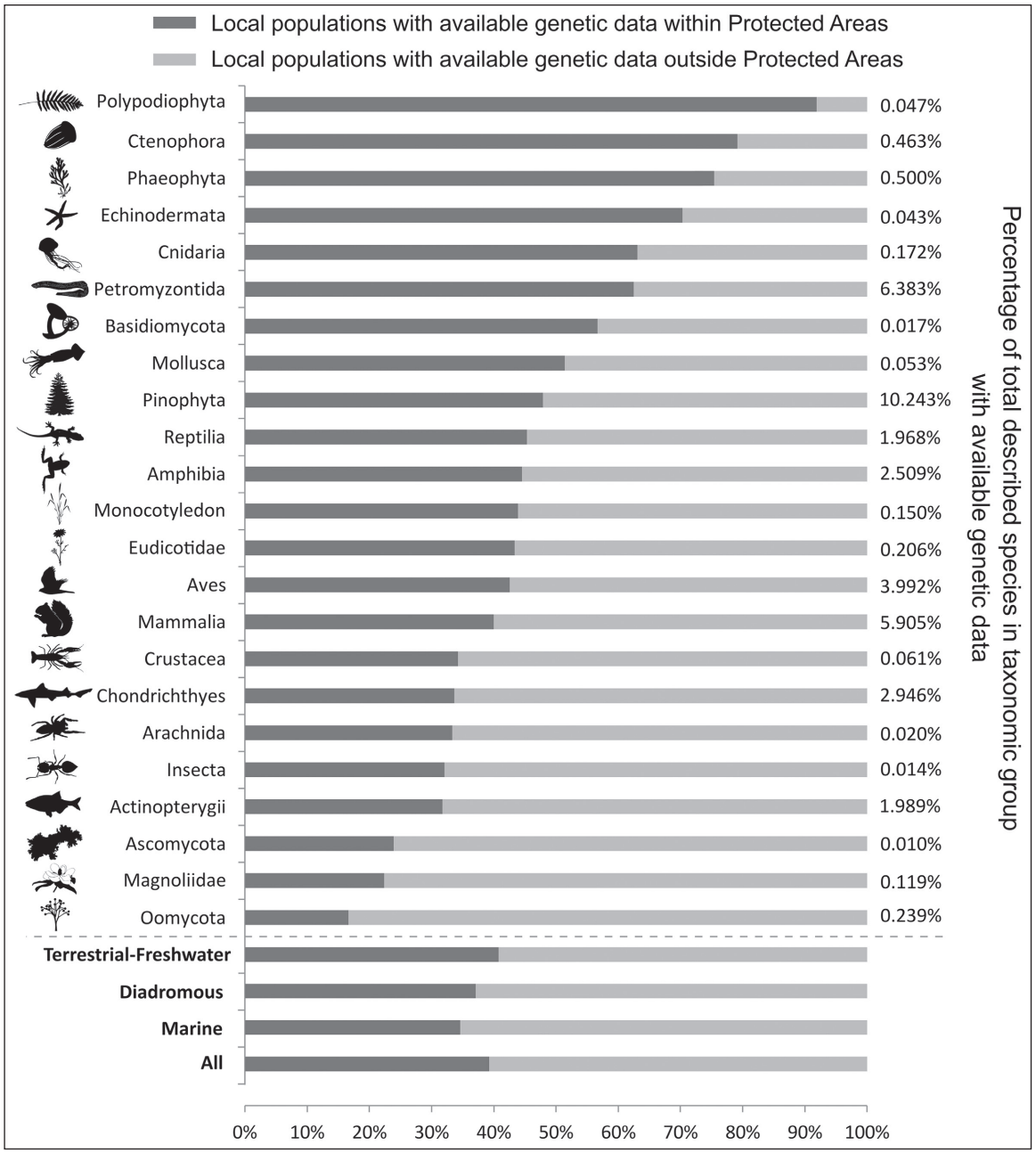

Figure 2. Percentage of local populations with available genetic data within (dark gray) and outside of (light gray) protected areas (PAs). Percentages are displayed both per taxonomic group and per species' primary habitat type (bottom four categories in bold). Taxonomic groups with <20 local populations in the meta-database are only included in the bolded categories (and not shown individually). Numbers along the right side of the figure represent the percentage of total described species in each taxonomic group with available genetic data (regardless of whether they are inside or outside of PAs) as compared to the total number of known species within the taxonomic group. Silhouettes courtesy of PhyloPic (www.phylopic.org; Cnidaria, Pinophyta, Mammalia, and Actinopterygii silhouettes are in the public domain, while the other living form silhouettes are reproduced under the CC0 1.0 Universal license).

to nor associated with the same drivers across taxa and regions (Leigh *et al.* 2021; Figuerola-Ferrando *et al.* 2023; Schmidt *et al.* 2023b). Large initiatives like the African BioGenome Project, an effort by African researchers to sequence the genomes of 105,000 endemic species (Ebenezer *et al.* 2022), and other regional and taxon-specific projects within the Earth BioGenome Project (Gupta 2022) may help to lay a solid foundation for future population genetic and genomic surveys.

In the interim, multiple approaches can be used to integrate existing genetic data into biodiversity protection and monitoring. First, in data-rich regions, existing data can be repurposed to assess genetic variation and connectivity within and outside of PAs (eg Figuerola-Ferrando *et al.* 2023) and to integrate DNA-based genetic criteria into the design of new PAs. These data also provide contemporary baselines for temporal genetic monitoring programs (Clark *et al.* 2025).

Second, to bridge global data gaps, researchers could correlate existing genetic data with geographic, environmental, and taxonomic variables to identify informative proxies when genetic data are not available (Schmidt *et al.* 2023b). For instance, macrogenetic analyses (Leigh *et al.* 2021) can identify drivers of genetic diversity and connectivity, as well as biotic/abiotic correlates such as PA design (eg size, shape, connectivity to other PAs). Third, the sparsity of genetic data in many regions, coupled with the costs of generating sequence data, underscores the need to develop proxies that can be estimated without genetic data. For instance, the headline indicator A.4 for Goal A and Target 4 of the GBF (CBD 2022; Hoban *et al.* 2023) uses the proportion of populations with an effective population size of >500, where effective population size could be approximated using population abundance or density estimates, area covered, or knowledge from Indigenous communities and other experts (Hoban *et al.* 2023, 2024). These proxies could inform decision-making by allowing rapid assessments of both the genetic status of and trends for populations when genetic data are unavailable. Genetic data collection could then be prioritized for species, populations, or regions in need of in-depth DNA-based analyses or conservation management actions (eg translocations, hybrid management, ex situ breeding; Hoban *et al.* 2024). Fourth, increased efforts to gather, harmonize, and share existing genetic data, particularly in data-poor regions, may improve the global coverage of available data. Regarding this last objective, recent and rapid growth in the conservation genomic data literature (Neaves *et al.* 2024) suggests the potential to add more data from new publications, open data repositories, and other resources, provided that those data have the necessary metadata to facilitate their reuse (eg geographical coordinates; Leigh *et al.* 2024). A recent comprehensive survey of genomic datasets available in the INSDC found that 87% lacked key spatiotemporal metadata (eg geographic coordinates of sampling sites) necessary for reuse (Toczydlowski *et al.* 2021). However, tools for retroactively georeferencing existing datasets are available (Leigh *et al.* 2021, 2024). Adopting universal reporting and archiving standards for genetic and genomic data could also improve the reusability of future data for monitoring progress toward achieving global conservation targets (Leigh *et al.* 2024).

Conclusions

Area-based conservation initiatives, like 30 × 30, offer opportunities to enhance biodiversity protection, including genetic diversity, in the next decade and beyond. Although genetic data to assess and inform PA design and efficacy remain sparse globally and for many taxonomic groups, targeted efforts can help fill these gaps. Integrating genetics into PA assessments could help safeguard genetic diversity alongside other biodiversity levels, helping to meet multiple biodiversity goals and targets (eg GBF Targets 3 and 4; CBD 2022). In some regions, there is the potential to inform efforts to protect intraspecific genetic variation and connectivity within and between PAs. Overall, increased integration of intraspecific genetic data with spatial conservation planning tools (Andrello *et al.* 2022; Nielsen *et al.* 2023) can help to ensure comprehensive conservation of species, populations, and their unique genetic variation, in new protected areas.

Acknowledgements

We thank S Hoban and R Fisher for insightful comments and suggestions. IP-V was supported by the US Geological Survey (USGS) Powell Center for Synthesis and Analysis. This work was conducted as a part of the "Standardizing, Aggregating, Analyzing and Disseminating Global Wildlife Genetic and Genomic Data for Improved Management and Advancement of Community Best Practices Working Group" supported by the John Wesley Powell Center for Analysis and Synthesis, funded by the USGS. RDC and MLP were supported by US National Science Foundation #OISE-1743711; CJG and EK were supported by a Natural Sciences and Engineering Research Council of Canada Discovery Grant. Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the US Government.

Data Availability Statement

Complete citations for all relevant public data used in this study are provided in Appendix S1: Table S1. The metadata database (supplementary data file 1) and data summaries (supplementary data file 2) are available in the Figshare repository: https://doi.org/10.6084/m9.figshare.28639895.v1 (Paz-Vinas *et al.* 2025a) and https://doi.org/10.6084/m9.figshare.28639898.v1 (Paz-Vinas *et al.* 2025b), respectively.

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Supporting Information

Additional material can be found online at http://onlinelibrary.wiley.com/doi/10.1002/fee.2867/suppinfo

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