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Genomic approximations for the study and conservation of mammals

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Genomics is the study of the genome's structure, function, evolution and mapping, including gene interactions with each other and with the environment. Genomics is a tool that allows studying fine evolutionary processes in non-model mammals. These approximations provide valuable information regarding levels and distribution patterns of neutral and adaptive genetic variation. Additionally, genomics allows studying organisms responses to environmental changes and anthropogenic activities. This information has high potential applications in the development of management and conservation plans for threatened mammalian populations and species. The present work provides information so that the reader can understand and outline a mammal conservation genomics project. This is an introductory guide for the use of genomics in the study of mammals, with emphasis in the link between genomics and conservation biology. This guide explains some general aspects of the genomics approximation that allow studying mammals such as sequencing methodologies, reduced representation sequencing, mitogenomes, whole genome sequencing, low coverage whole genome sequencing, metagenomics and transcriptomics; including some examples of their applications in conservation. We conclude this document with some challenges and perspectives for the application of mammal conservation genomics.

Keywords: Conservation genomics, mammals, mitogenomes, next generation sequencing, pangenome, reduced representation sequencing, transcriptomics, whole genome sequencing.

La genómica es el estudio de la estructura, función, evolución y mapeo de genomas, incluyendo la interacción de los genes entre sí y con el ambiente. La genómica es una herramienta que permite el estudio de procesos evolutivos finos en mamíferos no-modelo, aportando información muy valiosa respecto a niveles y patrones de distribución de la variabilidad genética neutral y adaptativa, así como sobre la respuesta de los organismos a los cambios ambientales y a las presiones antropogénicas. Por lo anterior, esta información tiene alto potencial para el desarrollo de planes de manejo y conservación de especies y poblaciones de mamíferos en riesgo. El presente trabajo provee la información necesaria para comprender y delimitar un proyecto de genómica para la conservación. Presentamos una guía introductoria a la genómica aplicada en el estudio de mamíferos con énfasis en la conexión de la genómica con la conservación. La guía aborda distintas aproximaciones genómicas que permiten el estudio de mamíferos, como las plataformas de secuenciación, representación reducida de genomas, mitogenomas, secuenciación de genomas completos, secuenciación de genomas completos a baja resolución, metagenómica y transcriptómica; incluyendo algunos ejemplos de su aplicación en la conservación. Concluimos con algunos retos y perspectivas respecto a la aplicación de la genómica para la conservación de mamíferos.

Palabras clave: Genómica de la conservación, mamíferos, mitogenomas, secuenciación de nueva generación, pangeno, secuenciación de representación reducida, transcriptómica, secuenciación del genoma completo.

Conservation genetics and genomics

Conservation genetics refers to the application of population genetics, evolutionary theory and molecular tools in combination with ecological data for the conservation of wildlife (Frankham 2003; Allendorf *et al.* 2010; Ouborg *et al.* 2010). Traditional conservation genetics approaches have been useful to solve phylogenetic uncertainty, to understand the levels and distribution of genetic diversity, and its correlation to extinction risk.

Conservation genetics aims at better understanding the extent of the impact of human activities, such as habitat fragmentation and habitat loss, on the loss of genetic diversity and the disruption of population structure. Also, conservation genetics has been applied to infer biological aspects of inconspicuous or understudied species, to assess the levels of inbreeding and the risk of inbreeding depression to propose genetic rescue, and in wildlife forensics (Frankham 2003; 2005; 2010; Allendorf *et al.* 2010; Ouborg *et al.* 2010; Shafer *et al.* 2015; Whiteley *et al.* 2015; Hedrick and Garcia-Dorado 2016).

Initially, conservation genetics relied on data obtained from isozymes. Then, with the technical advances of molecular biology and Sanger Sequencing, studies focused more on mitochondrial DNA (mtDNA; see Supplementary Materials S1 for a list of abbreviations), which is maternally inherited and provides a window into evolutionary processes that occur over geological time, such as lineage divergence, speciation, adaptive radiations, and extinctions. The design of species-specific nuclear microsatellite loci allowed the analysis of biparentally inherited loci, which provides information about historical processes on an ecological scale such as connectivity between populations or gene flow, inbreeding and kinship, genetic drift, effective population size and human-mediated bottlenecks, and natural selection (Sunnucks 2000; Schlötterer 2004; Selkoe and Tonnen 2006; Allendorf *et al.* 2010).

The combined use of mtDNA and nuclear microsatellite loci allowed making inferences regarding breeding strategies, sex proportions, and evolutionary vs. historical processes. Today, with the advent of next-generation sequencing and the genomic era, we have the potential to unlock the information contained in whole genomes from non-model species, mitogenomes, reduced representation of genomes, metagenomics, transcriptomics, and other omics approaches (Schlötterer 2004; Allendorf *et al.* 2010; Ouborg *et al.* 2010; Shafer *et al.* 2015; Allendorf 2017).

This review will provide a concise guide for applying genomics and transcriptomics in the conservation of mammals. We expect that this information is useful to uncover the potential of genomic tools for the study and conservation of mammals, and we will provide basic information and concepts (Supplementary Materials S2) for mammalogists who are getting started in the field of conservation genomics.

Next- Generation Sequencing platforms

The introduction of Next Generation Sequencing (NGS) made it possible to obtain the genetic information of a species in a relatively short time. Initially, this approach was very expensive, but with technologic advancement and increases in the demand for this methodology, sequencing costs have gradually decreased, making it accessible to laboratories with modest budgets. NGS conforms to a group of advanced sequencing technologies that allow for the rapid sequencing of DNA and RNA. The advantages of NGS lie in technological advancements, speed, cost-effectiveness, and data output capabilities (Goodwin *et al.* 2016). Moreover, NGS allows incrementing the quantity of loci from few loci to thousands of loci, thus providing higher statistical power to analyses; also, it allows sequencing multiple fragments simultaneously. NGS data can be used in adaptive genomics, to study loci involved in adaptation to environmental changes, to assess levels of neutral and genetic variation and to understand resilience to climate change and habitat fragmentation (Li *et al.* 2020).

NGS uses massively parallel sequencing where millions of DNA fragments are sequenced simultaneously. NGS varied platforms use different technologies, such as sequencing by synthesis (Illumina), nanopore sequencing (Oxford Nanopore), or real-time sequencing (PacBio), allowing to obtain millions of sequences in a short time (Hu *et al.* 2021). The Illumina platform (i.e. HiSeq, NovaSeq; www.illumina.com) produces short reads that are typically 50-300 bp long, offer high accuracy, low cost per base, and high throughput. Short-reads are suitable for applications, such as re-sequencing, population genomics, and metagenomics (Simon *et al.* 2009). In particular, for monitoring genetic diversity, detecting inbreeding in populations, identifying candidate loci under selection and determining population connectivity. It is also useful in resolving phylogenomic relationships among populations and species, especially with conservation concerns. Lastly, it can be used to detect the presence of species in environmental samples, which helps monitor elusive or endangered species (Fuentes-Pardo and Ruzzante 2017). However, short-reads often struggle to resolve repetitive regions, structural variants, and complex genomes due to their limited length.

On the other hand, technologies like PacBio (www.pacb.com) and Oxford Nanopore (nanoporetech.com/es) produce long-reads that are several kilobases long (thousands of bases long). Long reads allow sequencing and assembling the repetitive regions in the genome, thus producing highly contiguous genomes. Long-read technologies have the caveat of higher error rates than short-read sequencing (but this has been improving in recent years) and are generally more expensive compared to short-read technologies (Cuber *et al.* 2023). Using long-reads for *de novo* genomic assemblies produces high-quality reference genomes for species without existing data, that are assembled to the chromosome level. Thanks to long reads spanning large regions of the genome, it is possible to identify structural variants in the genome, such as large insertions, deletions, or rearrangements that might be linked to adaptation or disease susceptibility (Lu *et al.* 2016).

Each sequencing approach offers unique strengths: short-reads provide high accuracy and depth, while long-reads offer extended sequencing that can span complex genomic regions. Both types can be integrated and offer the possibility of hybrid sequencing approaches that can achieve superior genome assemblies and variant detection (Whibley *et al.* 2021). In conjunction, this hybrid approach allows for an understanding of the genetic makeup of endangered species. Current technologies, such as high-throughput chromosome conformation capture (Hi-C) and PacBio high fidelity (HiFi), produce highly accurate long reads, provide uniform coverage and allow us to assemble genomes to the chromosome level (www.pacb.com).

NGS technologies have revolutionized conservation genomics by enabling the collection of detailed genetic data, previously limited by traditional sequencing. This information can be used to understand the biological and

ecological factors that affect species' survival, adaptation, and resilience, informing more effective conservation strategies. NGS allows for the comprehensive assessment of genetic diversity at the whole-genome level. This allows detecting single nucleotide polymorphisms (SNPs), microsatellites, and other types of genetic variation such as transposable elements and structural variants across entire populations, offering a detailed picture of genetic variability to identify adaptive traits, make informed management strategies, detect hybridization and monitor genetic health (Supple and Shapiro 2018).

For example, in the Mountain Gorillas (*Gorilla beringei beringei*), a species critically endangered due to habitat loss, poaching, and disease, a high-quality reference genome was obtained through the combination of short-reads (Illumina) and long-reads (PacBio), overcoming the challenges posed by its complex repetitive genome structure. This high-quality genome assembly revealed regions of the genome susceptible to inbreeding depression and identified genetic variants linked to immune function, helping inform breeding programs to maintain the genetic diversity of the Mountain Gorilla (Xue *et al.* 2015).

Massive parallel sequencing offers a wide range of possibilities for the study of wildlife which are detailed in the following sections and compared in Table 1.

Reduced Representation Sequencing (RRS)

There are several genotyping-by-sequencing (GBS) methodologies to obtain SNPs based on Reduced Representation Sequencing (RRS). These methods are based on the use of restriction enzymes for library preparation, followed by fragment size selection, adaptor ligation, PCR amplification and multiplexing (see review in Andrews *et al.* 2016). Sequencing is performed with a short-read platform. The most used methods for the study of mammals are restriction site-associated DNA sequencing (RADseq) and double digest restriction site-associated DNA sequencing (ddRADseq), which use one or two restriction enzymes, respectively, to cut DNA (Miller *et al.* 2007; Baird *et al.* 2008; Peterson *et al.* 2012).

RRS refers to sequencing a small fraction of the genome to obtain SNPs; typically, between 1 and 10 % of the genome is covered (Peterson *et al.* 2012; Andrews *et al.* 2016, Figure 1). This approach allows obtaining genomic data from hundreds of individuals, and it is usual to obtain thousands to tens of thousands of SNPs (Davey *et al.* 2011; 2013; Andrews *et al.* 2016). The number of SNPs or coverage required will depend on the study's objective, for example, higher coverage will be needed if we want to search for signals of selection (Andrews *et al.* 2016; Ahrens *et al.* 2018).

To implement this type of study, several aspects should be considered, such as the restriction enzymes to be used to digest the DNA, as the type and number of enzymes will have an impact on the number of SNPs obtained depending on the genome size of the studied species, and the number of SNPs required (Davey *et al.* 2011; 2013; Peterson *et al.* 2012; Andrews *et al.* 2016; Fu *et al.* 2016).

Other methodological aspects to consider are biases and errors that could be introduced during library preparation (Mastretta-Yanes *et al.* 2014; O'Leary *et al.* 2018). The number of reads per sample (coverage and depth of coverage) will also impact the number of SNPs discovered; this will depend on the objective of the study, the number of SNPs to uncover, and the genome size of the species (O'Leary *et al.* 2018). As previously mentioned, to discover candidate loci under selection, a higher number of SNPs is required. Previous studies conducted on the same or on closely related species may serve as a guide; also, if this information is not available for our study species, we could conduct pilot studies to test different enzyme combinations and different sequencing depths (Davey *et al.* 2013; O'Leary *et al.* 2018).

SNPs discovery based on RRS can be performed with and without a reference genome (see O'Leary *et al.* 2018;

Table 1. Comparison of Whole Genome Sequencing (WGS), Low-coverage WGS (lcWGS), and Reduced Representation Sequencing (RRS) in evolutionary and conservation studies.

Feature / Application	WGS	lcWGS	RRS
Genome coverage	High (>20× recommended for SMC). Complete breadth.	Low (<5× typical). Random but complete breadth.	Very low (<10% of genome). Sparse/ fragmented breadth.
Primary variant type	SNPs, Indels, and Structural Variants (SVs).	Primarily SNPs via genotype likelihoods.	Primarily SNPs at targeted restriction sites.
Genetic load & inbreeding	Excellent; gold standard for Runs of Homozygosity (ROH)	Reliable for population-level inbreeding coefficients.	Limited; misses rare variants and many ROH due to data gaps.
Selection (adaptation)	High; identifies narrow genomic islands of divergence	High; enables genome-wide selection scans and genotype-environment association.	Lower; likely to miss localized adaptive signals.
Demographic Inference	High resolution for deep and recent history (MSMC/PSMC).	Robust for recent history; accurate Site Frequency Spectrum models.	Reliable for broad signals, but may miss specific parameters
Reference requirement	Essential; requires high-quality assembly.	High; requires a species-specific or related reference	Low; can be used *de novo* without a reference genome.
Main advantage	Capture of all variation types, including complex SVs.	Cost-effective population screening while retaining individual info.	Low cost; high individual sample sizes possible.
Main limitation	High sequencing and computational costs.	Requires specialized probabilistic tools (e.g., ANGSD).	Biased by "null alleles" and lack of functional genome context.

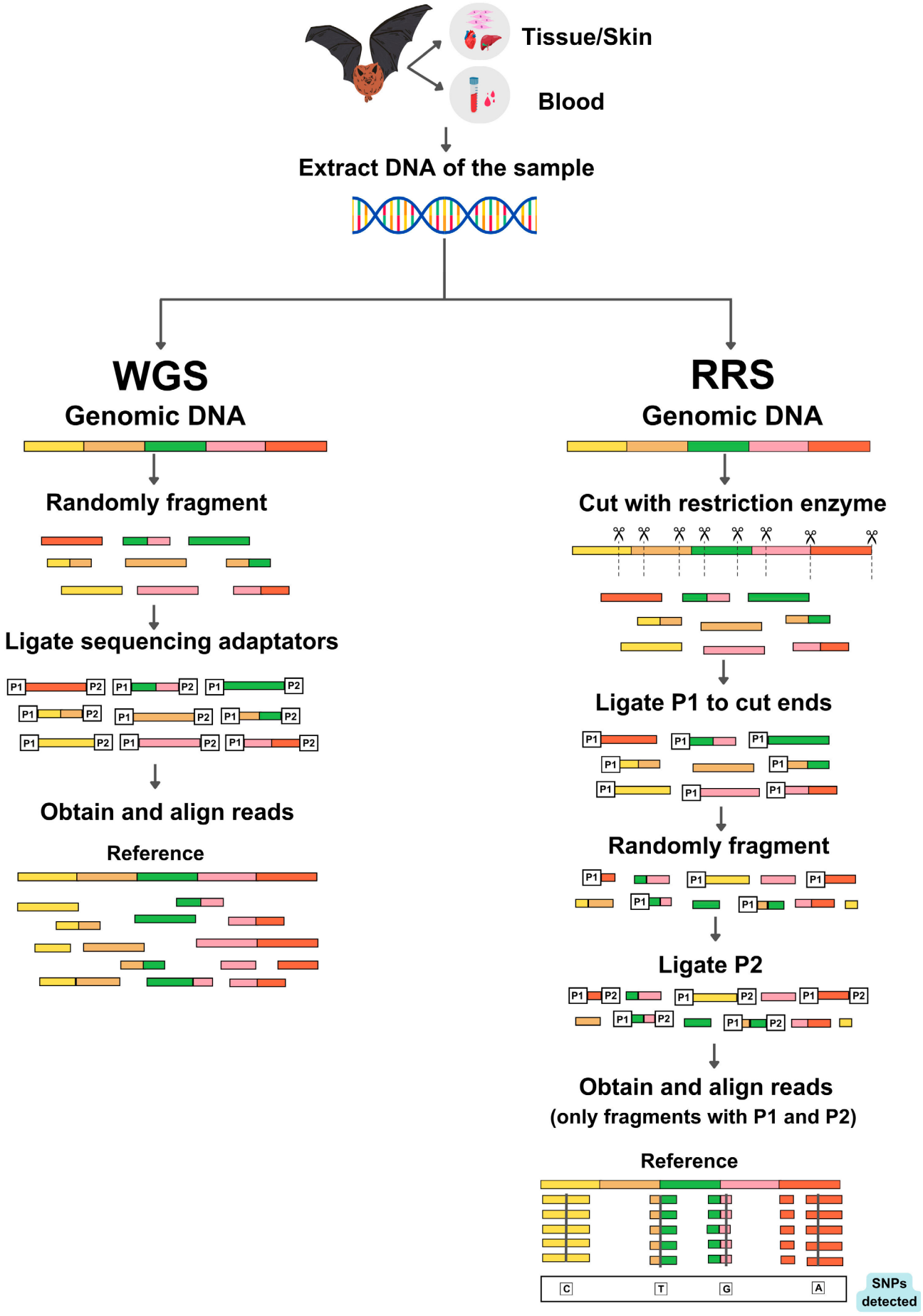

Figure 1. Overview of library preparation for whole genome sequencing (WGS) and reduced representation sequencing (RRS) for the study of mammals.

Bohling 2020). The selection of a reference genome will impact variant calling pipelines: the closer the species, the better the results (Bohling 2020). When a reference genome is not available (*de novo* variant calling), it is recommended to implement optimization protocols to define parameter values to identify SNPs (Paris *et al.* 2017).

RRS is useful for estimating levels of genetic diversity and genetic structure that allows us to propose conservation actions such as defining management units and assessing connectivity between populations. This approach was used to assess the impact of urbanization on genetic variation and genetic differentiation in the eastern grey squirrel (*Sciurus carolinensis*) (Fusco *et al.* 2023). The authors used a landscape genomics approximation to assess connectivity in rural and urban areas within the species' native range. Accordingly, connectivity was higher than expected in urban areas, whilst connectivity was lower than expected in areas impacted by agriculture.

Also, RRS provides accurate measures of inbreeding and allows performing robust kinship and relatedness analyses (Luikart *et al.* 2019). For example, relatedness analyses were used to assess if kinship influences home range overlap in an urban population of bobcats (*Lynx rufus*) (Payne *et al.* 2025). These analyses were performed by combining positioning data, to estimate individual home range and home range overlap, with SNPs data, to estimate relatedness between pairs of individuals. Accordingly, there was higher relatedness between female pairs than between male pairs and male-female pairs; also, mother-daughter pairs showed higher home-range overlap than unrelated individuals. Results suggest that urbanization doesn't seem to have a negative effect on genetic variation in this population yet, but expansion of the urban matrix will likely have major impacts on population fragmentation, isolation, and inbreeding, as has been reported in other urban bobcat populations. Moreover, this study shows that these felines are not as solitary as previously thought.

One of the advantages of genomics data is the implementation of genotype-environmental association studies and other methods to search for candidate loci under selection in non-model organisms and without a reference genome, such as *FST* outlier tests (Davey *et al.* 2011; Andrews *et al.* 2016; Ahrens *et al.* 2018). The latter permits uncovering processes of local adaptation and identifying putatively adaptive genetic variation that could be considered in conservation actions (Luikart *et al.* 2019). This approach was used to uncover candidate loci, associated with local adaptation, resulting from habitat specialization, in two species of *Dromiciops*, a marsupial endemic to the Valdivian Forest in Chile and Argentina (Quintero-Galvis *et al.* 2024). These authors also assessed the potential changes in allele frequencies as a response to future environmental change. This study helped identify vulnerable areas for the preservation of both species (*D. bozinovici* and *D. gliroides*), and to prioritize populations for conservation taking future environmental change into consideration.

RRS, in combination with fecundity and survival data, is useful to assess inbreeding depression. For example, a study used ddRADseq data to assess inbreeding depression in North Atlantic right whales (*Eubalaena glacialis*), a highly endangered marine mammal (Crossman *et al.* 2024). Even though these authors found low correlation between inbreeding and fecundity, they identified a few SNPs with potential involvement in reproduction that may be associated with fecundity. They suggest that several factors, such as body size and anthropogenic stressors, may affect fitness.

RRS is a promising genomic approximation for the conservation of mammals given that its lower costs allow sequencing a higher number of individuals than whole genome sequencing (WGS) and low coverage whole genome sequencing (lcWGS). Moreover, this approach provides higher resolution than other types of molecular markers (i.e. mtDNA and microsatellite loci) for the estimation of key population parameters such as effective population sizes and kinship, as previously mentioned. Finally, the possibility of differentiating and measuring neutral and adaptive genetic variation offers a great opportunity for the study and preservation of species and their potential to respond to environmental change.

Mitogenomics

The mitochondrion is an organelle with its own genetic material (the mitogenome), present in nearly all eukaryotic cells, whose origin dates to ancient bacterial endosymbiosis (Jin *et al.* 2020). The mitogenome is a circular, double-stranded molecule, approximately 16 to 18 kb in length in animals (Nicholls and Minczuk 2014). This molecule contains 13 protein-coding genes (PCGs) involved in oxidative phosphorylation (aerobic respiration), 2 ribosomal RNA genes, 22 transfer RNA genes, and a non-coding control region (CR) which is approximately 1 kb in length (Gibson *et al.* 2004; Ladoukakis and Zouros 2017). The synteny of the mitogenome in mammals is highly conserved and the array does not change between taxonomic units (Meganathan *et al.* 2012). Each of the two strands of the mitogenome contains an origin of replication and is labeled as "heavy" (OH) and "light" (OL) origins (Nicholls and Minczuk 2014).

The mitogenome is characterized by maternal inheritance and a compact synteny, meaning that coding sequences are separated by only a few bases, lacking introns, or even exhibiting small overlaps (Fernández-Silva *et al.* 2004). Many of the protein-coding genes can have incomplete stop codons (such as TA or T), for which stop codons are generated through the process of polyadenylation (addition of a repetitive adenine nucleotide sequence) after transcription (Donath *et al.* 2019). Although the primary function of mitochondria is to participate in the process of oxidative phosphorylation, they are also related to a wide variety of cellular processes such as apoptosis, aging, signaling, metabolic homeostasis, and the biosynthesis of macromolecules

such as pyrimidines, amino acids, phospholipids, folate coenzymes, heme and urea (Attardi and Schatz 1988; Ladoukakis and Zouros 2017).

The mitogenome has an estimated average of 9.04×10^{-9} substitutions per nucleotide per year in mammals (Soares *et al.* 2013). Synonymous mutations are more common than non-synonymous mutations (Konrad *et al.* 2017). Asymmetric replication is the main explanation for the high mutation rate of the mitogenome (Hassanin *et al.* 2005; Nicholls and Minczuk 2014). Most mutations occur in the non-coding region, making the presence of a conserved (coding) and a less conserved (non-coding) region sources of genetic diversity among species, or even among individuals within the same population (Gibson *et al.* 2004; Ladoukakis and Zouros 2017). Studies on molecular evolution of the mitochondrial genome in mammals have shown that the protein coding regions (PCGs) are mainly subject to purifying selection, but substitution rates, as well as the strength and patterns of selection, are heterogeneous (da Fonseca *et al.* 2008; Shen *et al.* 2010; Botero-Castro *et al.* 2018; Rocamontes-Morales *et al.* 2025). Such variation has been related to metabolic demands or other life history attributes (da Fonseca *et al.* 2008). For example, changes in selection regimes along the mitochondrial genome have been associated with the evolution of sanguivory and nectarivory in bats (Botero-Castro *et al.* 2018; Rocamontes-Morales *et al.* 2025).

The study and characterization of the mitogenome and mitochondrial markers have served as the foundation for molecular analyses of phylogeny, phylogeography, and population connectivity in a wide range of mammal species (Avise and Ellis 1986; Jin *et al.* 2020). Intra- and inter-population genetic diversity is also addressed using mitochondrial markers. This is often studied to propose new conservation strategies based on connectivity, gene flow, and the preservation of diversity. Recently, there has been a suggestion that the widespread influence of both direct and indirect selection on mitochondrial markers makes any conclusions drawn from it unclear or open to interpretation. In mammals, indirect selection on mtDNA can result from linkage disequilibrium with maternally inherited traits (Hurst and Jiggins 2005; Mohammadi *et al.* 2019). The combined use of mitochondrial markers with nuclear markers provides better resolution for integrative systematic studies of a taxonomic group, enabling the ability to differentiate between species, individuals, or populations. This approach allows researchers to gain a more comprehensive understanding of evolutionary relationships and genetic diversity within and among species or populations. Combining both types of markers facilitated the identification of mitochondrial-like sequences within the nuclear genomes of numerous animals known as nuclear-mitochondrial DNA segments (NUMTs), which are common in mammalian genomes and have the potential to be used for phylogenetic inference (Calabrese *et al.* 2017; Uvizl *et al.* 2023). NUMTs themselves can be useful molecular tools for phylogenetic and population genetic studies, because of their fast evolution (Zhang and Hewitt 1996; Toews and Brelsford 2012; Calabrese *et al.* 2017; Uvizl *et al.* 2023).

Recently, the complete assembly of mitogenomes has been achieved through the implementation of NGS. This allows for comparative inferences and evolutionary phylogenetics. Despite the abundance of mitogenome reconstructions made possible by different methods, complex regions such as the repetitive ones and segmental duplications found in the CR have been difficult to resolve (Heyer *et al.* 2001; Bronstein *et al.* 2018; Formenti *et al.* 2021). In theory, when repeats longer than the sequencing reads are present, assemblies are constrained within the confines of these repetitive elements (Picardi and Pesole 2012).

Currently, mitogenome assemblies have a low margin of error and are highly accurate (Formenti *et al.* 2021; Nachtigall *et al.* 2021; Uliano-Silva *et al.* 2023). Comparisons between mitogenomes facilitate the retrieval of phylogenetic relationships within the study group. The quantity, quality, and diversity of complete mitogenome assemblies and datasets available for mammals enable a precise phylogenetic comparison of sequence data and assembly approaches to describe it and enable the development of a new line of research in the field of mammalian genomics.

Mitogenomes have been widely used in phylogenomics of mammals, to obtain a better understanding of relationships between species and within species (Castellanos-Morales and Gutiérrez-Guerrero 2025). A study obtained 93 mitogenomes for six species of the genus *Dasyprocta* (Ruiz-García *et al.* 2022) and found that this genus requires taxonomic revision. Several species may be constituted by more than one lineage, while others were not supported by the analysis. These results are relevant for conservation as some of the taxa that require revisions are endemic to islands and may be endangered.

Whole genome sequencing (WGS) and Pangenomics

WGS is a comprehensive technique used to sequence the complete DNA of the genome (Figure 1). WGS covers the entire genome, including nuclear and mitochondrial DNA, allowing us to study a full picture of genetic variation (Ng and Kirkness 2010).

Covering the entire genome of an organism offers insights into both coding and non-coding regions that regulate gene expression or have other important functions. WGS allows researchers to examine all types of genetic variation, from single nucleotide polymorphisms (SNPs) to larger structural variants like insertions, deletions, and duplications (Ekblom and Wolf 2014). As provided in the previous section, through NGS technologies, short and long-read technologies (i.e. Illumina, PacBio) facilitate the production of high-quality genome assemblies.

In conservation, WGS has proven useful for the identification of population bottlenecks, inbreeding, and

adaptive traits in endangered species. For example, the Tasmanian devil (*Sarcophilus harrisii*) is endangered due to transmissible cancer known as Devil Facial Tumor Disease (DFTP). Through WGS analysis it was possible to identify genetic variants associated with disease resistance, aiding conservation managers to plan breeding programs to enhance the chances of survival for this species (Stahlke *et al.* 2021).

In another study, WGS was implemented to assess inbreeding depression in black bears (*Ursus americanus*), brown bears (*U. arctos*), and polar bears (*U. maritimus*) through runs of homozygosity (ROH). These authors detected higher variance in the amount of inbreeding and detrimental variants within species than between species; smaller, isolated, or recently bottlenecked populations had higher genetic load than larger and connected populations. Overall differences in genetic load between species were related to historic effective population size, where polar bears showed lower genetic load because small historic effective population sizes may have allowed the purge of deleterious alleles. This study also highlights the applicability of WGS in conservation by identifying populations that require management to reduce genetic load (Clendenin *et al.* 2025).

Beyond the single reference genome approach, the emerging field of pangenomics is the study of all genomic content within a species or across populations. Pangenomics includes core genes shared by all individuals and accessory genes that vary between individuals or populations (Tettelin and Medini 2020). Accessory genes can reflect local adaptations or environmental pressures (Whelan *et al.* 2021). Pangenomics captures a broader spectrum of genomic variation, offering a more complete picture of species diversity than single-genome sequencing.

Pangenomics has been more commonly applied in microbial genomics and to study crops, mainly because of the complexity and size of mammalian genomes which can be challenging and costly to sequence to construct a pangenome. The genomes of bacteria and archaea range from 0.6 to 14.3 Mb, while the reported genome sizes in mammals go from 1.6 to 6.3 Gb (Kapusta *et al.* 2017; Martinez-Gutierrez and Aylward 2022); plus, in mammals 40% of the genome is constituted by repetitive elements, while coding regions represent ~2-8%. The latter impacts the availability of high-quality genomes; for example, by March 2024 there were complete genomes available at NCBI for only 1,011 mammalian species; moreover, a small fraction of these genomes have curated annotations (Castellanos-Morales and Gutiérrez-Guerrero 2025).

Pangenomics is starting to be applied in mammalian representatives, such as the case of the domestic pig (*Sus scrofa*) pangenome are now available (Li *et al.* 2023). In a study based on 250 individuals from 32 breeds across Eurasia, it was possible to identify 3,438 novel genes absent from the current reference genome. The catalog sequences were characterized as presence/absence variations (PAVs) within pigs. The authors found that 16.8% of the genes in the pangenome catalog undergo PAV. They also found several genes associated with adaptation that are relevant to immune responses (e.g. swine leukocyte antigen, respiratory syndrome virus) (Li *et al.* 2023). This example highlights the importance of studying pangenomes, which revealed hidden layers in the diversity of pigs, and can be applied to mammalian species with a focus on conservation.

The Human Pangenome Project is another example of current pangenomics that seeks to obtain the pangenome of humans (Wang *et al.* 2022). Pangenome projects face the challenge of managing an enormous amount of data and require robust computational resources and bioinformatics expertise. However, the potential for integrating pangenomics with the other 'omics' approaches (i.e., transcriptomics, epigenomics) could provide a more holistic understanding of species adaptation and resilience, and the link between genotype and phenotype, which could be highly valuable for mammalian conservation efforts.

Pangenomics studies on human genomes and crops have uncovered intraspecific structural variation. Structural variants (SVs) change the total amount of DNA such as gene duplications, insertions and deletions, or change the sequence of DNA such as translocation, inversions, and fissions/fusions (Smeds *et al.* 2024). These studies highlight the importance of SVs in functional genomic variation, molecular evolution, and rapid adaptation to environmental changes. Therefore, obtaining multiple high-quality genomes for endangered species will allow performing analyses on SVs to better understand fitness-associated traits of conservation interest (Wold *et al.* 2021). Implementing this approximation for the study of wildlife is still methodologically challenging, but steps are being taken with promising results. For example, in Scandinavian wolves (*Canis lupus*) it has been demonstrated that in a small, isolated and inbred population, SVs increased genetic load and may play a role in inbreeding depression—as this type of variants will have significant effects on protein function—, while immigration reduced genetic load and provided a means for genetic rescue (Smeds *et al.* 2024).

Another approach is to obtain low-coverage genomes. lcWCS allows for cost-effective population screening. This approach focuses on overall population characteristics such as allele frequencies and patterns of variation across SNP throughout the genome, patterns of linkage disequilibrium, identity by descent segments, selection scans to detect signatures of selection and adaptive divergence, among others (Lou *et al.* 2021).

One of the main constraints to applying lcWGS to non-model organisms is the need for a reference genome to map short-sequence reads, but if a reference genome for the target species is not available, a reference genome of a closely related species can be used. An alternative is using a reference transcriptome to map short-reads. There are still several limitations and challenges for the implementation

of lcWGS to wildlife (e.g. required quantity and quality of DNA, need of bioinformatic skills and access to a computer cluster to conduct analyses), but this approach may be particularly useful to study rare or endangered species where obtaining a large sample size could be difficult (Lou *et al.* 2021). This approach can also help take advantage of samples from mammalogical collections, where a few samples per locality may be available, depending on the species of interest.

A study compared results from mid-coverage WGS (30x), lcWGS (9x) and RRS (RADseq) data regarding the population structure and historical demography of the North American mountain gout (Martchenko and Shafer 2023). All data sets (WGS and RADseq) revealed similar results for population differentiation, demographic history, and signals of adaptation, suggesting that the long-term adaptive capabilities of the North American mountain gout may be compromised as the species has low genetic variation (Martchenko and Shafer 2023). According to these authors, WGS provides certain advantages over RADseq as it is more adequate for inferring adaptive processes and for calculating inbreeding through ROH.

Metagenomics

Metagenomics refers to the production of comprehensive genomic data from samples that contain more than one taxon, such as environmental samples (soil, water, or fecal samples) or individual samples (swaps, blood, urine, feces). Initially, metagenomics was developed to study communities of microorganisms. Currently, metagenomics' application has extended because it provides valuable information about genome-wide variation of communities and taxonomic groups (Seeber and Epp 2022).

Metagenomics is being used to study spatial and temporal changes in biological communities, to record rare species that are difficult to sample or observe in the wild, for early detection of invasive species, to analyze the microbiome and its relationship with health or susceptibility to disease, to characterize diet items, etc. (Bohman *et al.* 2014; Thomsen and Willerslev 2015; Ruppert *et al.* 2019). In this section, we will focus on two applications of metagenomics: (a) metabarcoding (amplification of a specific DNA region to identify taxa) to study mammalian communities or specific taxa through a single sample, and (b) the study of the mammalian microbiome (communities of microorganisms associated with mammals).

Moreover, it is now possible to assemble complete mitochondrial genomes from metagenomic data by performing NGS of total DNA extracted from environmental or fecal samples; for example, the mitochondrial genomes of four large vertebrates (giant panda (*Ailuropoda melanoleuca*), Asian black bear (*Ursus thibetanus*), Sunda pangolin (*Manis javanica*) and North Atlantic right whale (*Eubalaena glacialis*) were assembled from metagenomics of scat samples (Baeza *et al.* 2023). This is a valuable tool for monitoring rare, inconspicuous, and endangered mammals.

Metagenomics has emerged as a powerful tool in ecological studies and species monitoring, garnering significant interest from molecular ecologists (Ruppert *et al.* 2019; Liu *et al.* 2020). Although this type of analysis may not identify all species with absolute certainty, it provides valuable data for ecological inference, assessing species responses to current environmental changes, and monitoring invasive species and disease vectors of public health concern (Liu *et al.* 2020). Metagenomics enables to evaluate the impact of anthropogenic activities on mammalian communities, the functional characterization of microbiomes and their implications for mammalian health, to record the presence/absence of endangered species and to obtain mitochondrial genomes for rare, inconspicuous and elusive species, from environmental and paleontological samples.

Metabarcoding. Metabarcording of environmental DNA (eDNA) is a useful, rapid, and non-invasive tool to recognize mammalian communities, populations and species that are endangered, invasive, or common species that are difficult to observe in an ecosystem by traditional field methods such as footprints, camera traps or scats (Bohmann *et al.* 2014; Harper *et al.* 2019). Environmental DNA (eDNA) is obtained from a sample of water, sediment, or free DNA that organisms transfer to the environment through feces, secretions, sperm, blood, urine, leaves, roots, pollen, or fruit that contains a mixture of genetic material from different organisms (Bohmann *et al.* 2014; Thomsen and Willerslev 2015). Through eDNA we can analyze ecological and evolutionary processes of aquatic or terrestrial biodiversity, rare taxa or environmental information and answer research questions from areas such as molecular biology, paleontology, and environmental sciences (Thomsen and Willerslev 2015; Aivelo and Medlar 2018).

DNA metabarcoding methods change slightly depending on the organisms and on the type of sample (Aivelo and Medlar 2018; Brassea-Pérez *et al.* 2019; Harper *et al.* 2019; Liu *et al.* 2020). There are several steps to implement an eDNA metabarcoding methodology for the study of mammals (Bohmann *et al.* 2014; Thomsen and Willerslev 2015; Haarsma *et al.* 2016; Ruppert *et al.* 2019; Liu *et al.* 2020; Hassan *et al.* 2022, Figure 2). First, identify the eDNA barcoding region to answer the research question and build a reference database of all possible DNA barcodes that may occur in the study area with barcode repositories or specimens from natural history museums, scientific collections or research institutions (Haarsma *et al.* 2016). When selecting an appropriate DNA barcode, several key factors must be considered. The barcode should be a universal and highly conserved region to facilitate sequence alignment across diverse species (Yang *et al.* 2018). Additionally, a short fragment (<1000 bp) DNA is recommended to ensure amplification, even from degraded samples (Yang *et al.* 2018; Ruppert *et al.* 2019). Ideally, the selected region should exhibit low intraspecific variation but high interspecific variation

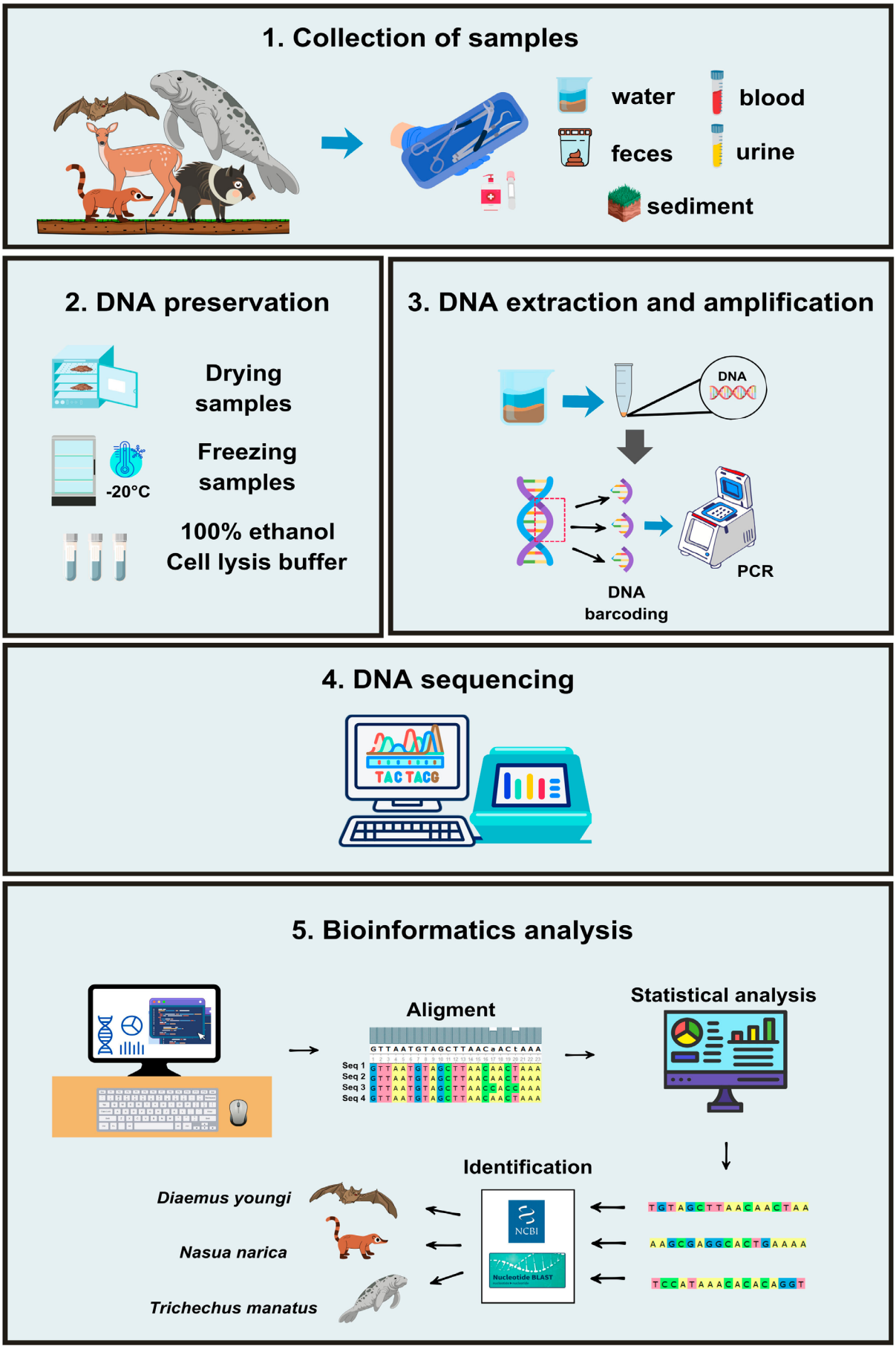

Figure 2. Overview of steps needed to conduct a metagenomics study of mammals.

to identify the target group (Ruppert *et al.* 2019). The barcode sequence commonly used in mammals and other vertebrates is the cytochrome c oxidase subunit I (COI or COX) from mtDNA (Ivanova *et al.* 2012). There are international repositories such as BOLD database (boldsystem.org) and NCBI's GenBank where reference sequences are deposited (www.ncbi.nlm.nih.gov).

Several details should be considered when sampling to optimize detection (depending on type of substrate), and to minimize contamination with exogeneous DNA (Seeber and Epp 2022). To ensure eDNA sample quality and minimize contamination, sterile equipment should be used, washed with soapy water or ethanol between samples, and accompanied by gloves, sterile vials, and a negative control (Aivelo and Medlar 2018; Liu *et al.* 2020). Proper storage is crucial as temperature, pH, and light exposure influence DNA degradation (Ruppert *et al.* 2019). For drying samples, freezing at -20°C is recommended to prevent DNA degradation (Creer *et al.* 2016, Figure 2).

After sample collection, DNA is extracted and a target DNA segment corresponding to a barcode is amplified via polymerase chain reaction (PCR); PCR products are purified and sequenced (Ruppert *et al.* 2019). The obtained DNA sequences are analyzed using bioinformatics tools and databases like BOLD and NCBI, or a reference database can be built for a specific study, to search for similarity and identify the taxa in the samples (Thomsen and Willerslev 2015; Chaves *et al.* 2025). Methods for obtaining eDNA are improved continuously as new technological advancements are incorporated (Thomsen and Willerslev 2015).

The analysis and alignment of metabarcoding data are essential steps for identifying organisms within a sample (Galhardo *et al.* 2018). The application of eDNA with other traditional field tools has improved biodiversity monitoring and has enabled the detection of species, such as the rare longfinned pilot whale (*Globicephala melas*) and the endangered hellbender salamander (*Cryptobranchus alleganiensis*), which were detected from water samples (Bohmann *et al.* 2014). The eDNA method is an efficient approach for biodiversity assessment because it offers a less invasive sampling method, and facilitates the identification of rare or endangered species, while minimizing stress to study organisms (Bohmann *et al.* 2014; Thomsen and Willerslev 2015; Liu *et al.* 2020).

Metabarcoding has been successfully used to detect mammals in a tropical forest, when compared to other commonly used sampling techniques such as mist-nets, pitfalls, grids and camera traps which are designed for certain focal groups. Accordingly, non-invasive eDNA sampling complements conventional sampling techniques and allows conducting rapid assessments for monitoring, management and conservation of mammals. This approach allows evaluating changes in the composition of mammalian communities through space and time, for example, contrasting different types of habitats, contrasting sites in a habitat perturbation gradient, or monitoring the effect of management and restoration programs (Coutant *et al.* 2021; Mena *et al.* 2021).

Metabarcoding from fecal samples has been used to determine animal diets. For example, this approach was used to assess dietary range and overlap between co-occurring mammals to assess potential competition (Kanishka *et al.* 2025). Another study used eDNA from scats to assess changes in diet of the yellow footed antechinus (*Anthechinus flavipes*), heath mouse (*Pseudomys shortridge*) and bush rat *(Rattus fuscipes*) after fire in a woodland ecosystem in Australia. This method was time-effective and successful to determine the baseline diet of the three species, and to detect changes in diet associated with the availability of critical food resources after a fire. Accordingly, these analyses allow considering the effect of fire management actions in the identified food resources (Wanniarachchi *et al.* 2022).

Microbiome. Metagenomics can also be used to study the mammalian microbiome. The microbiome is the community of microorganisms (bacteria, viruses, protozoa and fungi) that inhabit in or reside on an organism. The microbiome has influenced the course of mammalian adaptation and diversification. It has been associated with dietary transitions to herbivory, specialization and resistance to toxic food items, phenotypic plasticity and the evolution of innate and adaptive immune mechanisms in mammals. In some species, there is even host dependence on its microbiome to perform certain functions (Moeller and Sanders 2020).

There can be differences in the microbiome between individuals, and even between parts of the body. Moreover, there is a close interaction between the host and its microbiome (via structural elements, metabolites and signal molecules), and the microbiome composition of an individual may affect many of the individual's attributes (health, nutrition, physiology, immunity and development) and its fitness. The microbiome changes in response to differences in environmental conditions, for example, between lowland and highland populations or between captive and wild populations (Bahrndorff *et al.* 2016; Ange-Stark *et al.* 2023; Wang *et al.* 2025). Also, it has been suggested that captivity disrupts the gut microbiome of organisms because of changes in diet, the use of antibiotics, homogeneous environment, increased stress and close contact with humans (Dallas and Warne 2023; Dai *et al.* 2025). This, in turn, may affect the prevalence of pathogenic bacteria and the immune response of organisms (Dai *et al.* 2025). Differences in gut microbiome between captive and wild populations have been linked to low fecundity in captivity. Microbiome studies are useful for the development of prebiotics and probiotics for the reintroduction and management of threatened populations (Dallas and Warne 2023; Wang *et al.* 2025).

A study on black rhinoceros (*Diceros bicornis*) compared the microbiome of wild and captive animals. There were differences in beta diversity between captive and wild

rhinoceros. In captive individuals, some microbes were replaced with microbes typically found in livestock. Moreover, analysis of the microbiome found different functional bacterial communities, with higher abundance of glycolysis and amino acid synthesis pathways in captive rhinoceros, which results in differences in the acquisition of certain nutrients from the diet. Accordingly, management of the captive population should include changes in diet, and the administration of probiotics or fecal transplants to restore gut microbiome diversity (Gibson *et al.* 2019).

Analyzing the microbiome of wild mammals may be challenging, but methodological advancements make it feasible nowadays. Comparative studies on the gut microbiome of small mammals suggested that diet may influence the composition of the gut microbiome. In this case, sympatric species showed similarities in their microbiome composition; other aspects such as diet, life history, and phylosymbiosis may influence microbiome composition (Moeller and Sanders 2020; Li *et al.* 2022). In addition, microbiomes are being studied in relation to susceptibility to disease, such as the white nose syndrome (caused by *Pseudogymnoascus destructans*), a fungal pathogen responsible for mass mortality of bats in North America (Vanderwolf *et al.* 2021). In this sense, even if the effects of the white nose syndrome on bat microbiomes vary between bat hosts, it has been demonstrated that the presence of certain microorganisms may influence host resistance (Vanderwolf *et al.* 2021; Ange-Stark *et al.* 2023).

Transcriptomics

Transcriptomics focuses on the study of the products of the transcription of the genome from DNA to RNA in any of its forms (mRNA, rRNA, tRNA and noncoding RNA), to characterize molecular responses to external stimuli such as ecological, environmental or anthropogenic factors. This discipline allows characterizing genetic expression profiles, and to identify and quantify genes that turn on or off under certain conditions; taking into consideration that each organism has an evolutionary history that influences the genetic expression of gene profiles under different environmental conditions (Jaris *et al.* 2012). Transcriptomics allows studying the molecular mechanisms of adaptation, and to use this information in management and conservation planning to conserve the adaptive potential of species (Alvarez *et al.* 2015; Theissinger *et al.* 2023).

Species respond to environmental changes through two main mechanisms: phenotypic plasticity and changes in the genome that confer adaptation (Bernatchez *et al.* 2024). Phenotypic plasticity is the ability of one genotype to face environmental changes by expressing an alternative phenotype; phenotypic plasticity could become fixed as permanent changes that improve species fitness (Aubin-Horth and Renn 2009; Weeks *et al.* 2022; Yeaman 2022). Genetic adaptation involves heritable changes in the allele frequencies of genes that impact fitness (Yeaman 2022). In this sense, transcriptomics arises as an approximation to understand the role of gene expression in the responses of organisms to different environmental conditions, which drives evolutionary adaptation (He *et al.* 2016) and ecological divergence during speciation (Jeukens *et al.* 2010; Pavey *et al.* 2010).

RNA-seq technology was developed to characterize complete transcriptomes, without information from a reference genome, to identify the gene profiles with downregulated or upregulated expression in a specific condition, to identify the use of alternative splicing, secondary structures of RNA, to characterize metabolic pathways, and the genetic regulation process. Additionally, this methodology allows the quantification of gene expression with high accuracy even from genes with low expression (Wang *et al.* 2009; Loeffler *et al.* 2023).

Regarding population genotyping, RNA-seq allows us to characterize and quantify the variation in gene expression at a population level (Jaris *et al.* 2012; Lopez-Maestre *et al.* 2016). Such variation occurs not only on the coding sequences (it is estimated that 60% of the adaptive sites associated with selection signals occur in these regions), but also on *cis* and *trans* regulation elements (such as promoters, enhancers, silencers, binding sites for transcription factors, miRNA, etc.), which contribute to phenotypic or adaptive divergence of species (Jehl *et al.* 2021).

The integration of gene expression and population genomics to identify genetic variants such as SNPs from RNA sequences also enables estimating genetic diversity parameters (nucleotide diversity, structure, differentiation, and gene flow) for making evolutionary inferences (Jaris *et al.* 2012; Yu *et al.* 2023). For example, adaptation to altitudinal variation has been studied in the deer mice (*Peromyscus maniculatus*). This study found differential abundance in 11.7% of evaluated genes between individuals from highland (n = 10) and lowland populations (n = 10), and differences in gene expression in 0.7% of the genes. Few differentially expressed genes were associated with the response to differences in altitude. In this case, regulatory plasticity contributed to physiological adaptation to highlands. Accordingly, regulatory plasticity may play an important role in niche breadth and in potential response to environmental changes (Cheviron *et al.* 2013).

Another application of transcriptomics analyses is in landscape transcriptomics, which refers to the study of fluctuations in genome expression across populations in response to environmental gradients to establish management. This approach provides interesting information about adaptive local responses and the potential resilience of populations to rapid environmental change. Also, anthropogenic perturbations may lead to genetic differentiation between wild populations, and changes in connectivity, which could drive species to extinction (Keagy *et al.* 2023).

The potential of this tool is clear; however, there are many more reports of its use for studying the response to stress or environmental changes in model plants, fish, and

insects than for non-model mammals. Initially, one of the main limitations for the applicability of transcriptomics for the study of mammals and particularly endangered species, was that it required euthanizing individuals to obtain samples from specific organs or tissues, such as the brain, the kidneys, the lungs, the heart or the liver, to mention a few, depending on the research question (Huang *et al.* 2016). Nonetheless, thanks to technological advances, nowadays it is possible to conduct single-cell transcriptomics or to study the transcriptome from blood samples, making it feasible to study endangered species (Huang *et al.* 2016; 2019; Hilton *et al.* 2019).

Here we highlight some interesting studies that used RNA-seq to study ecological-evolutionary processes, such as identifying conserved sequences, expansion or contraction of gene families in specific lineages implicated in molecular evolution, genome complexity which drives species adaptation to new environments, and signals of selection. For example, 39 differentially expressed genes (DEG) were identified to be under positive selection in lung tissue of the yak (*Bos grunniens*) when compared with cattle (*Bos taurus*). The yak is a unique bovine that can live in high-altitude regions such as the Tibetan Plateau; accordingly, identified DEGs were associated with survival in oxygen-deficient environments (Lan *et al.* 2018).

Another study found that, in some cattle lineages, selective pressures have relaxed on traits associated with behavior in wildlife. In addition, there was an increase in the strength of positive selection in genes associated with amino acid metabolism, immune response, reproductive traits, hormone biosynthesis, and response to stress associated with an increase in temperature. The latter, together with non-conserved sequences in genes associated with lipid metabolism, could be used to improve the production and quality of meat (Cortez *et al.* 2022).

Transcriptomics allows to identify biomarkers that are indicative of the amount of genetic variation within and between populations to gain a better assessment of functional variability; this is useful information when defining management units and when identifying populations with low adaptive potential (Xu *et al.* 2014; 2016). The use of biomarkers allows monitoring population health, levels of genetic diversity, detection and prevalence of disease, and the response to environmental stress (He *et al.* 2016; Tarlinton *et al.* 2021). These aspects are highly relevant when selecting individuals for reintroduction and for implementing assisted reproduction techniques (Bowen *et al.* 2022; Gad *et al.* 2024); particularly for endangered mammals that require higher precision and efficacy in their management (Gao *et al.* 2022; Theissinger *et al.* 2023).

An RNA-seq approach was used to identify a biomarker for detecting kidney disease in koalas (*Phascolarctos cinereus*). The koala is a vulnerable species that is distributed in Australia, where two genetic clusters have been identified, a northern and a southern cluster. The southern cluster shows low levels of genetic variation, and individuals are carriers of several diseases that impact fitness. The gene *SLC26A6* was differentially expressed when comparing the northern and southern populations, and differential expression was associated with kidney disease; thus, this gene may function as a biomarker to detect susceptibility to kidney disease in koalas (Tarlinton *et al.* 2021).

In the bighorn sheep (*Ovis canadensis*), several genes (TGFb, AHR, IL1b and MX1) were associated with the initial phases of pneumonia, which cause a mortality rate of 90%. These genes can be used as biomarkers for monitoring populations for early detection of the disease, and to implement an adequate management plan (Bowen *et al.* 2022).

Transcriptomic data have also been used to develop biomarkers that allow assessing ecological risks for the presence of toxins in the marine surface, changes in temperature regimes, and the presence of pathogens in the bottlenose dolphin (*Tursiops truncatus*) from Bahía Sur de Baja California. In this case, two genes (UBQLN4 and TXNDC11) were associated with response to environmental stress such as fluctuations in temperature (Trego *et al.* 2019).

Finally, the characterization of the transcriptome in early embryonic development provides information that allows optimizing the process for embryo selection, fertilization, and the selection for individuals for *ex situ* conservation and reintroduction (Chitwood *et al.* 2017; Gad *et al.* 2024). The southern population of white rhinoceros (*Ceratotherium simum*) consists of only two non-reproductive individuals; in this case, assisted reproduction may be a viable alternative to increase population size. This analysis showed that four miRNA (miR-149b, miR-148a, miR-451 and miR-21) are highly active during embryonic development; these loci may be key for implementing successful assisted reproduction (Gad *et al.* 2024).

The application of transcriptomics for mammal conservation is only starting, but this approach is promising for gaining a better understanding of species' capacity to respond to environmental changes. In addition, obtaining transcriptomic data has a lower cost than obtaining genomic data; therefore, this approach represents a viable alternative for laboratories with restricted budgets.

Challenges and perspectives

There are still some challenges in implementing genomics for the study and conservation of mammals. A strong population genetics' theoretical background is advisable to implement adequate analyses and to help interpret the data. In this sense, population genetics courses for managers must be designed.

Another challenge is building technical capabilities (both in equipment and human resources) for the construction of genomic libraries and gaining access to next-generation sequencing technologies, particularly in countries from the global south. In this sense, expertise in bioinformatics is needed to conduct data analyses and develop user-friendly software that provides easier access

to data analysis for non-experts. The latter comes hand in hand with access to high-performance computer clusters because genomic approaches produce a large amount of data that cannot be analyzed on a personal computer.

Finally, translating complicated technical language into an accessible language for non-experts and grounding research findings in their practical implications and applications for conservation will help raise awareness in the public. Moreover, this is a crucial step in linking scientific researchers with wildlife managers and decision-makers.

The transition from conservation genetics to genomics will become increasingly common as massive sequencing costs decrease and technologies become more accessible. The application of genomics in combination with non-invasive sampling is still challenging, as DNA from this type of sampling is usually found in low concentrations and it is degraded. Although there have been advances in these areas, future efforts should optimize the application of genomic tools to non-invasive samples (Russello *et al.* 2015; Andrews *et al.* 2018; Ramírez-García *et al.* 2025) and museum specimens, which hold valuable information about historical patterns of genetic diversity (Card *et al.* 2021; Raxworthy and Smith 2021; Fong *et al.* 2023). In addition, genomics, transcriptomics, epigenetics and other omics (such as metabolomics and proteomics) will contribute with a better understanding of how species, populations and biological communities will respond to climate change and to address the biodiversity crisis (Tiwari and Rajwanshi 2022; De León *et al.* 2023; Bernatchez *et al.* 2024). In conjunction with environmental data and future projections of niche models, genomics and other omics will help predict potential allele turnover, dispersal potential, and the role of gene flow to climate change (Fitzpatrick and Keller 2015; Capblancq *et al.* 2020; Aguirre-Liguori *et al.* 2021; Bernatchez *et al.* 2024); as well inbreeding and inbreeding depression, hybridization and adaptive introgression. We hope that mammalogists (current and future) found this review useful as a starting point for implementing genomics studies for the conservation of mammals.

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Declaration of Artificial Intelligence use

The authors declare that no AI was used in the preparation of this manuscript.

Author contributions

Gabriela Castellanos-Morales led the writing and development of the present manuscript. Gabriela Castellanos-Morales and Jorge Ortega were responsible for manuscript conceptualization. All authors performed literature searches and revision for different sections and writing of original draft. Anahí Canedo-Texón composed the abbreviature and concept lists, Jesús Antonio Rocamontes-Morales prepared Table 1 and Katia Hernández-Bolaños prepared figures. All authors contributed to reviewing and editing of previous versions of the manuscript. All authors approved the final version of this manuscript.

Supplementary Data

SD1. List of abbreviations used in the present article.
SD2. List of concepts frequently used in genomic studies.

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