



Research Paper

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Gaps and biases in vertebrate wildlife genetics from a global biodiversity hotspot

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Summary

Biodiversity knowledge gaps and biases persist across low-income tropical regions. Genetic data are essential for addressing these issues, supporting biodiversity research and conservation planning. To assess progress in wildlife genetic sampling within the Philippines, I evaluated the scope, representativeness, and growth of publicly available genetic data and research on endemic vertebrates from the 1990s through 2024. Results showed that 82.3% of the Philippines' 769 endemic vertebrates have genetic data, although major disparities remain. Reptiles had the least complete coverage but exhibited the highest growth, with birds, mammals, and amphibians following in that order. Species confined to smaller biogeographic subregions, with narrow geographic ranges, or classified as threatened or lacking threat assessments were disproportionately underrepresented. Research output on reptiles increased markedly, while amphibian research lagged behind. Although the number of non-unique authors in wildlife genetics studies involving Philippine specimens has grown steeply, Filipino involvement remains low. These results highlight the uneven and non-random distribution of wildlife genetic knowledge within this global biodiversity hotspot. Moreover, the limited participation of Global South researchers underscores broader inequities in wildlife genomics. Closing these gaps and addressing biases creates a more equitable and representative genetic knowledge base and supports its integration into national conservation efforts aligned with global biodiversity commitments.

Introduction

Much of Earth's biodiversity – species identity, distribution, ecology, traits, and evolutionary history – remains incomplete or largely unknown (Hortal et al. 2015). These knowledge gaps hinder biodiversity research, slow scientific progress, and obstruct the development of effective, evidence-based conservation strategies (Baranzelli et al. 2023, Diniz-Filho et al. 2023, Guedes et al. 2025). Where biodiversity knowledge does exist, it is often unevenly distributed, disproportionately favoring certain geographic regions and distorting the view of the natural world (Hughes et al. 2021). These biodiversity knowledge gaps and biases are particularly evident in low-income tropical regions, where biodiversity is both abundant and underexplored (Wilson et al. 2016, Hughes et al. 2021, Moura & Jetz 2021, Linck & Cadena 2024). Addressing this disparity is challenging given limited resources and capacity for many low-income biodiverse countries, but it is essential for progress in biodiversity knowledge and its real-world applications (Rodrigues et al. 2010, Oliveira et al. 2017, Etard et al. 2020, Gumbs et al. 2024, Moura et al. 2024). Efforts must start with a systematic assessment of existing data to evaluate its scope and representativeness. This approach should identify research priorities, inform conservation strategies, and guide more pragmatic and impactful actions toward safeguarding biodiversity.

Genetic data, fundamental to understanding species and their populations, are absent for a quarter of living terrestrial vertebrates (Šmíd 2022). This data gap exacerbates biodiversity knowledge shortfalls, extending its impact beyond scientific understanding to practical applications. Absence of genetic data obscures phylogenetic and evolutionary insights, also known as Darwinian shortfall, limiting their integration into policy, planning, and conservation practice (Diniz-Filho et al. 2013). For instance, missing genetic data likely explains why at least one-third of tetrapod species in “fully sampled” phylogenies have imputed relationships, which can introduce uncertainty and bias into evolutionary analyses and downstream conservation applications (Guedes et al. 2024). Moreover, species' genetic makeup shapes their adaptive capacity: while some populations can respond to environmental change, others may struggle to persist, risking genetic diversity loss in wild populations globally (Shaw et al. 2025). Generating data on species' genetic diversity, population size, and evolutionary history is therefore essential for developing more effective and informed conservation strategies (Hohenlohe et al. 2021, Hoban et al. 2022, Gumbs et al. 2023, McLaughlin et al. 2025). Given these considerations, understanding species and populations at genetic level is critical for integrating this fundamental biodiversity component into conservation frameworks. However,

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technical challenges in generating and interpreting genetic data have historically limited their use in conservation (Taylor et al. 2017, Hoban et al. 2024a). Despite these challenges, the importance of genetic data continues to grow, driven by advances in conservation genetics and a global push to incorporate genetic diversity into policy and practice.

The United Nations Convention on Biological Diversity (CBD) adopted the Kunming-Montreal Global Biodiversity Framework in 2022, which outlines 23 global targets for biodiversity conservation to be achieved by 2030 (CBD 2022a). Among these, Target 4 highlights protection of genetic diversity across all species, a significant step forward to recognizing and safeguarding this often-neglected biodiversity component. Under this framework, signatory countries must report their progress on Target 4, with genetic data playing a pivotal role. Genetic data can be used to monitor genetic diversity, track changes over time, and identify at-risk species and populations – all these inform practical conservation strategies (Hohenlohe et al. 2021, Hoban et al. 2022, 2024b). However, genetic data availability is uneven, disproportionately favoring certain taxonomic groups and regions (Reddy 2014, Šmíd 2022, Linck & Cadena 2024). This imbalance, coupled with biases in genomics research towards (and involving) Global North countries (Linck & Cadena 2024, Carneiro et al. 2025), can further exacerbate challenges for countries with limited resources and capacity to handle, analyze, and interpret genetic data. Such disparities may hinder skills and technology transfers to improve genetic data and research on wildlife (hereafter ‘wildlife genetics’) in resource-constrained regions (see Ramírez-Castañeda et al. 2022, Bertola et al. 2024). Reviewing existing knowledge in wildlife genetics is a crucial first step in identifying deficiencies, prioritizing overlooked areas and guiding resources toward targeted actions (Hoban et al. 2024c).

Building upon the global context of wildlife genetics gaps and challenges they present (Thurjell et al. 2022, Paz-Vinaz et al. 2023, Schmidt et al. 2023), this paper examines these issues through the lens of a global biodiversity hotspot: the Philippines. This tropical island archipelago – characterized by high and threatened biodiversity, high endemic richness, and limited capacity and resources – reflects common challenges faced by many biodiversity hotspots worldwide (Vilaça et al. 2024). As such, the Philippines provides a valuable case study for assessing wildlife genetics, offering insights broadly applicable to other biodiverse but resource-constrained countries. As a step toward assessing developments in genetic sampling of Philippine biodiversity, given its growing role in conservation and policy, I examined the scope and representativeness of publicly available genetic data for Philippine endemic vertebrates and analyzed trends in data growth and research use from the 1990s to 2024. Endemic vertebrates, vulnerable and reliant on local research and conservation action, are often the focus of conservation planning and priority-setting in the Philippines (Supsup et al. 2023, Fidelino et al. 2025). This targeted focus provides practical and policy-relevant lens to evaluate how genetic research can inform conservation priorities, particularly for genetically overlooked and undersampled species. I also evaluated the involvement of Filipino scientists in wildlife genetics research to gauge their representation and contribution in the field. This review offers a timely resource for the Philippines as it moves toward incorporating genetic considerations into conservation policy and practice in response to global biodiversity commitments.

Methods

Database assembly

A total of 769 Philippine endemic vertebrates were collated from publicly accessible databases (Table S1), accounting for 52.7% of all vertebrate wildlife in the archipelago (~1,458 vertebrate species). Collated dataset includes 99 amphibians (Class: Amphibia) from Amphibian Species of the World 6.2 (Frost 2024); 262 birds (Class: Aves) from Checklist of Birds of the Philippines (Brinkman et al. 2024); 144 mammals (Class: Mammalia) from the American Society of Mammologists’ Mammal Diversity Database v1.13 (Mammal Diversity Database 2024); and 264 reptiles (Class: Reptilia) from The Reptile Database (Uetz et al. 2024). The species list was curated to ensure the use of updated taxonomic treatments, using supplementary literature on Philippine biodiversity (Diesmos et al. 2015, Leviton et al. 2018, Weinell et al. 2019, Allen 2020).

Each species’ biogeographic distribution, conservation status, and geographic range were identified. The Pleistocene Aggregate Island Complexes (PAICs) framework was used as basis for species’ biogeographic distribution. PAICs are terrestrial biogeographic subregions of the Philippines, wherein Pleistocene sea-level fluctuations periodically connected islands separated by shallow waters (Brown et al. 2013). Islands within PAICs tend to have more similar present-day faunal compositions than those islands in different PAICs. The PAICs, ranked by land area, are: Luzon (including Babuyan Island Group to its north), Mindanao (including Mindanao, Samar, Leyte, Bohol, Basilan, and adjacent smaller islands), Palawan (including Busuanga, Coron, and Balabac islands), West Visayas (comprised of Panay, Negros, Cebu, Masbate, and smaller adjacent islands), Mindoro (including smaller Lubang and Semirara islands), Sulu Island Group (SIG; Sulu and Tawi-Tawi archipelago), and Romblon Island Group (RIG; Romblon, Tablas, and Sibuyan islands) (Figure 1 but see Meneses et al. 2024 for a detailed map with island names). Species occurring in two or more PAICs were indicated as ‘multiple’.

Conservation status was determined using the International Union for Conservation of Nature (IUCN) Red List v3.1 (IUCN 2024), categorized into threatened (critically endangered, endangered, and vulnerable species), non-threatened (least concern and near-threatened species), and no status (data-deficient and unassessed species). The IUCN’s geographic range criteria, specifically extent of occurrence (EOO), were used to classify ranges into small (<1000 km²), medium (1001–20 999 km²), and large (>21 000 km²). The geographic range category reflects species’ known distribution, as several species, although distributed in larger PAICs like Mindanao and Luzon, have smaller EOOs.

Publicly available DNA sequence data for each species, regardless the type and length, (hereafter ‘genetic data’) were manually searched in GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) from August to December 2024. GenBank is a genetic sequence database maintained by the U.S. National Institutes of Health’s National Center for Biotechnology Information. All searches were done using the species’ currently accepted scientific name, synonyms, and previously assigned names. This approach was necessary for species that had been split or lumped, as GenBank may not have updated their records to reflect latest taxonomic treatments (Hosner et al. 2022, Mulcahy et al. 2022). For entries where GenBank names did not align with current taxonomy, the original publication associated with genetic data was reviewed to confirm provenance of specimens, including entry if they were from the Philippines. Genetic data were then re-assigned to appropriate currently accepted taxonomic name.

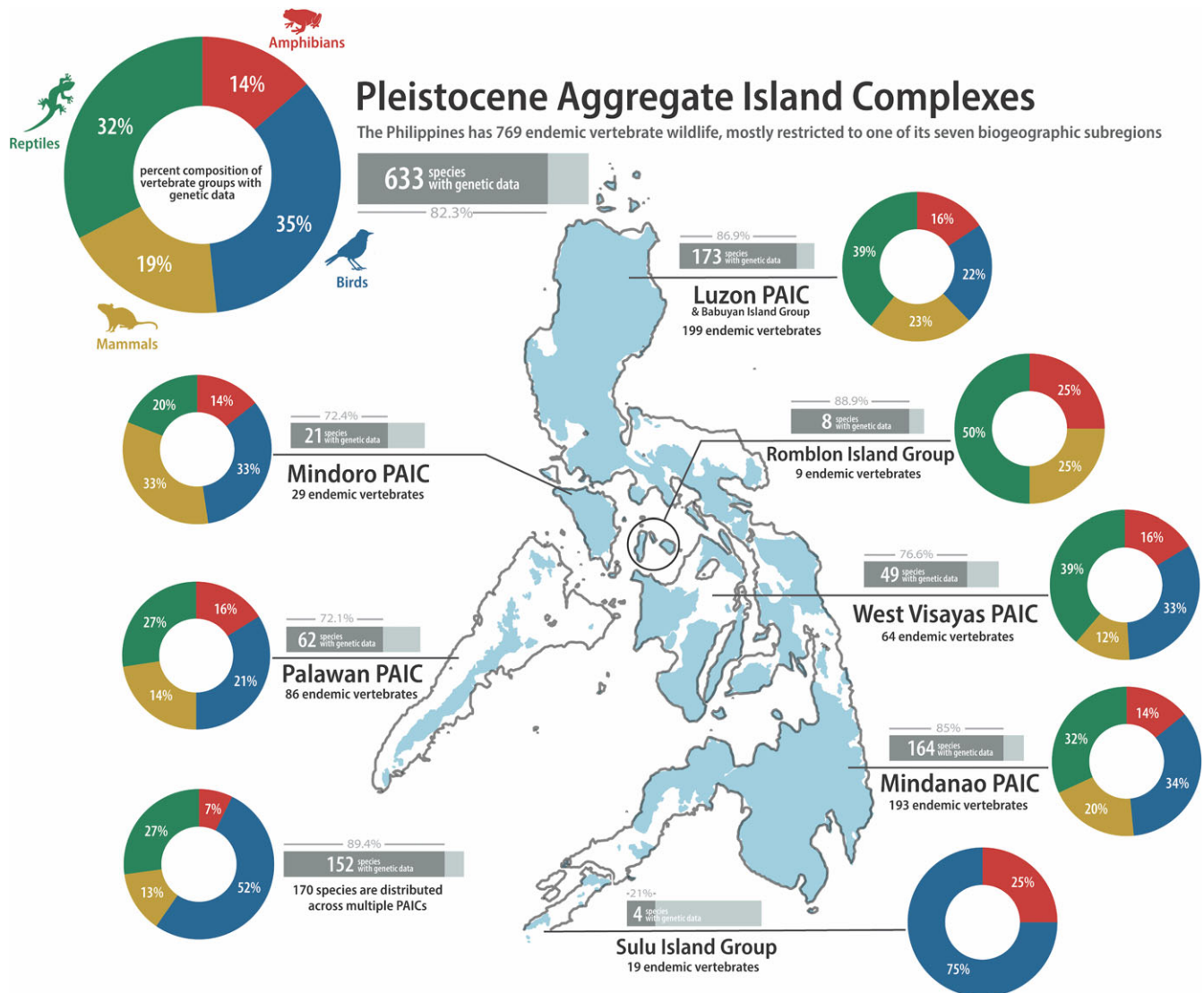


Figure 1. Map of the Philippines with its seven major biogeographic subregions (Pleistocene Aggregate Island Complexes, PAICs), outlined in dark grey. Doughnut charts represent percent composition of species with genetic data per vertebrate group: across the Philippines, for species distributed in multiple PAICs, and within each PAIC. Bars indicate proportion of species with genetic data (dark grey) relative to total species count (entire bar).

All returned nucleotide entries and from Sequence Read Archive (for entries generated from next-generation sequencing or NGS) were manually inspected to ensure they were not associated with sequences from other organisms (e.g., parasites, microbiome). Each species' genetic data for each year, from pre-2000 through 2024, were manually counted by checking each entry's revision history, only considering the year an entry first appeared in GenBank. Note that genetic data was based on unique entry, and multiple genetic data recorded for a species were likely derived from same specimens. This metric should reflect wildlife genetics research activity. Entries from Barcode of Life Data System were not separately searched as they mostly overlap with GenBank data (Šmíd 2022).

Wildlife genetics research

Publicly available, peer-reviewed literature associated with genetic data from GenBank was collated (Table S2). Phylogenetic studies that used genetic data from Philippine specimens but lacked

substantial discussion specific to the Philippines were excluded (e.g. Darst & Cannatella 2004, Winkler et al. 2014). Regional studies or those conducted in Southeast Asia and neighboring Pacific islands involving multiple Philippine specimens, which influenced taxonomic decisions for Philippine species, enhanced understanding of Philippine evolutionary history, or otherwise contextualized Philippines in their discussions were included (e.g. Lim et al. 2014, Heckeberg et al. 2016, Shankar et al. 2021, Blanck et al. 2023). Complementary searches in Web of Science and Google Scholar were conducted to include studies involving non-endemic but native species in the Philippines to supplement data (e.g. Kirchman 2009, Veron et al. 2020, Karin et al. 2024). Although some studies may have been missed, the compiled papers are expected to largely reflect the current state of wildlife genetics research on Philippine vertebrates. Studies were skimmed to identify general research focus, with an emphasis on population-level studies (i.e., genetic samples were from multiple individuals from multiple localities largely representative of species' geographic range) and conservation genetics.

To assess involvement of Filipino scientists in wildlife genetics research, each study was manually reviewed to identify first author's affiliation (Philippine or foreign), proportion of authors affiliated with Philippine institutions, and proportion of Filipino authors (regardless of current affiliation). Filipino authors were identified based on their publicly available information (e.g., raised and educated in the Philippines) or published studies (e.g. previously affiliated with Philippine institutions), an approach made more feasible by the relatively small number of Filipino scientists working in wildlife genetics (see Meneses et al. 2024).

Status and trends in wildlife genetics

A total of 56 928 genetic datasets were initially recovered from GenBank, excluding *Carlito syrichta* due to its extensive entries (400 000+) (Table S1). Genetic data from three studies were also removed because a few species with high entry counts (>1000) skewed temporal trends (Figure S1) and model outputs (Table S3) for taxonomic groups: *Kaloula conjuncta*, *K. kalingensis*, *K. kokacii*, *K. picta*, *K. rigida*, and *K. walteri* (>1000 genetic data for each species; Alexander et al. 2017), *Crocodyrus beata*, *C. grayi*, *C. mindorus*, *C. negrina*, *C. ninoyi*, *C. palawanensis*, and *C. panayensis* (>1000 entries for each species; Giarla & Esselstyn 2015), and *Crocodylus mindorensis* (1797 entries; Tabora et al. 2012). After excluding these sequences, the thinned dataset included 17 399 genetic data from 766 species used for analyses (Table S4), closely reflecting trends over the 1990s–2024 not skewed by outlier data. Despite removing genetic data from a few species, results from the thinned dataset were broadly consistent with the full dataset (Figure S1, Table S3). However, the thinned dataset was used for consistency across all analyses.

The total number and proportional completeness (number of species with genetic data divided by total number of species) of genetic datasets were calculated for each category: taxonomic group, biogeographic subregion (PAICs), threatened status, and geographic range. Vertebrate composition with genetic data was further analyzed by PAIC to gain finer understanding of spatial patterns of genetic availability. For calculating proportional completeness, *C. syrichta*, as well as the recently described *Limnonectes cassiopeia* and *Coura philippinensis* for which available genetic data were not accessed for downstream analyses, were still included. To assess how genetic data varied across categories, each category (taxonomic group, biogeographic subregion, threatened status, and geographic range) was modeled separately using generalized linear model (GLM) with negative binomial error to account for overdispersion, with the total number of genetic data as the response variable and categories as the categorical predictor. For each model, the null deviance (from the intercept-only model) and the residual deviance (from the full model with the predictor variable) were compared using a likelihood ratio test to determine whether the inclusion of the predictor variable improves the model fit over the intercept-only model (i.e., whether the model with multiple-level categories provides a significantly better explanation of the data than the reference level alone). Post-hoc pairwise comparisons, adjusted for multiple comparisons using Tukey's method, were then conducted using the R package *emmeans* (Lenth 2025) to identify which levels within each category were significantly different from each other at $\alpha = 0.05$.

Trends in genetic data accumulation over time were visualized using locally estimated scatterplot smoothing (LOESS) curves with 95% confidence intervals. These analyses were also performed

separately by taxonomic group to assess whether patterns in biogeographic subregion, threat status, and geographic range held across taxa (Figures S2–S4). Mean annual rate of increase (average number of genetic data added per year = sum of annual increases/number of years) and overall rate of increase (proportional growth relative to starting point in the 1990s = final value – initial value/final year – initial year) were calculated for each category. These summary statistics were derived from aggregated trends across all 766 species, which show general trends at the category level while still being based on species-specific data.

Lastly, total number of wildlife genetics publications across vertebrate groups was computed, and trends over time were visualized using LOESS curves with 95% confidence intervals. To visualize temporal trends in research involvement of Filipino researchers, the cumulative number of non-unique authors per publication were plotted over time (i.e., total authorship counts irrespective of individual identity). This metric reflects publication activity and collaborative involvement in wildlife genetics research using Philippine specimens, rather than a direct measure of human resource capacity or unique researcher counts. All analyses and visualizations were performed in R version 4.2.2 (Supplementary Material).

Results

Genetic data on Philippine endemic vertebrates

Six hundred and thirty-three of the 769 Philippine endemic vertebrate species had genetic data (82.3% proportional completeness; Figure 1), although 590 had ≤ 20 GenBank entries. Birds and reptiles, being the most speciose groups, accounted for a significant portion of species with genetic data both country-wide and across most PAICs, except for smaller Romblon Island Group and Sulu Island Group. Despite amphibians having fewer species overall, they had the highest proportional completeness (87%; Figure 2A). In comparison, about 84% of mammals and birds and 78% of reptiles had genetic data.

Of the thinned 17 399 genetic data obtained from 766 species from GenBank, 16 582 were generated by traditional sequencing methods (e.g., Sanger) while only 817 genetic data from 158 species were generated through NGS (~5% of thinned dataset; Table S1). Reptiles had 6250 of these genetic data (mean \pm SD, 23.76 \pm 57.60), birds had 4750 (18.13 \pm 33.28), mammals had 3,939 (27.54 \pm 59.47), and amphibians had 2460 (25.10 \pm 68.55), mirroring species richness among groups. There was insufficient evidence to suggest that taxonomic group predicts the total number of genetic data (LRT $\chi^2 = 7.62$, df = 3, $p = 0.055$; Table 1). Post-hoc tests revealed that no pairwise differences between levels within the taxonomic group were statistically significant (Table 1).

Reptiles saw the highest growth over time in genetic data, although mammals had a faster increase over the 1990s–2024 (Figure 2B). Cumulative increase in genetic data was highest in reptiles (250%), followed by birds (190%), mammals (158%), and amphibians (98.4%). Genetic data for mammals increased almost linearly after 2002 (mean annual rate of increase: 1.06 \pm 10.3), while data for amphibians began to grow around 2010 and continued steadily through 2024 (0.965 \pm 10.6). Birds and reptiles exhibited similar trends, with genetic data on birds showing a sharp rise post-2010 after a steady slow increase in the early 2000s (0.697 \pm 5.71). Reptiles started increasing slowly then steeply increased post-2010, overtaking birds (0.914 \pm 10.4).

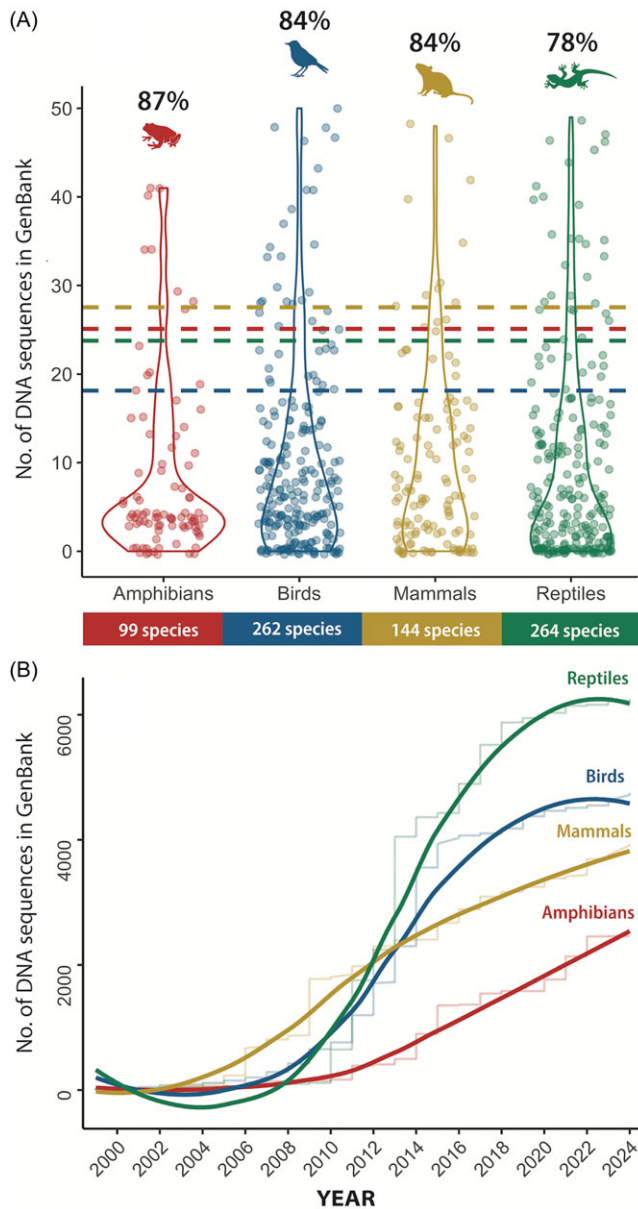


Figure 2. Genetic data for terrestrial vertebrate groups in the Philippines. (A) Violin plots of DNA sequence data from GenBank. Points represent individual species, dashed lines indicate mean for each vertebrate group, bars display total number of endemic species per group, and percentages at the top denote proportional completeness (species with genetic data relative to total species). The y-axis is capped at 50 for better visualization. (B) Cumulative growth of genetic data by vertebrate group. Solid lines show LOESS smoothing with 95% confidence intervals, while transparent lines represent annual cumulative sums.

Biogeographic subregion (PAIC) significantly predicted the total number of genetic data ($LRT \chi^2 = 102.94$, $df = 7$, $p < 0.001$; Table 1). Species distributed across multiple PAICs had significantly more genetic data than species restricted to a single PAIC, a pattern that held true for birds when analyzed by taxonomic group (Figure S2). More broadly, species occurring in larger PAICs generally had higher numbers of genetic data (Table 1; Figure S2). Vertebrates in PAICs with larger land areas harbored more genetic data on average and exhibited higher proportional completeness, likely reflecting higher endemic species richness in these regions (Figure 3A). This trend

complements cumulative increase in genetic data, which was highest in species distributed across multiple PAICs (281%), followed by species endemic to larger PAICs like Luzon (173%) and Mindanao (159%), with species endemic to smaller PAICs showing low overall increase ($<50\%$).

Mean annual rate of increase in genetic data was highest for species distributed across multiple PAICs (1.60 ± 13.9), with a steady rise beginning in 2005 and steeply increasing through 2024 (Figure 3B). Genetic data for species endemic to Mindanao and Luzon PAICs started increasing after 2006, with Mindanao (0.794 ± 7.71) initially leading Luzon (0.840 ± 9.00). However, genetic data for Luzon-PAIC-endemic species saw a sharp increase in early 2010s, surpassing genetic data for Mindanao-PAIC-endemic species. Genetic data for West-Visayas-PAIC-endemic species (0.560 ± 4.75) showed gradual increases from 2010 onward, but this trend has slowed in the last decade. Genetic data for species endemic to Palawan PAIC (0.365 ± 3.42) and Mindoro PAIC (0.320 ± 2.31) exhibited slower, more steady increases in the past decade. Genetic data for species endemic to SIG showed the lowest mean annual increase (0.047 ± 4.75).

Extent of occurrence (EOO) significantly predicted the total amount of genetic data ($LRT \chi^2 = 101.89$, $df = 2$, $p < 0.001$; Table 1). Species with large geographic ranges (larger EOO) had significantly more genetic data than species with smaller ranges, a pattern that remained consistent across taxonomic group (Table 1; Figure S3). Vertebrates with larger geographic ranges accumulated more genetic data on average and exhibited higher proportional completeness (87% vs. $<80\%$ for species with smaller ranges; Figure 3C). These results align with the cumulative increase in genetic data, highest in species with large EOO (570%), followed by medium EOO (89.8%) and small EOO (36.3%). Genetic data for species with large geographic ranges began increasing steadily in 2005 and continued to rise steeply through 2024 (mean annual rate of increase: 1.20 ± 11.4 ; Figure 3D). Genetic data for species with medium (0.485 ± 4.08) and small (0.262 ± 1.78) ranges showed slower increases.

Threatened status was also a significant predictor of the total number of genetic data ($LRT \chi^2 = 74.29$, $df = 2$, $p < 0.001$; Table 1). Threatened species and those species without IUCN threat assessments (including data-deficient species) were predicted to have lower genetic data than non-threatened species (Table 1). Notably, threatened species had more genetic data than unassessed species in birds and mammals; however, the opposite pattern was observed in reptiles and amphibians (Figure S4). Non-threatened species had 90% proportional completeness (vs. $<80\%$ for species with either threatened or no threat status; Figure 3E) and had the highest cumulative increase in genetic data throughout (571%) compared to threatened species (75.9%) or species with no status (48.8%). Genetic data for non-threatened species increased sharply after 2005 and continued to rise through 2024 (mean annual rate of increase: 1.15 ± 10.9), while genetic data for species with threatened status (0.503 ± 4.19) and no status (0.328 ± 4.64) saw slower increases over the 1990s–2024 (Figure 3F).

Wildlife genetics research

A total of 213 published, peer-reviewed wildlife genetics studies from the 1990s to 2024 involving Philippine specimens were collated. These studies included 72 on reptiles, 62 on birds, 54 on mammals, and 25 on amphibians. On average, 2.04 ± 2.16 studies were published annually across all vertebrate groups. Among vertebrate groups, reptiles experienced the fastest growth in

Table 1. Generalized linear models with negative binomial error predicting genetic data as a function of taxonomic group, biogeographic subregions, geographic range, and threatened status. In the pairwise comparisons column, levels within categories that share at least one letter are not significantly different at $\alpha = 0.05$.

Model	Categorical predictors	Estimate \pm SE	Pairwise comparisons
Genetic Data ~ Taxonomic Group	Intercept (Amphibians)*	3.223 \pm 0.1618	a
	Birds	−0.3254 \pm 0.1898	a
	Mammals	0.0929 \pm 0.2100	a
	Reptiles	−0.0548 \pm 0.1895	a
	Intercept (Multiple)*	3.7269 \pm 0.1165	e
Genetic Data ~ Biogeographic Subregions	Luzon*	−0.6430 \pm 0.1590	d
	Mindanao*	−0.6991 \pm 0.1602	cd
	West Visayas*	−1.0485 \pm 0.2239	bcd
	Palawan*	−1.4756 \pm 0.2030	b
	Mindoro*	−1.6094 \pm 0.3098	bc
	Romblon Island Group*	−1.6201 \pm 0.5285	abcd
	Sulu Island Group*	−3.5358 \pm 0.4202	a
	Intercept (Large)*	3.4441 \pm 0.0711	a
	Medium*	−0.9098 \pm 0.1351	b
Genetic Data ~ Geographic Range	Small*	−1.5243 \pm 0.1524	c
	Intercept (No Status)*	2.1429 \pm 0.1311	a
	Non-threatened*	1.2542 \pm 0.1488	b
Genetic Data ~ Threatened Status	Threatened*	0.4289 \pm 0.1840	a

*Significant coefficient at $\alpha = 0.05$.

research output (mean annual rate of increase: 2.77 ± 2.94 ; Figure 4A). While reptile studies had a slow start, they began to increase steeply after 2008, surpassing other taxa. Bird studies followed a similar trend, leading reptiles until 2017, after which their growth slowed down (mean annual increase: 2.42 ± 2.18). Mammal studies increased at a moderate, almost linear pace from 2000 to 2024 (2.00 ± 1.62), while amphibian studies showed a slower, steady increase starting around 2008 (0.96 ± 1.15). A crude assessment of research focus showed that ~90% of papers utilized phylogenetic approaches to answer questions related to systematics, evolutionary history, biogeography, and taxonomy of species, with 597 species (77.6%) having phylogenetic data. Only ~8% of studies included population-level sampling and ~5% addressed conservation genetics.

Filipino authors contributed on average 18% of the total volume of authorship activity ($n=1,100$ non-unique authors) over the 1990s–2024, although some are affiliated with foreign institutions (Figure 4B,C). Among vertebrate groups, bird studies involved the highest percentage of Filipino authors, with 21% affiliated with foreign institutions and 25% if author affiliations were not considered (Figure 4B). Mammals followed (16% and 20%, respectively), while reptiles (13% and 14%) and amphibians (11% and 12%) had lower Filipino involvement. Although the total number of authors contributing to wildlife genetics research using Philippine vertebrate specimens has risen sharply in the last two decades, Filipino involvement in these studies has lagged behind (Figure 4C).

Discussion

Over 80% of the Philippines’ endemic vertebrate species now have some genetic data available – a notable achievement that shows how much the country’s biodiversity science has advanced since the 1990s, when genetic studies on its wildlife first began (Brown et al. 2001, Heaney 2001). This synthesized dataset provides a valuable foundation for identifying species in need of further genetic sampling and exploring how genetic information can be integrated into national conservation planning in line with global biodiversity commitments. However, empirical evaluations of available genetic data and associated publications using Philippine

vertebrate specimens revealed gaps and biases. Although disparities are less obvious across broad vertebrate groups, they become more pronounced when analyzed by threat status, geographic range, and biogeographic subregion. These results reinforce the non-random and uneven distribution of knowledge in wildlife genetics, even within a biodiversity-rich country. Nonetheless, research progress has substantially advanced our understanding of the evolutionary history of this megadiverse, global biodiversity hotspot (Brown et al. 2013, Meneses et al. 2024). Yet, Filipino scientists involvement remains limited, pointing to broader inequities in the field of wildlife genomics (Link & Cadena 2024, Carneiro et al. 2025).

Approximately 17.7% of Philippine endemic vertebrates lack any genetic data, a figure that is lower compared to the global average of 24% (Šmíd 2022). This progress is encouraging, but much of available genetic data is derived from traditional mitochondrial DNA, typically obtained through Sanger sequencing. This method provides information from a limited number of genetic markers and often involves fewer specimens that may not be geographically representative of the species range. Although sufficient for generating phylogenetic information to address Darwinian shortfall (Guedes et al. 2024) and initial applications in conservation genetics (e.g., Essential Biodiversity Variables for genetic composition; Hoban et al. 2022), such data may be inadequate for detailed insights into genomes, species, and populations enabled by fine-scale genomic data produced by NGS (Hohenlohe et al. 2021, Bertola et al. 2024). These high-resolution data are required to answer a broad-range of questions that can offer deeper insights into wildlife populations and their evolutionary potential, critical for developing management strategies that consider genetic information fundamental to species’ persistence.

Among Philippine vertebrates, endemic reptiles have the least complete genetic data, whereas endemic birds and mammals are relatively well-sampled genetically, consistent with global trends (Šmíd 2022). Endemic amphibians, however, show the highest proportional completeness of genetic data, with 87% of species represented compared to the global average of 73.6% (Šmíd 2022). Globally, research attention has long been skewed toward birds and mammals, often due to their public appeal and biological traits

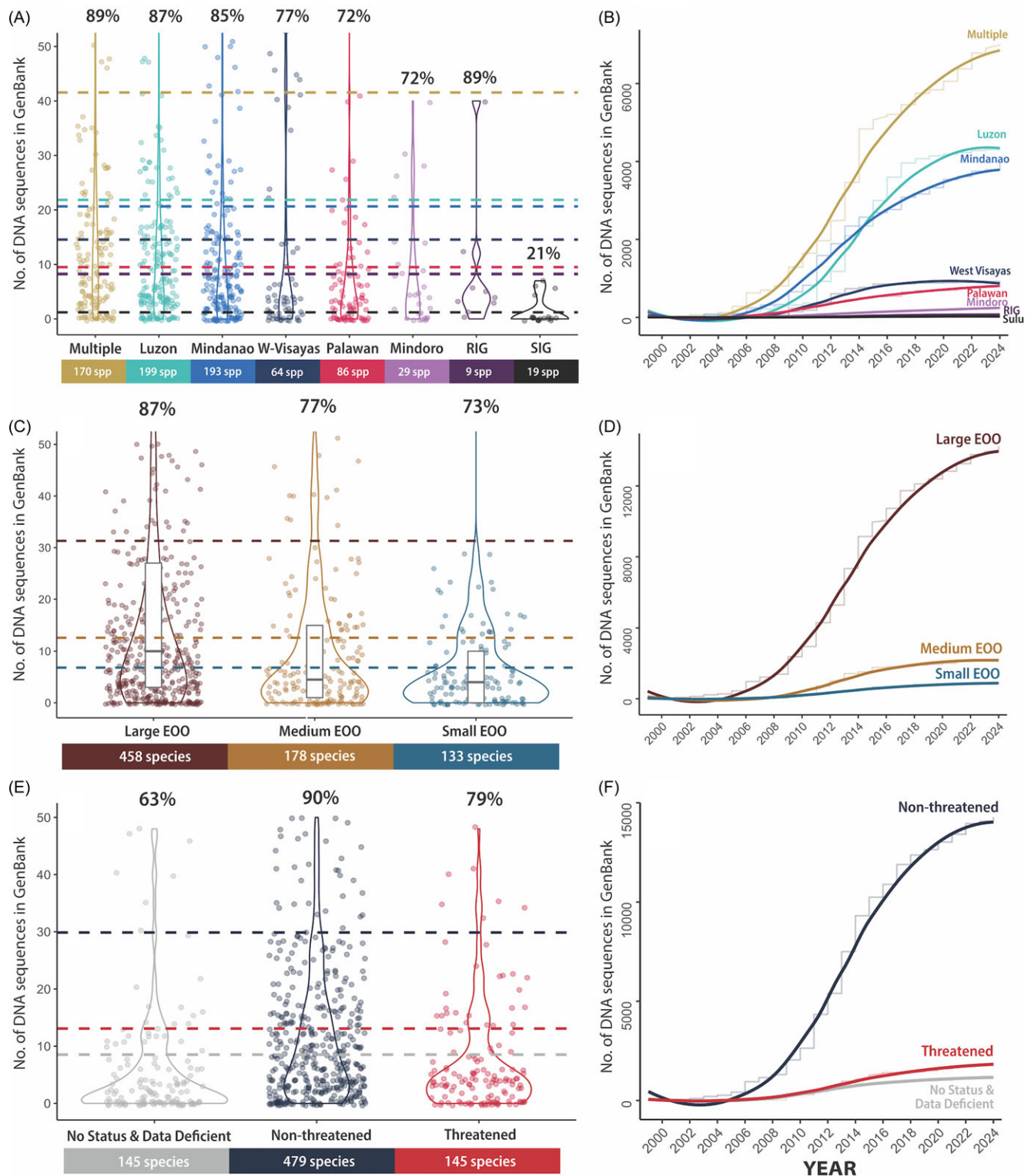


Figure 3. Genetic data for endemic vertebrates in the Philippines, categorized by biogeographic subregions (A & B), geographic range (C & D), and IUCN threatened status (E & F). (A, C & E) Violin plots of DNA sequence data from GenBank. Points represent individual species, dashed lines indicate mean for each category, bars display total number of endemic species per category, and percentages at the top denote proportional completeness (species with genetic data relative to total species). The y-axis is capped at 50 for better visualization. (B, D & F) Cumulative growth of genetic data by category. Solid lines show LOESS smoothing with 95% confidence intervals, and transparent lines represent annual cumulative sums. EOO= Extent of occurrence spp= species, W-Visayas= West Visayas.

that increase their detectability (Bonnet et al. 2002, Thomson & Shafer 2010, Titley et al. 2017, Guénard et al. 2025). This pattern is likely true for the Philippines as well, with recent local genomic

sequencing efforts focused on these vertebrate groups (e.g., Gaite et al. 2022, Bacus et al. 2025, Javier et al. 2025). In contrast, the relatively high genetic coverage of Philippine amphibians may

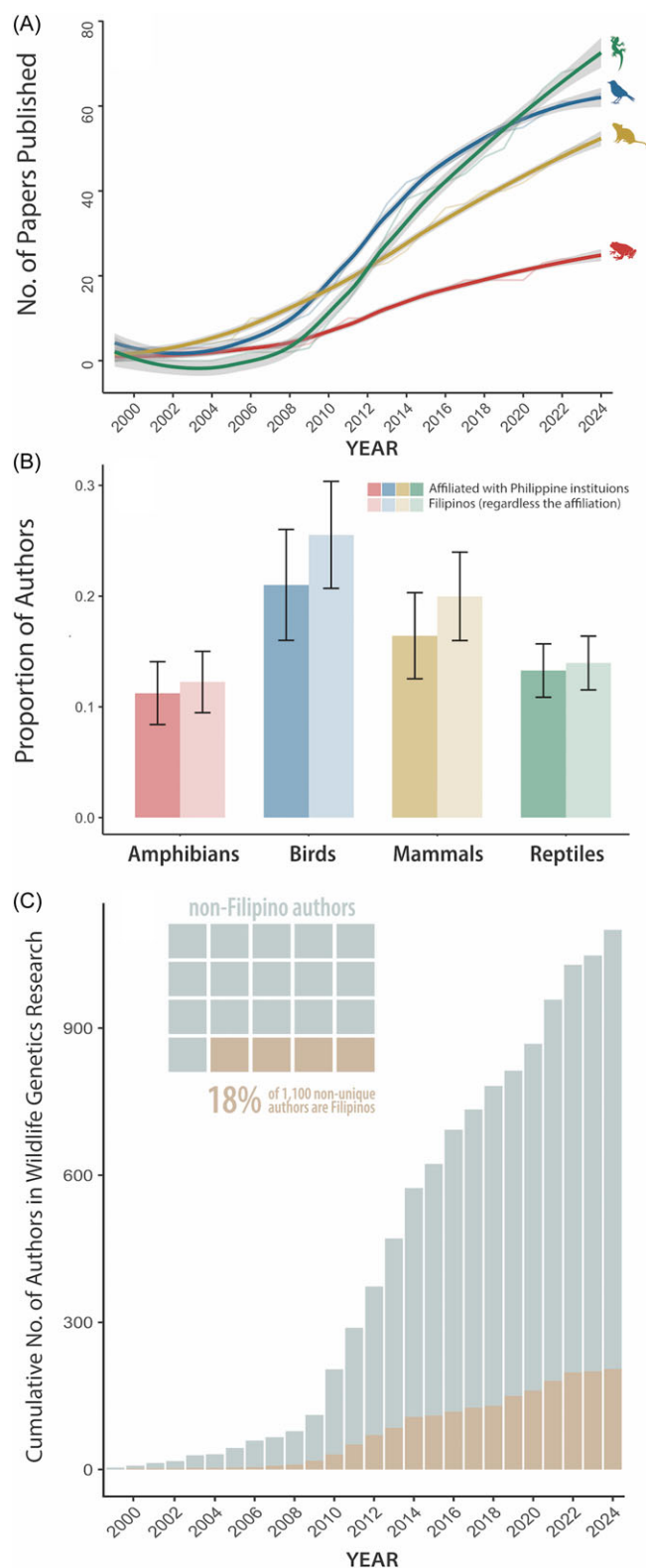


Figure 4. Wildlife genetics research on Philippine endemic vertebrates. (A) Cumulative growth of published peer-reviewed studies per vertebrate group. Solid lines represent LOESS smoothing with 95% confidence intervals, while transparent lines show annual cumulative sums. (B) Mean proportion of Filipino authors involved in these studies, categorized by those affiliated with Philippine institutions and those affiliated with either Philippine or foreign institutions. Bars indicate standard errors. (C) Cumulative number of non-unique authors (total authorship counts irrespective of individual identity) involved in these studies, with proportion of Filipino authors shown per year (pale brown). Inset waffle graph shows overall proportion of Filipino authors in total volume of authorship activity ($n = 1100$).

paradoxically reflect slower taxonomic and systematics progress in the group, with species richness likely underestimated and many cryptic species yet to be recognized or sampled genetically (Moura & Jetz 2021, Meneses et al. 2024). Philippine reptiles have seen a significant increase in new species descriptions over recent decades, but many older species described are from regions that remain challenging to survey, leaving their genetic data largely unavailable (Meneses et al. 2024). Recent advances in museomics demonstrate potential to recover genetic data from historical specimens even with degraded DNA, offering a promising avenue for filling these gaps (Nakahama 2021, Raxworthy & Smith 2021). Nevertheless, the long history of biological collections in the Philippines has provided invaluable materials that made genetic data, and resulting wildlife genetics studies, possible. Such progress underscores continued specimen-based surveys, particularly in historically undersampled regions and for poorly studied species and populations. Ethical and equitable accumulation of preserved specimens can significantly reduce phylogenetic knowledge gaps (Guedes et al. 2024), especially with 22.4% of Philippine endemic vertebrates lacking phylogenetic data.

Genetic data is disproportionately biased towards species with wide geographic ranges as well as non-threatened or with no conservation status, also reflecting global trends (Reddy 2014, Šmíd 2022, Guedes et al. 2024). These species traits often facilitate collection of larger number of specimens, increasing the availability of fresh materials suitable for genetic sampling. Species with broader ranges are more likely to be common in the wild and categorized as non-threatened, a pattern that is perhaps unsurprising given that IUCN Red List assessments explicitly incorporate range size as a key criterion. As such, fewer policy restrictions exist for collecting these species, making them abundant in museum collections and more likely to have genetic data (Berba & Matias 2022). However, many widespread Philippine endemic species may in fact represent species complexes or groups of morphologically similar but genetically distinct, range-restricted lineages that merit independent conservation attention (Sanguila et al. 2011, Brown et al. 2014, Hosner et al. 2018, Chan et al. 2020). Nevertheless, identifying evolutionarily significant units for widespread species facilitates strategies for species persistence amidst changing environments by delineating genetically, ecologically, and demographically distinct populations (Funk et al. 2012). Such information complements existing criteria used for broader area-based conservation measures in the Philippines, which are largely confined to species richness (Pitogo et al. 2024). Continued genetic data collection remains valuable even for genetically well-sampled species, as it tracks temporal genetic change (Shaw et al. 2025) and contributes population-level insights critical for achieving genetic diversity targets (Hoban et al. 2024b,c).

Species occurring across multiple or larger biogeographic subregions in the Philippines, particularly in the Luzon and Mindanao PAICs, are generally well-sampled genetically. In contrast, moderate-sized PAICs such as Mindoro, West Visayas, and Palawan and the small-sized SIG still have less than 80% of their endemic vertebrate species represented by genetic data. This pattern in moderate-sized PAICs is likely not due to inaccessibility, but rather the lack of sustained, collections-based fieldwork in these regions (see Meneses et al. 2024). This limits the availability of fresh tissue samples for sequencing, as reflected by the relatively slower increase of genetic data for vertebrates endemic in these PAICs. Beyond limited collection efforts, many species in these PAICs are neither common nor widespread. Although it may seem

intuitive that species in larger PAICs have broad geographic ranges, many are 'micro-endemic', being restricted for example to single mountain ranges, and require targeted sampling efforts. These species are logistically hard to sample, often lack threat assessments, or are likely to be classified as threatened due to their rarity and restricted distributions (Bland et al. 2015, Kittelberger et al. 2021, Cazalis et al. 2023). This targeted and strategic sampling of micro-endemic species in the Philippines is challenging and demands consistent effort (Řeháková et al. 2015, Supsup et al. 2021, Pitogo & Saavedra 2023), but it is indispensable for reducing genetic data gaps for narrow-range species that are either threatened or data deficient. A similar challenge exists for species inhabiting regions that are difficult to survey due to logistical, administrative, or security constraints, such as SIG and portions of Mindanao Island, which host numerous endemic species (Diesmos et al. 2015, Leviton et al. 2018, van de Ven et al. 2019, Allen 2020, Meneses et al. 2024). Getting genetic data for these species should be prioritized (Berba & Matias 2022), informing appropriate threat levels and corresponding conservation actions (Hohenlohe et al. 2021, Hoban et al. 2022). In cases where specimen collection is limited or prohibited, particularly for threatened species, non-invasive or minimally invasive methods for DNA sampling provide crucial alternatives (Carroll et al. 2018, Schultz et al. 2022).

Research output in wildlife genetics involving Philippine vertebrate specimens closely mirrors publicly available genetic data. Over recent decades, studies on reptiles, birds, and mammals have shown steady growth, while amphibian research has lagged behind. This gap is concerning given that amphibians are the most threatened vertebrates globally (Luedtke et al. 2023). Despite the few genetic studies on Philippine amphibians, recent research has begun to apply next-generation sequencing technologies to this group (e.g., Alexander et al. 2017, Chan et al. 2022, 2025), signaling a promising shift toward more comprehensive genomic investigations. Such studies can provide updates to their taxonomy and distribution, resolve species identities and range boundaries, assess inbreeding depression in isolated populations, and improve understanding of adaptive potential to climate change and habitat loss (IUCN SSC Amphibian Specialist Group 2024). However, while the decreasing costs of sequencing technologies have made broader sampling more accessible in theory, these advances have yet to fully benefit low-income biodiversity hotspots like the Philippines. Resource limitations, as well as infrastructural and technical capacity constraints, remain significant barriers to the generation and use of genetic data in Global South megadiverse countries (Vilaça et al. 2024).

Given these challenges, addressing knowledge gaps and biases in Philippine wildlife genetics will require sustained and inclusive multinational collaboration. However, available data suggest that such collaboration remains limited (see also Fontanilla et al. 2014). For instance, in studies primarily utilizing Philippine specimens, more than half lack Filipino co-authors (118 of 213 studies), highlighting missed opportunities for engagement, capacity building, and knowledge exchange with local scientists. This pattern may partly reflect the museum-based nature of many of these studies, which often rely on specimens collected in the past and now housed in foreign institutions – valuable resources, but settings that can inadvertently limit active involvement of Filipino researchers. Although museum collections offer invaluable potential for biodiversity research, maximizing their use alongside equitable collaboration is essential to avoid perpetuating dynamics often associated with parachute science (Asase et al. 2022, de Vos & Schwartz 2022). Acknowledging this equity gap is important, as its

persistence could undermine trust between local and foreign scientists, exacerbating the gap. Besides, Philippine access-and-benefit sharing policies explicitly require active involvement of Filipino scientists or local institutions throughout the research process. Even for studies that use existing genetic data from GenBank, included broadly as 'digital sequence information', the CBD emphasizes the fair and equitable sharing of non-monetary benefits arising from their use (CBD 2022b). These benefits may include: scientific cooperation in generating, analyzing, and interpreting genetic data; collaborative projects that meaningfully involve local scientists, including authorship opportunities; and broadly communicating research findings with stakeholders to support biodiversity conservation efforts (Asase et al. 2022, Collela et al. 2023, Carneiro et al. 2025).

Closing gaps and addressing biases in wildlife genetics have the potential to profoundly advance biodiversity knowledge (Diniz-Filho et al. 2013, Hortal et al. 2015, Guedes et al. 2024) and its application in conservation policy and practice (Hohenlohe et al. 2021, Hoban et al. 2022, Hoban et al. 2024a,b,c). Biodiversity hotspots like the Philippines stand to benefit immensely from targeted and inclusive collaborative efforts involving transdisciplinary stakeholders. Government agencies, indigenous peoples, and local communities can facilitate access to underexplored regions and streamline sample collection permits. Local and international scientists need to equitably collaborate to generate robust evidence from genetic data, which policymakers and conservation practitioners can integrate into actionable strategies. These inclusive partnerships underpins the enabling environment that is critical for advancing wildlife genetics (Bertola et al. 2024). Although genetic information is gaining traction beyond scientific fields, it remains underutilized in the Philippine biodiversity conservation landscape. However, the country's progress in wildlife genetics presents a timely opportunity to embed genetic considerations into a national conservation framework aligned with global commitments (Hoban et al. 2024c). This approach could seamlessly integrate genetic information with other biodiversity attributes – species and ecosystems – shaping a more holistic and impactful conservation strategy for safeguarding the unique and threatened wildlife of this global biodiversity hotspot.

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