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RESEARCH ARTICLE

Disproportion between the Peruvian Amazonian megadiverse mammalian fauna and the available molecular information

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https://zoobank.org/80DD1B0B-381D-4180-95D2-84FE48EFC64F

ABSTRACT. Peru holds a high mammalian diversity in its Amazonian region, with 326 species. However, our knowledge about the actual diversity is still considered incomplete, and the molecular information for those species in genetic databases is even less comprehensive. To assess the availability of genetic information for Peruvian Amazonian mammals relative to known diversity, we surveyed the Amazonian mammals with at least one molecular marker in the most widely used repositories for nucleotide sequences, GenBank and BOLD Systems. Our survey focused on widely used molecular markers in evolutionary biology—cytochrome b [cyt-b], cytochrome oxidase I [COI], 12S ribosomal RNA [12S], and the mitogenome [mit]—derived from Peruvian Amazon mammals. Additionally, to gain insights into the current mammalian sampling effort in Peruvian Amazonia, we generated a map of unique sampling localities and a heat map, utilizing 41951 records, which identified six major information gaps. This comprehensive analysis found 1597 genetic sequences corresponding to 180 mammalian species (55.2% of Peruvian Amazonian species): COI (38 species), cyt-b (167 species), 12S (56 species), and mitogenome (16 species). Taxonomically, Rodentia (53 species, four markers), Chiroptera (63 species, three markers), and Didelphimorphia (27 species, four markers) represented most molecular data, with a concentration of molecular markers in the orders Chiroptera (703) and Rodentia (499). Geographically, the Loreto department has the largest genetic information (530 records, 99 species). These results confirm a worrying underrepresentation of Peruvian Amazonian diversity in molecular databases. Consequently, we advocate for the use of scientific collections as an alternative source to systematically generate genetic information for the Amazonian mammal diversity in Peru to compensate for the current underrepresentation.

KEY WORDS. Biodiversity, barcoding, bioinformatics, museomics, Neotropics.

INTRODUCTION

The western Amazonian subdivision of the Neotropical lowland rainforests was defined by Wallace (1854) as the region that extends west of the Rio Negro and Rio Madeira. Zoogeographically, it was recognized as a western Amazonian subregion by Voss and Emmons (1996). This subregion is renowned for its status as a biodiversity hotspot, particularly for several faunistic groups (Erwin et al. 2004, Stotz et al. 1996, Young et al. 2004, Ceballos and Ehrlich 2006), and

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it stands out as the most biodiverse Amazonian subregion for mammals (Voss and Emmons 1996, Arévalo-Sandi et al. 2021, Pacheco et al. 2021).

Situated below 1000 m above sea level (m.a.s.l.), western Amazonia has an annual rainfall of more than 2000 mm (FAO 1988, Voss and Emmons 1996, Cavalcante et al. 2020). Notably, unlike other Amazonian subregions, it presents extensive areas of intact tropical humid forest, and it is likely to maintain stable climatic conditions in the face of global warming (Killeen et al. 2007). However, the region faces significant threats from anthropogenic activities, including human population growth, an increase in transportation routes (e.g., the Interoceánica highway), illegal mining, and deforestation. These activities cause pollution, habitat destruction, and biodiversity loss, which threatens the sustainability of resources in the region (Fearnside 1996, 2006, García-Dávila et al. 2014, 2015) and the survival of many indigenous ethnic groups, which have proven to contribute with the conservation of biota (Orta-Martínez and Finer 2010, Fernández-Llamazares et al. 2021, Villén-Pérez et al. 2022).

The Peruvian Amazonia has an area of 661,000 km^2 (Oliveira et al. 2007) and belongs to the Selva baja ecoregion (sensu Brack-Egg 1986). This ecoregion, characterized by a tropical lowland forest ecosystem situated on the eastern flank of the Andes, spans across several departments, including Loreto, Ucayali, Madre de Dios, and portions of the Amazonas, Ayacucho, Cajamarca, Cusco, Huancavelica, Huánuco, Junín, Pasco, San Martín, and Puno (Finer et al. 2008). Also, this ecoregion harbors an impressive diversity of mammals, with 326 species equivalents to 56.50 % of the total Peruvian mammal species (Pacheco et al. 2021, Rengifo et al. 2022). Despite this substantial diversity and the pivotal ecological roles played by mammals in their ecosystems, their current diversity is still underestimated (Pacheco et al. 2021) and their molecular information is even less comprehensive (Noreña et al. 2018). This lack of information is also mirrored at the regional level since the diversity of mammals in only two departments was thoroughly analyzed: the Loreto department with 261 species of mammals (Diaz et al. 2021, Graham-Angeles et al. 2021, Sánchez-Vendizú et al. 2021) and the Ucayali department with 192 species (Quintana et al. 2009); however, the molecular information available for the species of mammals occurring in both departments were not estimated.

Biodiversity assessments and the molecular information on species are critical to prioritizing conservation strategies (Karp et al. 1997, Arif and Khan 2009). In this contribution, we aim to update our knowledge of the diversity of mammals throughout the Peruvian Amazonia by identifying regions with limited or no mammal records, and assessing the quantity of genetic information available for mammalian specimens collected in the Peruvian Amazonian region in the most used public databases, Barcode of Life Data Systems (BOLD) and National Center for Biotechnology Information (NCBI; GenBank).

MATERIAL AND METHODS

Study area

The Peruvian Amazonian region encompasses the territory on the eastern flank of the Andes, below 1000 m.a.s.l., which is equivalent to the “lowland rainforest” (sensu Voss and Emmons 1996). The biogeographic studies have also divided the lowland rainforest into two ecoregions: “selva baja” and “sabana de palmeras” (sensu Brack-Egg 1986) or recently into three: “Bosque Húmedo Amazónico”, “Bosque Muy Húmedo Premontano”, and “Bosque Seco Oriental” (sensu Britto 2017). The Peruvian Amazonia contains several major river basins, such as the Marañón River (1414 km) and the Ucayali River (1771 km), which join to form the Amazonas River with an extension of 713 km in Peruvian territory.

Specimen records

A preliminary mammal species list was built based on Gardner (2007), Pacheco et al. (2009, 2020, 2021), and Patton et al. (2015). The records of these species were then downloaded from the online databases GBIF (https://www.gbif.org) and VERTNET (http://vertnet.org). These include data from the most important worldwide collections, such as the American Museum of Natural History, New York (AMNH); Field Museum of Natural History, Chicago (FMNH); Museum of Vertebrate Zoology, University of California, Berkeley (MVZ); Museum of Natural Science, Louisiana State University, Baton Rouge (LSUMZ); Florida Museum of Natural History, University of Florida, Gainesville (FLMNH); University of Kansas Biodiversity Institute, Kansas (KU); Natural History Museum of Los Angeles County, Los Angeles (LACM); Museum of Comparative Zoology, Cambridge (MCZ); Museum of Southwestern Biology, Albuquerque (MSB); Michigan State University, East Lansing (MSU); Oklahoma Museum of Natural History, Norman (OMNH); Royal Ontario Museum, Toronto (ROM); The Texas A&M Biodiversity Research and Teaching Collections, Texas, formerly the Texas Cooperative Wildlife Collection, College Station (TCWC); Museum of Texas Tech University, Lubbock (TTU); Museum of Zoology, University of Michigan, Ann Arbor (UMMZ); and the National Museum of Natural History, Washington (USNM). A major source of information was the mammalian collection of the Museo de Historia Natural, Universidad Nacional Mayor de San Marcos, Lima (MUSM). The nomenclature was updated based Pacheco et al. (2020, 2021) and recent literature. Geographic coordinates, elevation, and locality data were verified using gazetteers in Gardner et al. (2007), Patton et al. (2015), Diaz et al. (2021), Graham-Angeles et al. (2021), and Sánchez-Vendizú et al. (2021). These data are contained in Supplementary File 1.

To gain a comprehensive understanding of mammal sampling area throughout the Peruvian Amazonia, we compiled a dataset encompassing all available mammalian records in these collections (Supplementary File 1). This dataset was used to prepare two maps. The first map shows a representation of unique localities (each record with different geographic coordinates) over the three ecoregions (sensu Britto 2017): Bosque Húmedo Amazónico (BHA), Bosque Muy Húmedo Pre-Montano (BMHP), and Bosque Seco Oriental (BSO). The second map (heat map), elaborated using the Kernel density method with 3 km cells and a 25 km ratio, shows the areas with the largest concentration of collection records and those with gaps of information (i.e., areas with none or less than 1% of all records). Maps were built with ArcMap v.10.3. In addition, we scaled the availability of records and unique localities per ecoregion, estimating the effort per area (1000 km^2) in each case. Analyses were performed in ArcMap v.10.3.

Molecular data

The search in GenBank was carried out in the Nucleotide database of NCBI (https://www.ncbi.nlm.nih.gov/nuccore) using the advanced mode search tool, with the command (((genus) AND species) AND molecular marker). After entering the command, we carried out a manual search, looking for records from Peru. Because this geographic information is sometimes missing, we checked in the metadata for the catalogue number, the title of the journal article, or any other information that would indicate that the sequence was generated from a specimen collected in Peru. When a catalog number was available, we searched the online database of the corresponding museum; and for journal articles, the accession number of GenBank was searched within the article or the supplementary information if needed. The search in BOLD (http://www.boldsystems.org) was carried out looking for "scientific name" + Peru using the search tool. The molecular markers assessed were cytochrome b (cyt-b), cytochrome oxidase I (COI), 12S ribosomal RNA (12S), and the mitochondrial genome (mit). The search process was done until the end of August 2023. Valid records were interpreted as those with current scientific names, synonyms, and geographic data. Records obtained were sorted in a main database as follows: order>family>genus>species. A list of Amazonian mammalian species with records of nucleotide sequences per department and type of marker is presented in Supplementary File 2, that include recent taxonomic changes (Silva et al. 2022, Cláudio et al. 2023, Sandoval et al. 2024). Moreover, a list of threatened and endemic Peruvian species from Amazonia was built, based on the Servicio Nacional Forestal y de Fauna Silvestre (SERFOR 2018), describing whether or not they have genetic information.

RESULTS

We assembled a comprehensive dataset of 41,951 mammalian records from 1237 unique localities for 326 species from the Peruvian Amazonia (Fig. 1A, Supplementary File 1). Our data showed that the Bosque Húmedo Amazónico (BHA) and the Bosque Muy Húmedo Pre-Montano (BMHP) comprised most mammalian records with 65.7 and 43.2 records per 1000 km^2, respectively (Fig 1A, Table 1), whereas only 8.8 records per 1000 km^2 come from the Bosque Seco Oriental (BSO) (Table 1). However, estimates of the number of unique localities per 1000 km^2 showed that the BSO (the smallest area) has the same number of unique localities sampled per area (1.9) as the BHA (the largest area), whereas the BMHP has only 1.2 unique localities per 1000 km^2 (Table 1).

The heat map showed several areas with none or less than 1% of mammalian records, which are considered major information gaps (Fig. 1B). These critical regions include: 1) Putumayo area; 2) northern Marañón area; 3) Marañón-Ucayali interfluvial area; 4) Yavarí-Ucayali interfluvial area; and 5) Ucayali and Madre de Dios area. The first four critical areas are mostly in the Loreto department, and the Ucayali and Madre de Dios area is in the Ucayali and Madre de Dios departments. All these critical areas are in remote areas relatively far from large cities. For example, area 5 is about 250 km from Puerto Maldonado, and area 1 is about 400 km from Iquitos.

The molecular search in GenBank or BOLD recovered 1597 DNA sequences (genes and mitochondrial genomes), which correspond to 180 of the 326 species of Peruvian Amazonian mammals (55.21%) (Supplementary Files 2–4). The orders Chiroptera (n = 703 sequences) and Rodentia (n = 499) had the largest number of DNA sequences, where-

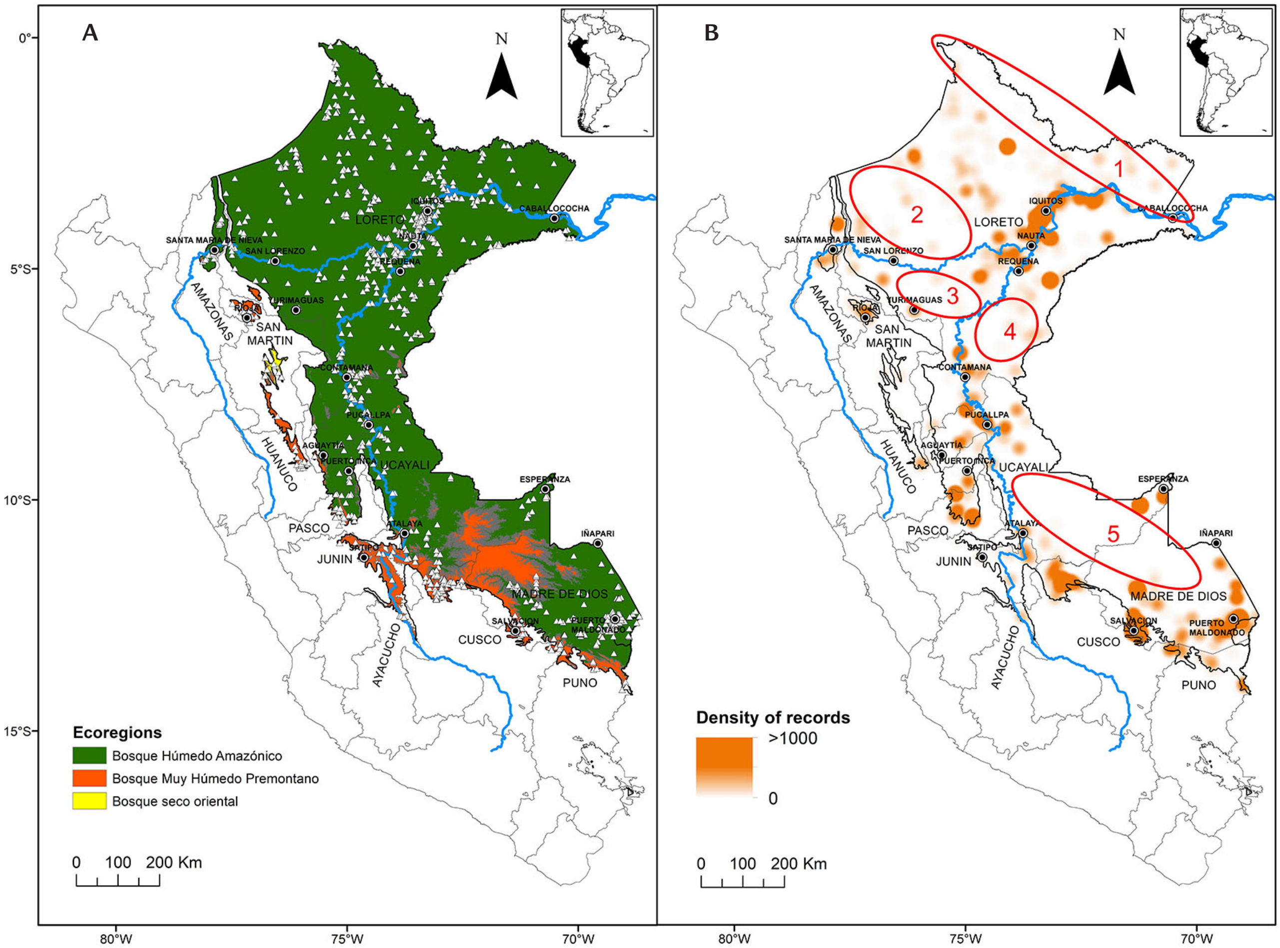

Figure 1. (A) Distribution map of unique localities sampled for mammals over the Peruvian Amazon ecoregions sensu Britto (2017). (B) Heat map of the Peruvian Amazonian region showing record densities of mammals available in collections. The red ellipses highlight major information gaps identified: 1) Putumayo area, 2) northern Marañón area, 3) Marañón-Ucayali interfluvial area, 4) Yavarí-Ucayali interfluvial area, 5) Ucayali and Madre de Dios area.

Table 1. Number of records and unique record localities for mammalian specimens from the Peruvian Amazonia by ecoregions sensu Britto (2017).

Ecoregion	Area (km²)	Number of records	Records / 1000 km²	Number of unique localities	Unique localities / 1000 km²
Bosque húmedo amazónico	540288.1	35490	65.7	1049	1.9
Bosque muy húmedo premontano	148947.8	6428	43.2	181	1.2
Bosque seco oriental	3731.5	33	8.8	7	1.9
Total		41951		1237	

as no genetic data is available for Sirenia and Cingulata (Fig. 2A, Supplementary File 4). The orders Chiroptera and Rodentia had the largest number of species with sequence data (63 and 53 species, respectively), whereas the orders Pilosa (2), Lagomorpha (1), and Perissodactyla (1) showed the lowest number of species with sequence data (Fig. 2A, Supplementary File 4). The orders Artiodactyla, Didelphimorphia, Perissodactyla, Pilosa, and Rodentia have species with nucleotide sequences for all the molecular markers assessed in this study (12S, COI, cyt-b, and mit). The orders Primates and Chiroptera included species with sequences for three molecular markers (12S, COI, and cyt-b), Carnivora

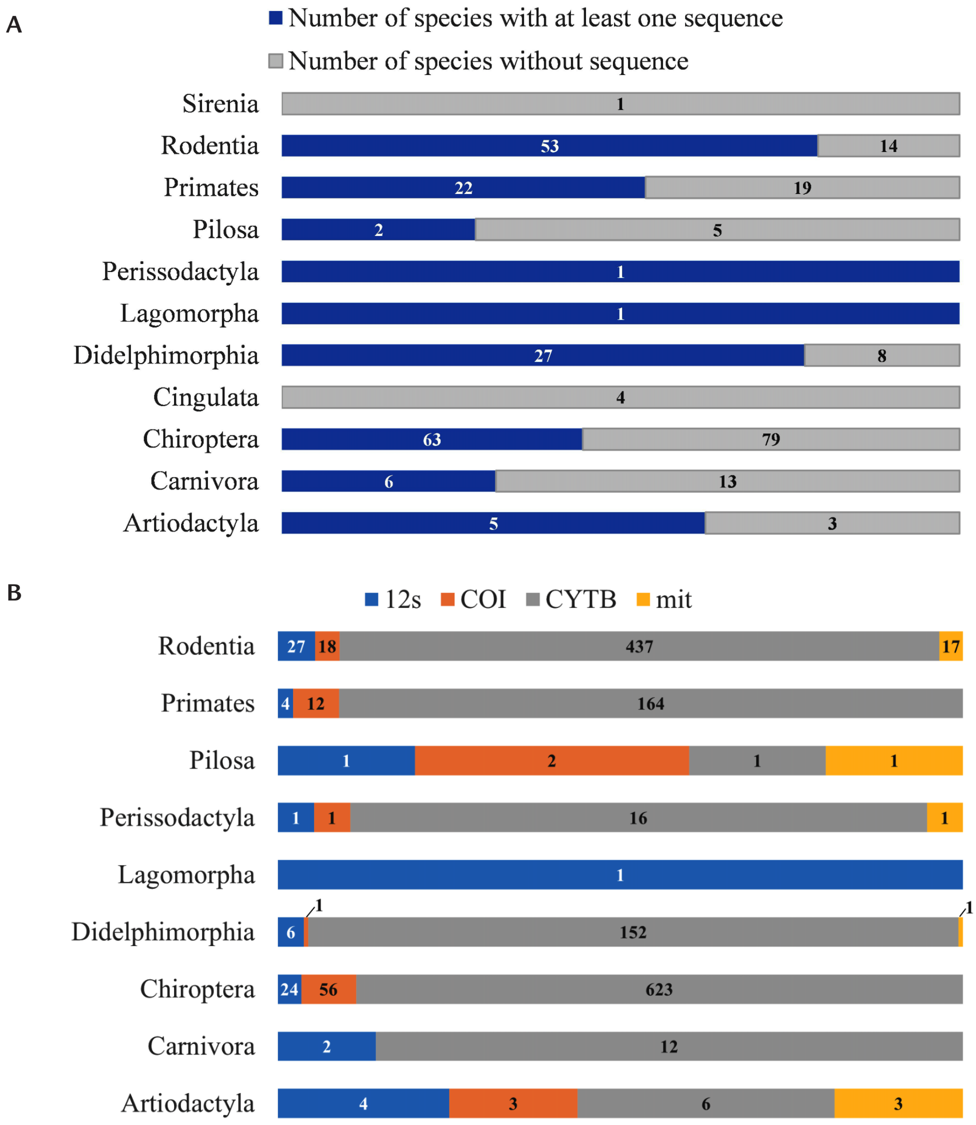

Figure 2. (A) Number of species per order of Peruvian Amazonia mammals and nucleotide sequences availability. (B) Number of nucleotide sequences per molecular marker and taxonomic order.

diversity was represented with two molecular markers (cyt-b and 12S) and Lagomorpha with only one molecular marker (Fig. 2B, Supplementary File 4).

Cytochrome b (cyt-b) was the molecular marker with the highest number of records (1411 records for 167 species), whereas the complete mitochondrial genome was the less frequent (23 for 16 species) (Table 2, Supplementary Files 3, 4). The markers 12S and COI are represented by 70 (56 species) and 93 sequences (38 species), respectively (Table 2, Supplementary Files 3, 4). By order, the cyt-b had the highest frequency in Chiroptera (623 sequences for 54 species) and Rodentia (437 sequences for 52 species), whereas the lowest number of cyt-b sequences was recorded for Artiodactyla (6 sequences for 5 species) (Fig. 2B, Supplementary Files 3, 4).

The COI marker had the highest frequency in Chiroptera (56 sequences for 18 species) and the lowest in Perissodactyla (1) and Didelphimorphia (1). The molecular marker 12S registered the largest number of species in Rodentia (27 sequences for 19 species) and Chiroptera (24 sequences for 21 species), whereas Perissodactyla, Lagomorpha, and Pilosa had only one sequence each. The highest number of mitogenomes were found in Rodentia (17 in 10 species), whereas

Didelphimorphia, Pilosa, and Perissodactyla had only one mitogenome each (Fig. 2B; Supplementary Files 3, 4).

At the family level, Cervidae, Tayassuidae, Didelphidae, Tapiridae, Bradypodidae, Cuniculidae, Echimyidae, and Sciuridae had species with nucleotide sequences for all the molecular markers assessed, whereas Felidae, Procyonidae, Atelidae, Pitheciidae, and Dasyproctidae had sequences only for cyt-b. The family Choloepodidae had sequences only for COI. The families Furipteridae, Leporidae, and Dinomyidae had sequences only for the marker 12S (Supplementary File 3).

Loreto is the department with the largest number of species with at least one molecular marker (99), followed by Cusco (56) and Madre de Dios (52) departments, whereas Ayacucho (3), and Pasco (3) departments have the lowest number of species (Table 3). Loreto is also the department with the highest number of sequences (530), followed by Cusco (141), and Madre de Dios (135), whereas Ayacucho and Pasco departments have the lowest number of sequences (3 and 6, respectively) (Table 2).

According to SERFOR (2018), 22 Peruvian Amazonian species of mammals are considered threatened, and 11 of them are not represented by any molecular data obtained from Peruvian Amazonian specimens. With regard to endemism, 3 of the 5 known endemic species are not represented by any molecular data (Table 4).

Table 2. Number of nucleotide sequences available for mammalian species from Peruvian Amazon listed by molecular marker and department.

Department	12S	COI	cyt-b	mit	Total
Amazonas	11	7	61	5	84
Ayacucho	0	0	3	0	3
Cajamarca	0	0	17	0	17
Cusco	15	7	119	0	141
Huánuco	1	5	60	0	66
Junín	0	0	12	0	12
Loreto	26	45	449	10	530
Madre de Dios	8	10	113	4	135
Pasco	0	0	6	0	6
Puno	1	1	13	1	16
San Martín	0	0	38	0	38
Ucayali	2	4	17	0	23
No locality	6	14	503	3	526
Total	70	93	1411	23	1597

Table 3. Number of mammalian species from the Peruvian Amazonia with nucleotide sequences available, arranged by molecular marker and department.

Department	12S	COI	cyt-b	mit	Sequenced species
Amazonas	10	6	33	4	39
Ayacucho	0	0	3	0	3
Cajamarca	0	0	7	0	7
Cusco	15	5	46	0	56
Huánuco	1	4	22	0	23
Junín	0	0	7	0	7
Loreto	23	17	88	7	99
Madre de Dios	7	7	49	3	52
Pasco	0	0	3	0	3
Puno	1	1	5	1	5
San Martín	0	0	12	0	12
Ucayali	2	4	8	0	12
No information	5	4	18	3	19
Total	64	48	301	18	

DISCUSSION

Peru is renowned for hosting an impressive array of mammalian species (579 species) and is the country with the highest mammalian diversity in western Amazonia (326 species) (Pacheco et al. 2021, Rengifo et al. 2022). However, here we show that significant information gaps persist in at least five under-sampled areas across the Peruvian Amazonia (Fig. 1B). These areas situated at considerable distances from major cities, pose significant challenges to comprehensive sampling due to the extraordinary effort and costs required for access (Mena et al. 2021). Our identified information gaps align with previous analyses conducted for the Loreto and Ucayali departments by Quintana et al. (2009), Diaz et al. (2021), Graham-Angeles et al. (2021), and Sánchez-Vendizú et al. (2021). Among these areas, the Northern Marañón, the Marañón-Ucayali, and the Madre de Dios areas are of the greatest concern because very few or no records document their diversity.

The number of available sequences of Amazonian mammalian species deposited in genetic databases generated from Peruvian specimens (1597 DNA sequences for 180 species) clearly is not representing the hyper diverse status recognized for the Peruvian Amazonia (326 species). This under representation can be attributed to various factors, including the inaccessibility of remote regions for specimen collection, resource limitations in generating genetic data within regional laboratories, scarcity of accessible laboratories, or legal restrictions on genetic data access (Aguilar et al. 2010, Pacheco et al. 2021).

Our data is also consistent with earlier genetic assessments emphasizing the scant representation of Peruvian mammalian species in genetic databases. Rojas et al. (2018) found that for all sequences of vertebrates available for the

Table 4. Threatened species of mammals from the Peruvian Amazonia according to SERFOR (2018), including information on endemism (E) and nucleotide sequences availability in genetic repositories. None = Lack of nucleotide sequences).

Order	Family	Species	Threat category	Endemic	Nucleotide sequences in repositories
Artiodactyla	Cervidae	*Blastocerus dichotomus*	VU		None
Carnivora	Canidae	*Atelocynus microtis*	VU		None
Carnivora	Mustelidae	*Pteronura brasiliensis*	EN		GenBank
Chiroptera	Phyllostomidae	*Vampyressa melissa*	VU		GenBank
Cingulata	Chlamyphoridae	*Priodontes maximus*	VU		None
Didelphimorphia	Didelphidae	*Marmosa andersoni*	EN	E	GenBank
Pilosa	Myrmecophagidae	*Myrmecophaga tridactyla*	VU		None
Primates	Atelidae	*Alouatta seniculus*	VU		GenBank
Primates	Cebidae	*Aotus miconax*	VU	E	None
Primates	Atelidae	*Ateles belzebuth*	EN		GenBank
Primates	Atelidae	*Ateles chamek*	EN		GenBank
Primates	Pitheciidae	*Cacajao calvus*	VU		GenBank
Primates	Pitheciidae	*Callicebus lucifer*	VU		GenBank
Primates	Pitheciidae	*Callicebus oenanthe*	CR	E	None
Primates	Cebidae	*Callimico goeldii*	VU		None
Primates	Atelidae	*Lagothrix lagothricha*	EN		None
Primates	Cebidae	*Saguinus labiatus*	EN		None
Primates	Cebidae	*Saguinus tripartitus*	VU		GenBank
Rodentia	Dinomyidae	*Dinomys branickii*	VU		GenBank
Rodentia	Cricetidae	*Neusticomys peruviensis*	VU	E	GenBank
Rodentia	Cricetidae	*Rhipidomys modicus*	VU	E	None
Sirenia	Trichechidae	*Trichechus inunguis*	VU		None

Loreto department, only 8.92% corresponded to mammals. On a different scale, Noreña et al. (2018) estimated that only 1.13 % of the Peruvian mammals are represented with genetic sequences in GenBank and only 13 records in BOLD System. We then posit that the low representation of Peruvian biodiversity in genetic databases is of great concern. This becomes even more critical when considering nuclear data, which are generated in lower proportion than mitochondrial data. For example, only six new species of sigmodontine rodents described in the last decade have included nuclear data (Dalapicolla and Percequillo 2020).

The genetic marker most frequently employed for Amazonian mammals varied by taxonomic group. For example, cyt-b was largely the most frequent molecular marker for rodents and marsupials, likely due to the marker reliability in phylogenetic reconstructions and molecular identification at the species level (Graybeal 1993, Bradley and Baker 2001, Tobe et al. 2010). Whereas the marker COI was preferred for genetic identification of bats (Clare et al. 2011) due to the development of the Barcoding project and the BOLD system platform (Hebert et al. 2013). On the other hand, the low representation of mitogenomic sequences is likely a methodological constraint. Mitogenomes for mammals are on average ~18 to 20kb in size (Rand 1993) and are generally assembled either by whole genome sequencing (WGS) with genome skimming (Trevisan et al. 2019, Janiak et al. 2022), or by tiling PCRs where genomes are assembled in many pieces (Schenk et al. 2017, Totawa et al. 2020). WGS methods require high quality samples with unfragmented DNA, which are not easily available, and both methods require access to high throughput sequencing (HTS) capabilities. Although HTS has resulted in ways to generate full mitogenomes at low cost by multiplexing, the technology itself is not widely distributed globally (Watsa et al. 2020a, Urban et al. 2023), and difficult to access within Peru (Carrillo-Larco et al. 2022). Fortunately, the 17 mitogenomes generated for rodents show the transition to the Genomic era in rodent systematic as pointed out by Lessa et al. (2014) and D'Elía et al. (2019).

Regarding taxonomic level, our data showed the disproportion of genetic data available among taxonomic orders. The orders Chiroptera and Rodentia comprised the largest amount of genetic data (1202 sequences). Although these are the two most diverse orders in Peru (Pacheco et al. 2021), the genetic data represented only the 44.4% and 79.1% of their species present in Peruvian Amazonia, respectively. On the other hand, medium-size or large charismatic species such as primates and carnivores had comparatively little genetic data (only 235 sequences for only 64 species).

Apparently, there is still the perception that medium-size or large mammals lack taxonomic problems; therefore, studies of genetic structure and genetic variability have not been developed with similar intensity as in small rodents, bats, or marsupials. Recent publications on the felid genus *Leopardus* (Nascimento et al. 2021) and the howler monkeys of the genus *Alouatta* (Ruiz-García et al. 2017) that have analyzed the phylogeographic structure of these taxa have resulted in taxonomic changes. Also, the difficulty in obtaining collecting permits for large species is a deterrent for scientific research (Gannon et al. 2007). Fortunately, non-invasive methods are now available to obtain genetic material, such as from hair, saliva, blood (Waits and Petkau 2005, Henry et al. 2011, Flagstad et al. 2012, Ferreira et al. 2018, Aylward et al. 2022), which help to partially overcome the need of collecting medium size or large mammals. However, vouchers and associated information are desirable by museum collections, when possible, to carry on research that could be impossible or difficult without whole-organism specimen such as the discovery and description of new species, the origins and spread of infectious diseases among other topics (Bakker et al. 2020, Thompson et al. 2021, Johnson et al. 2023, Nachman et al. 2023).

From the conservation point of view, it is of great concern the lack of genetic information in three Amazonian endemic species and 11 threatened species according to SERFOR (Table 4). We raise awareness of these concerns and call for an urgent program to study these important species. Several of these endemic and threatened species are difficult to find or collect because rareness, secretive habits or restricted by the Peruvian legislation, obtaining tissue samples from museum specimens is an alternative, since scientific collections are currently recognized as an important museomic resource (Gauthier et al. 2020, Jin et al. 2020, Castañeda-Rico et al. 2022, Fong et al. 2023). For example, several genes and mitogenomes have been obtained from Amazonian species from Peruvian scientific collections (e.g., Abreu-Jr et al. 2020, Ruelas and Pacheco 2022, Pacheco and Ruelas 2023). Museum collections have become an important and diverse genetic resource that can help fill the genetic information gaps of species for conservation, systematic, or economic purposes (Watsa et al. 2020b, Mulcahy et al. 2022).

We also found that our results for the Loreto department (99 species with 530 sequences) are higher than the 34 species and 175 sequences reported by Rojas et al. (2018), although this difference could be due to the search tool employed. Rojas et al. (2018) used a data mining algorithm implemented in the Rentrez package for R (Winter 2017), whereas our data was constructed using an exhaustive approach, analyzing species by species in the molecular repositories. Our data showed that the Rentrez algorithm in Rojas et al. (2018) recovered only 34.34 % of the genetic sequences available, mainly because some sequences on repositories have incomplete data. For example, if a sequence missed the word "Peru" it will never be recovered by informatic methods. Exhaustive search, species by species, although laborious, recovered 65.66 % more information than the Rentrez package. Therefore, we strongly suggest the researchers include complete geographic data of localities in GenBank and linked to the complete information of the museum or collection where the record was taken, as is currently done in BOLD System. The BOLD is a platform specifically built to work with biodiversity data (Hebert et al. 2013) and let to make updates since taxonomic changes could happens in the light of more genetic, morphological, or ecological information.

Our findings underscore a significant gap in the representation of genetic information for the Peruvian Amazonia, indicating a lag behind contemporary research standards. The inclusion of molecular data from Peruvian Amazonia, in an integral approach with non-molecular data, could help to resolve the systematic status of several species complex (Sanchez-Vendizú et al. 2018, Velazco and Patterson 2019, Ruelas and Pacheco 2022). Moreover, what we know of the diversity of mammals in the Peruvian Amazonia remains notably incomplete. With only a fraction of the Peruvian Amazonian species documented in genetic databases, it is imperative to undertake swift and comprehensive measures. Urgent initiatives, expanded inventories, enhanced scientific collections and laboratories, and collaboration with government entities are essential to safeguard these species from extinction.

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Competing Interests

The authors have declared that no competing interests exist.

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Supplementary Material 1

Supplementary File 1. List of mammalian records of the Peruvian Amazonia employed for preparing maps in Fig. 1. Geographic coordinates, elevation, and locality data were verified using gazetteers (see Material and Methods), but most specific names remain as have appeared in the original database.

Authors: V Pacheco, J Martínez-Altamirano, JL Mena, et al.

Data type: Gazetter data.

Link: https://doi.org/10.3897/zoologia.41.e23110

Supplementary Material 2

Supplementary File 2. Updated list of mammalian species from Peruvian Amazonia and nucleotide sequence availability per department and type of marker. (Am) Amazonas, (Cu) Cusco, (Hu) Huánuco, (Lo) Loreto, (Ma) Madre de Dios, (Pu) Puno, (Uc) Ucayali, (N) no nucleotide sequence. The column labeled "n.l." designates records lacking specific locality information, except for their presence in Peru.

Authors: V Pacheco, J Martínez-Altamirano, JL Mena, et al.

Data type: Species list.

Link: https://doi.org/10.3897/zoologia.41.e23110

Supplementary Material 3

Supplementary File 3. Nucleotide sequence account per molecular marker available for Peruvian Amazonian mammal grouped by the taxonomic categories of order and family.

Authors: V Pacheco, J Martínez-Altamirano, JL Mena, et al.

Data type: Sequence account.

Link: https://doi.org/10.3897/zoologia.41.e23110

Supplementary Material 4

Supplementary File 4. Number of mammalian species from the Peruvian Amazonia with molecular information arranged by molecular marker and taxonomic order.

Authors: V Pacheco, J Martínez-Altamirano, JL Mena, et al.

Data type: Species account.

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