International Journal of Molecular Zoology 2024, Vol.14, No.3, 154-165
http://animalscipublisher.com/index.php/ijmz

Research Report **Open Access**

Evolutionary Conservation Genomics of Carnivores: Insights from Felids

Qineng Si
BIotechnology Reseach Center, Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China
Corresponding email: qineng.si@cuixi.org

International Journal of Molecular Zoology, 2024, Vol.14, No.3 doi: 10.5376/ijmz.2024.14.0015
Received: 30 Mar., 2024
Accepted: 11 May, 2024
Published: 31 May, 2024

Preferred citation for this article:
Si Q.N., 2024, Evolutionary conservation genomics of carnivores: insights from felids, International Journal of Molecular Zoology, 14(3): 154-165 (doi: 10.5376/ijmz.2024.14.0015)

Abstract Conservation genomics is crucial for understanding the evolutionary history of species and maintaining their genetic diversity. As top predators, felids play a key role in maintaining ecological balance, making their conservation essential. This study aims to explore the genomic landscape of felids to guide and enhance conservation strategies. We investigated the evolutionary history of felids, tracing their origins, diversification, and phylogenetic relationships, highlighting major evolutionary events. Using advanced sequencing technologies and genomic data analysis methods, we studied genetic variation within and among felid species. Through a detailed case study of the tiger (*Panthera tigris*), we gained insights into its genetic diversity, population structure, and conservation efforts, providing valuable experience for other felid species. We explored adaptive genomic traits related to habitat, disease resistance, and behavior. We assessed threats to felid genomic diversity, including habitat fragmentation, human-wildlife conflict, and climate change. We discussed conservation strategies based on genomic data, including breeding programs, habitat restoration, and policy recommendations. This study emphasizes the critical role of genomics in felid conservation. By integrating genomic research with ecological data, robust conservation strategies can be developed to maintain felid biodiversity. Future directions include leveraging emerging technologies and setting long-term conservation goals to ensure the survival of these majestic predators.

Keywords Conservation genomics; Felids; Genetic diversity; *Panthera tigris*; Adaptive traits

1 Introduction

Conservation genomics is an emerging field that leverages genomic data to address conservation challenges (Allendorf, 2017). By analyzing the genetic material of organisms, researchers can gain insights into genetic diversity, population structure, and evolutionary history, which are critical for developing effective conservation strategies. Advances in sequencing technologies have enabled the generation of high-quality genomic data for a wide range of species, including those that are not traditional model organisms (Johnson and Koepfli, 2014). These genomic tools have revolutionized our understanding of biodiversity and the genetic factors that contribute to species survival and adaptation (Samaha et al., 2021).

Felids, or members of the cat family, are of particular interest in conservation genomics due to their ecological roles as apex predators and their vulnerability to environmental changes (Primmer, 2009). Felids such as tigers, lions, leopards, and cheetahs have experienced significant population declines and habitat fragmentation, making them prime candidates for genomic studies aimed at conservation (Kim et al., 2016). The genetic diversity within felid populations is crucial for their adaptability and long-term survival. Studies have shown that felids often exhibit low genetic diversity, which can increase their susceptibility to diseases and reduce their ability to adapt to changing environments (Azizan and Paradis, 2021). Understanding the genetic makeup of felids can help identify populations at risk and inform conservation efforts to maintain or enhance genetic diversity (Smith et al., 2017).

This study conducts a systematic review of the current state of conservation genomics in felids, synthesizing findings from recent genomic studies to provide a comprehensive understanding of the genetic factors influencing felid conservation; explores the genetic diversity, population structure, and evolutionary adaptations of various felid species. By integrating data from multiple studies, this study hopes to identify common patterns and unique challenges faced by different felid species and aims to highlight the potential of genomic tools in developing effective conservation strategies for felids and emphasize the importance of preserving their genetic diversity for future generations.

2 Evolutionary History of Felids

2.1 Origins and diversification

The evolutionary history of modern felids traces back to relatively recent divergence and speciation events that occurred less than 11 million years ago. This period marked the radiation of modern *Felidae*, producing successful predatory carnivores that have since spread worldwide. The diversification of felids was facilitated by at least 10 intercontinental migrations, which were influenced by sea-level fluctuations. These migrations and subsequent speciation events have been well-documented through a highly resolved molecular phylogeny, which includes autosomal, X-linked, Y-linked, and mitochondrial gene segments, as well as fossil calibrations1. The fossil record, however, underestimates the first occurrence of felid lineages by an average of 76%, indicating a low representation of felid fossils in paleontological remains (Johnson et al., 2006).

2.2 Phylogenetic relationships

The phylogenetic relationships among felids have been elucidated through comprehensive analyses of mitochondrial genomes. These studies have provided robust resolutions of both suprafamilial and intrafamilial relationships within the order Carnivora, to which felids belong. The divergence times among species of Carnivora, including felids, have been estimated using 21 fossil calibration points. These analyses suggest that major groups within Feliformia, the suborder that includes felids, diversified more recently during the Oligocene epoch. The basal divergence of the genus Nandinia, for instance, occurred at the Eocene/Oligocene transition (Hassanin et al., 2021). This phylogenetic framework has been crucial in understanding the evolutionary pathways and relationships among different felid species.

2.3 Major evolutionary events

Several major evolutionary events have shaped the history of felids. One significant event was the rapid radiation and spread of nimravid carnivores, which are closely related to modern felids. This radiation occurred during the late Eocene, following the decline or extinction of earlier carnivorous groups such as *Mesonychia* and *Oxyaenodonta*. The emergence of nimravids, characterized by hypercarnivorous features, marked a pivotal moment in the evolution of carnivorous mammals. The discovery of Pangurban egiae, an early nimravid from the Eocene of California, provides evidence for the swift diversification of nimravids during a period of global climatic instability. This event highlights the restructuring of North American ecosystems during the Eocene-Oligocene transition, which allowed carnivoraforms, including felids, to occupy high trophic level niches (Poust et al., 2022). In summary, the evolutionary history of felids is marked by recent divergence and speciation events, complex phylogenetic relationships, and significant evolutionary milestones that have contributed to their current diversity and ecological roles. The integration of molecular data and fossil records continues to enhance our understanding of these remarkable carnivores.

3 Genomic Techniques in Conservation Biology

3.1 Sequencing technologies

Advancements in sequencing technologies have significantly enhanced our understanding of the genetic diversity and evolutionary history of carnivores, particularly felids (Allio et al., 2021). High-quality reference genomes can now be obtained from various sources, including roadkill samples, which provide valuable genetic material for conservation studies. For instance, the genomes of the bat-eared fox and aardwolf were sequenced using a combination of Nanopore long reads and Illumina short reads, demonstrating the potential of these technologies in generating high-contiguity and gene-complete reference genomes. Additionally, cross-species genome alignments have been employed to discover single nucleotide variants (SNVs) in species such as cheetahs, snow leopards, and Sumatran tigers, using the domestic cat genome as a reference. This method has proven effective in identifying adaptive and deleterious alleles, which are crucial for conservation management (Samaha et al., 2021).

3.2 Genomic data analysis methods

Genomic data analysis methods are essential for interpreting the vast amounts of data generated by sequencing technologies. Techniques such as quantitative trait locus (QTL) mapping have been used to investigate the genetic architecture of adaptive traits in carnivores. For example, QTL mapping in haplochromine cichlid fish revealed the genetic basis of trophic diversity, which is relevant for understanding similar adaptive traits in carnivores (Feller and Seehausen, 2022). Phylogenetic analysis using mitochondrial DNA sequences, such as the cytochrome b gene, has also been employed to decipher the evolutionary history and genetic relationships among carnivore species. This approach provides insights into the origin, ancestry, and diversification of species, aiding in the prediction of future evolutionary trends (Bashir et al., 2020).

3.3 Applications in conservation

The application of genomic techniques in conservation biology has led to significant advancements in the management and preservation of felid species. For instance, the identification of orthologous chromosomal DNA segments through 3D comparative scaffotyping has facilitated the assignment of chromosome-scale DNA sequence scaffolds, reducing costs associated with karyotyping and physical mapping (Figure 1) (Corbo et al., 2022). Forensically informative nucleotide sequencing (FINS) has been used to differentiate closely related wild felids, such as the leopard cat, jungle cat, and fishing cat, based on mitochondrial gene variations. This method is crucial for preventing false identification in wildlife forensics and strengthening DNA databases for conservation purposes (Singh et al., 2020). Furthermore, studies on the genetic diversity of felid populations have highlighted the importance of factors such as generation length, habitat, and home range size in influencing genetic variation. These findings help identify priority species vulnerable to genetic diversity loss, guiding conservation efforts (Azizan and Paradis, 2021). In summary, the integration of advanced sequencing technologies, sophisticated genomic data analysis methods, and practical applications in conservation has provided valuable insights into the evolutionary conservation genomics of felids. These techniques are instrumental in enhancing our understanding of genetic diversity, adaptive traits, and evolutionary history, ultimately contributing to the effective management and preservation of carnivore species.

Corbo et al. (2022) found that comparative chromatin conformation analyses in five felid species—puma, tiger, leopard, cheetah, and clouded leopard—revealed significant chromosomal inversions and similarities in homologous synteny blocks. Their study utilized Evolution Highway for visualizing synteny blocks and Juicer plots to depict interaction frequencies between loci on chromosomal scaffolds. These analyses showed distinct chromosomal inversions greater than 1 Mb in size and variations in the frequency of interactions across species. The eigenvector values indicated chromatin structure differences at a 500-kb resolution. This study highlights the chromosomal structural variations and conserved elements across different felid species, contributing to the understanding of their evolutionary genomics.

4 Genomic Diversity in Felids

4.1 Genetic variation within species

Genetic variation within felid species is influenced by several factors, including geographic location, habitat type, and species-specific traits. A comprehensive study analyzing data from 135 population genetic studies on 28 wild felid species revealed significant differences in genetic diversity across continents. Populations in Africa and South America exhibited higher heterozygosity and allelic richness compared to those in other regions. Asiatic lions, in particular, showed the least genetic diversity among felids globally. Additionally, threatened species generally had lower genetic diversity than low-risk species, although genetic diversity was not correlated with body mass or geographic range. Generation length emerged as a critical factor, with species having shorter generation lengths displaying reduced genetic diversity. Habitat type and home range size also played roles, with species dependent on closed habitats and those with larger home ranges showing lower heterozygosity (Azizan and Paradis, 2021).

4.2 Comparative genomics among felid species

Comparative genomics has provided valuable insights into the evolutionary history and adaptive traits of felid species. Cross-species genome alignments using the domestic cat as a reference have enabled the discovery of millions of single nucleotide variants (SNVs) in species such as the cheetah, snow leopard, and Sumatran tiger. These alignments have facilitated the identification of population structures and functional genomic features, although they are less effective at detecting rare variants. Enrichment analyses of fixed and species-specific SNVs have shed light on adaptive traits and the pathogenesis of heritable diseases, underscoring the utility of cross-species genomic methods in conservation management (Samaha et al., 2021). Additionally, the conservation of chromatin conformation across carnivores, including felids, has been observed, highlighting the importance of maintaining three-dimensional chromatin architecture for conserved genome functions. This conservation has practical applications in reducing costs associated with karyotyping and physical mapping in biodiversity genome sequencing efforts (Corbo et al., 2022).

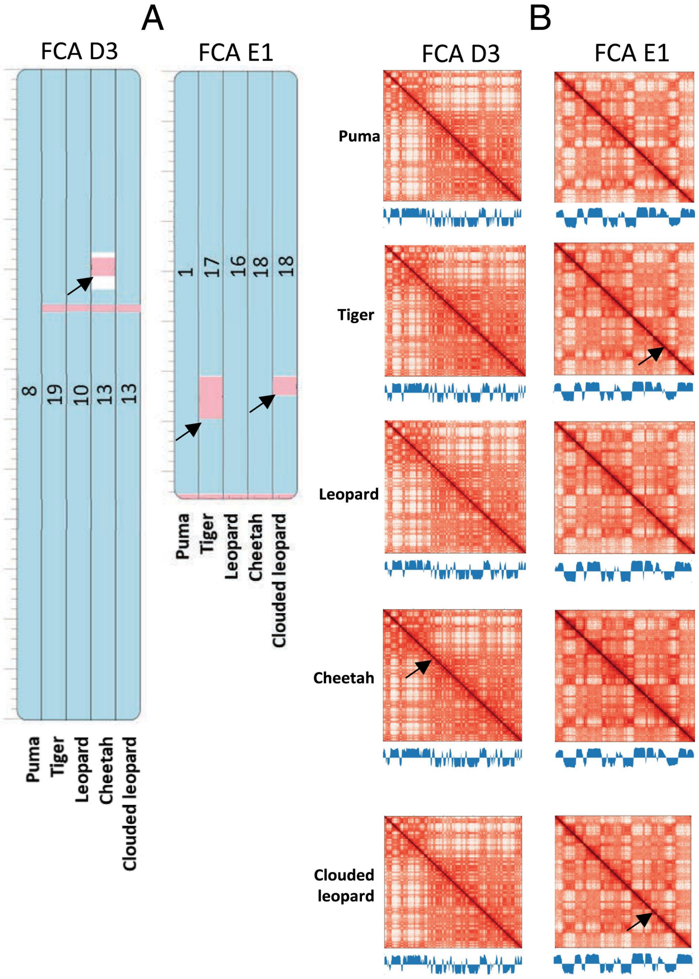

Figure 1 Comparative analysis of chromatin conformation in felids. Puma, tiger, leopard, cheetah, and clouded leopard C-scaffolds orthologous to cat chromosome D3 (FCA D3) and E1 (FCA E1) (Adopted from Corbo et al., 2022)

Image caption: (A) Homologous synteny blocks of the five felids visualized in Evolution Highway at 300-kb resolution. Blue indicates same sequence orientation as the reference genome. Pink depicts chromosome inversions (arrows indicate inversions bigger than 1 Mb). Numbers represent the scaffold identifier of the target species. (B) Juicer plots of orthologous C-scaffolds for the five felids as numbered in part A. Color intensity reflects the frequency of interactions between pairs of loci on C-scaffolds (range 1 to 1,000 for each map). Blue histograms depict eigenvector values for each species matrix at 500-kb resolution. Similar comparisons for all other cat chromosomes are shown in SI Appendix, Fig. S2. Alignment coordinates can be found in Dataset S3 (Adopted from Corbo et al., 2022)

4.3 Implications for conservation

The findings on genetic diversity and comparative genomics have significant implications for the conservation of felid species. Identifying species with low genetic diversity, such as the Asiatic lion, can help prioritize conservation efforts to mitigate the risks associated with reduced genetic variability. The use of cross-species genome alignments and the conservation of chromatin conformation can aid in the development of cost-effective genomic resources for non-model species, facilitating more informed conservation strategies. Furthermore, understanding the genetic basis of adaptive traits and disease susceptibility can inform breeding programs and habitat management practices aimed at enhancing the resilience of felid populations (Fan et al., 2018).

5 Case Study: *Panthera Tigris*

5.1 Genetic diversity and population structure

The genetic diversity and population structure of *Panthera tigris*, commonly known as the tiger, have been extensively studied to understand the implications for conservation. Recent genomic studies have revealed significant insights into the genetic makeup of various tiger subspecies. For instance, the near-chromosomal de novo assembly of the Bengal tiger genome has provided a high-quality reference that highlights the genetic hallmarks of apex predation and offers a comprehensive tool for conservation genetics5. This assembly has enabled the detection of longer stretches of runs of homozygosity, which are crucial for estimating genomic inbreeding levels. Additionally, the use of non-invasive methods such as eDNA from scat samples has proven effective in assembling complete mitochondrial genomes of the Amur tiger (*Panthera tigris altaica*). This approach has demonstrated that it is possible to retrieve accurate whole and nearly complete mitochondrial genomes without library enrichment protocols, providing a valuable resource for conservation strategies (Figure 2) (Baeza, 2022). These genomic resources are essential for understanding the genetic diversity and population structure of tigers, which is critical for their conservation.

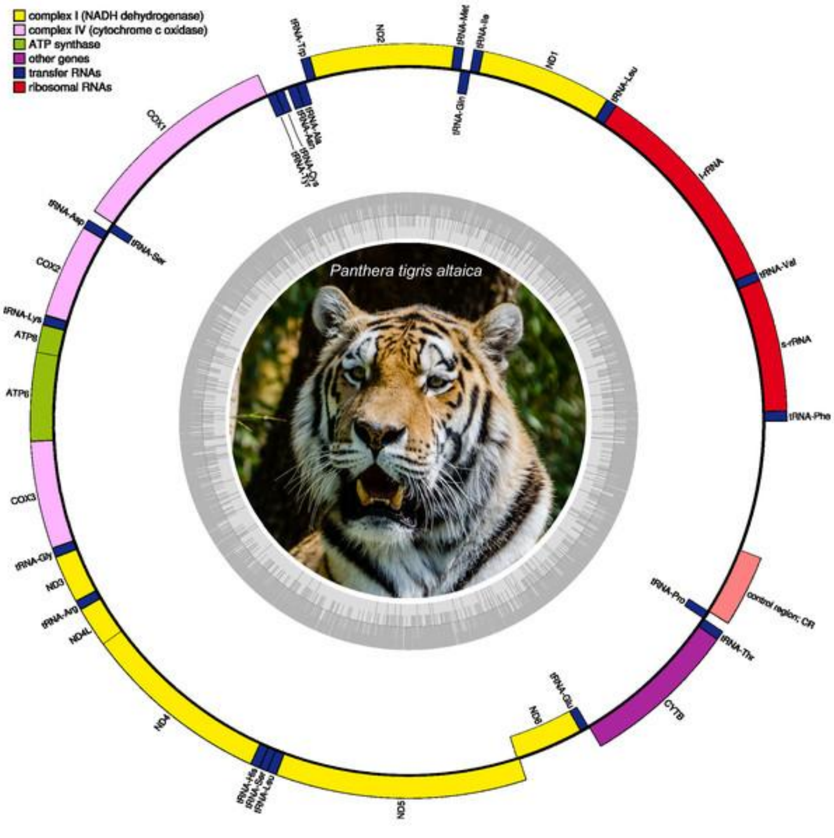

Figure 2 Circular DNA mitochondrial genome map of *Panthera tigris* altaica assembled from eDNA scat (Adopted from Baeza, 2022)

Image caption: The annotated map depicts 13 protein-coding genes (PCGs), two ribosomal RNA genes (rrnS: 12 S ribosomal RNA and rrnL: 16 S ribosomal RNA), 22 transfer RNA (tRNA) genes, and the putative control region (not annotated) (Adopted from Baeza, 2022)

Baeza (2022) found that the circular mitochondrial genome of the Siberian tiger (*Panthera tigris altaica*), assembled from environmental DNA (eDNA) scat samples, includes 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNA genes. Their analysis also identified a putative control region, although it was not annotated. This comprehensive mapping of the mitochondrial genome provides essential insights into the genetic structure and diversity of the Siberian tiger, aiding conservation efforts by enabling more accurate population monitoring and genetic health assessments. The study underscores the utility of eDNA in non-invasive wildlife genetics research, offering a valuable tool for studying endangered species like the Siberian tiger.

5.2 Conservation efforts and genomic insights

Conservation efforts for tigers have increasingly relied on genomic insights to inform management strategies. The high-quality genome assemblies of tigers have identified several gene families involved in key morphological features such as teeth, claws, vision, olfaction, taste, and body stripes, which are essential for their survival as apex predators5. These genomic insights have also revealed signatures of positive selection consistent with the Panthera lineage, providing a deeper understanding of the evolutionary adaptations of tigers. Moreover, the use of cross-species genome alignment methods has facilitated the discovery of single nucleotide variants (SNVs) in tigers, which are crucial for understanding population structure and functional genomic features. This method has been successfully applied to the Sumatran tiger (*Panthera tigris sumatrae*), yielding valuable data on adaptive traits, evolutionary history, and the pathogenesis of heritable diseases (Wultsch et al., 2016). These genomic insights are instrumental in developing effective conservation strategies that address the genetic health and viability of tiger populations.

5.3 Lessons learned for other felids

The genomic studies and conservation efforts focused on tigers offer valuable lessons for other felids. The successful application of non-invasive genetic methods, such as eDNA from scat samples, demonstrates the potential for similar approaches to be used in other felid species to gather genetic data without the need for invasive sampling techniques. This is particularly important for endangered and elusive species where traditional sampling methods may be challenging. Furthermore, the insights gained from high-quality genome assemblies and cross-species genome alignments highlight the importance of developing comprehensive genomic resources for other felids. These resources can provide critical information on genetic diversity, population structure, and adaptive traits, which are essential for informed conservation management (Shukla et al., 2022). By leveraging these genomic tools, conservationists can better understand the genetic health of felid populations and implement strategies to mitigate the risks of inbreeding and genetic drift. In conclusion, the case study of *Panthera tigris* underscores the significance of genomic research in conservation efforts. The lessons learned from tigers can be applied to other felids, enhancing our ability to protect and preserve these majestic species for future generations.

6 Adaptive Genomic Traits in Felids

6.1 Adaptations to different habitats

Felids exhibit a range of genomic adaptations that enable them to thrive in diverse habitats. One significant adaptation is the evolution of pattern recognition receptor (PRR) genes, which play a crucial role in immune responses. These genes have undergone positive selection in semi-aquatic species, suggesting that they have adapted to specific environmental pressures6. Additionally, the contraction of gene families related to starch and sucrose metabolism in felids indicates a dietary specialization that aligns with their carnivorous lifestyle, which is a critical adaptation for survival in various habitats (Figure 3) (Kim et al., 2016).

Kim et al. (2016) found that the identification of highly conserved regions (HCRs) across *Felidae*, *Hominidae*, and *Bovidae* revealed significant insights into genetic conservation and variation among these groups. The Venn diagram analysis showed shared and unique genes in the HCRs, with a notable number of conserved genes across all three families. The heatmap analysis of enriched gene ontology (GO) categories and KEGG pathways in the HCRs highlighted key biological processes and pathways, such as proteasome function, cell cycle regulation, and signal transduction pathways. These findings suggest that despite evolutionary divergence, there are critical conserved genetic elements among these families, which may play essential roles in their fundamental biological functions and evolutionary adaptations. The study emphasizes the importance of HCRs in understanding the genetic basis of phenotypic traits and species survival.

6.2 Disease resistance and health

The genetic architecture of felids also includes adaptations that enhance disease resistance and overall health. The PRR genes, which are essential for innate immunity, show a high degree of conservation across different felid species. This conservation suggests that these genes are under strong selective pressure to maintain their function in recognizing and responding to pathogens (Smith et al., 2017). Moreover, the low levels of genetic diversity observed in felid populations, such as those of tigers, lions, and leopards, highlight their vulnerability to diseases and the importance of maintaining genetic health for conservation purposes (Leaniz et al., 2007).

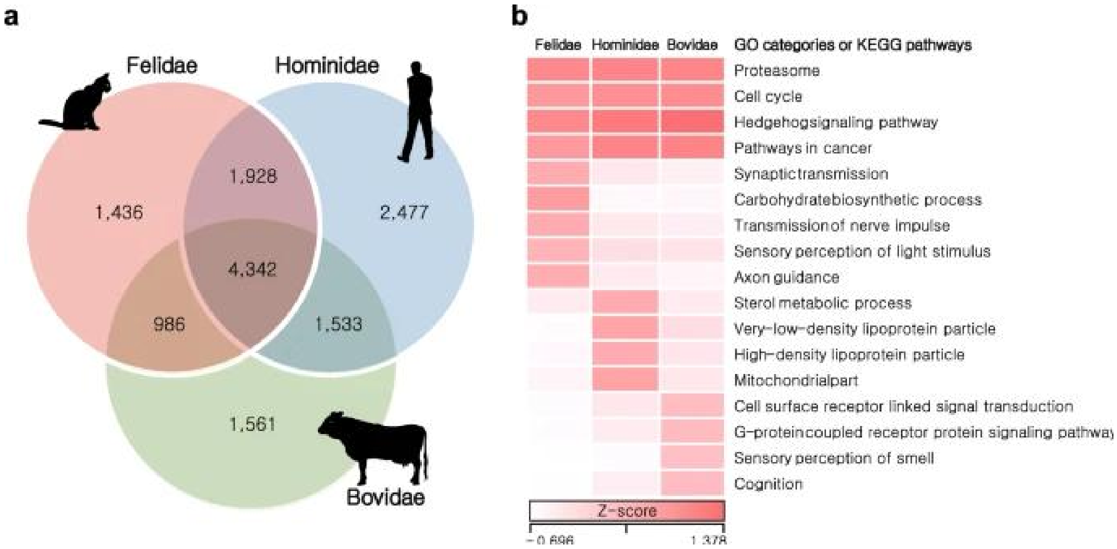

Figure 3 HCRs in *Felidae*, *Hominidae*, and *Bovidae* (Adapted from Kim et al., 2016)

Image caption: HCRs in the same family species were identified by calculating the ratios between numbers of conserved and non-conserved positions, a Venn diagrams of genes in the HCRs. b Heatmap of enriched gene ontology (GO) categories or KEGG pathways in the HCRs. Z-scores for the average fractions of homozygous positions are shown as a white-to-red color scale (Adapted from Kim et al., 2016)

6.3 Behavioral traits and genetics

Behavioral traits in felids are closely linked to their genetic makeup. For instance, genes associated with muscle strength and agility are crucial for hunting and meat consumption, which are key behavioral traits in carnivorous felids (Wu et al., 2022). These genetic traits not only influence their hunting efficiency but also their ability to adapt to different prey and hunting strategies. Additionally, the genetic evidence of low genetic diversity in felids suggests that their strict dietary requirements may limit their behavioral flexibility, making them more susceptible to environmental changes and human activities. In summary, the genomic traits of felids reflect their adaptations to various habitats, disease resistance mechanisms, and behavioral characteristics. These adaptations are crucial for their survival and highlight the importance of genetic diversity and conservation efforts to protect these species.

7 Threats to Felid Genomic Diversity

7.1 Habitat fragmentation and loss

Habitat fragmentation and loss are significant threats to the genomic diversity of felids. Fragmented landscapes can lead to isolated populations, reducing gene flow and increasing the risk of inbreeding. For instance, a study on jaguars, pumas, and ocelots in Belize demonstrated that habitat fragmentation has led to moderate levels of genetic differentiation among these species, with jaguars showing the lowest degree of genetic subdivision. Similarly, research on jungle cats in central India revealed that roads and human-dominated land-use negatively impact their movement, further fragmenting their habitats and reducing genetic connectivity (Tyagi et al., 2022). The importance of maintaining corridors and stepping stone habitat patches to facilitate movement and gene flow among fragmented populations is emphasized in conservation strategies (Ashrafzadeh et al., 2020).

7.2 Human-wildlife conflict

Human-wildlife conflict is another critical threat to felid genomic diversity. This conflict often results in direct killings, habitat destruction, and reduced prey availability, all of which can lead to population declines and genetic bottlenecks. For example, cheetahs are severely affected by human-wildlife conflict, with only approximately 7,100 individuals remaining in the wild. This has led to high inbreeding levels, particularly in the Critically Endangered Iranian and North-western subspecies, which exhibit the lowest genome-wide heterozygosity among big cats (Prost et al., 2022). The impact of human activities on felid populations underscores the need for effective conflict mitigation strategies to preserve their genetic diversity.

7.3 Climate change impacts

Climate change poses a significant threat to felid genomic diversity by altering habitats and affecting prey availability. Changes in temperature and precipitation patterns can lead to habitat shifts, forcing felids to move to new areas where they may face increased competition and reduced genetic diversity. A study on the genetic diversity of felids across different continents found that species in tropical regions, which are more vulnerable to climate change, have higher heterozygosity and allelic richness compared to those in non-tropical regions (Prost et al., 2022). This suggests that climate change could disproportionately impact felids in tropical areas, leading to a loss of genetic diversity. Additionally, the decline in prey species due to climate change can further threaten felid populations, as seen in the historical context of large-felid extinctions linked to prey loss (Sandom et al., 2018). In conclusion, habitat fragmentation and loss, human-wildlife conflict, and climate change are significant threats to the genomic diversity of felids. Addressing these threats through habitat conservation, conflict mitigation, and climate adaptation strategies is crucial for preserving the genetic diversity and long-term survival of these species.

8 Conservation Strategies Informed by Genomics

8.1 Breeding programs and genetic management

Genomic insights have significantly advanced our understanding of the genetic diversity and reproductive biology of felids, which is crucial for effective breeding programs and genetic management. Studies have shown that felids exhibit low levels of genetic diversity due to their strict dietary specializations and reduced population sizes, making them vulnerable to inbreeding and genetic drift (Ashrafzadeh et al., 2020). Conservation breeding programs must therefore prioritize maintaining and enhancing genetic diversity. Assisted reproductive technologies (ARTs), such as artificial insemination and embryo transfer, have been developed to overcome challenges in natural breeding and mitigate inbreeding. However, the success of these technologies is often limited by inconsistent responses to ovarian stimulation and variable quality of gametes and embryos, highlighting the need for further research and improvement in ARTs (Thongphakdee et al., 2020).

8.2 Habitat restoration and connectivity

Habitat loss and fragmentation are major threats to felid populations, necessitating strategies to restore and maintain habitat connectivity. Genomic studies have revealed the impact of landscape features on gene flow and genetic diversity among felid populations. For instance, roads and human-dominated land use negatively impact the movement of jungle cats, emphasizing the need for landscape-level management plans that consider multiple carnivore species. Additionally, maintaining corridors and stepping stone habitat patches along corridors is essential to facilitate the movement of individuals between fragmented habitats. Genetic monitoring of wild felids in fragmented landscapes has shown that while genetic diversity and gene flow are still relatively high, continued habitat loss and fragmentation could lead to decreased genetic connectivity (Knaus et al., 2011). Therefore, habitat restoration efforts should focus on creating and preserving corridors that enhance connectivity and support genetic exchange among populations.

8.3 Policy implications and recommendations

The integration of genomic data into conservation policies can provide more accurate and effective strategies for the preservation of felid species. Genomic analyses have identified priority species and populations that are particularly vulnerable to genetic diversity loss, such as the Asiatic lions and certain populations of fishers. These findings underscore the importance of targeted conservation efforts for these high-risk groups. Additionally, the use of whole-genome data rather than traditional genetic markers, such as the mitochondrial D-loop, can provide more reliable information for conservation decision-making (Wultsch et al., 2016). Policymakers should incorporate genomic data into wildlife management plans to ensure that conservation actions are based on the most accurate and comprehensive genetic information available. This approach will help to identify and protect critical habitats, enhance genetic diversity, and ultimately improve the long-term viability of felid populations. By leveraging genomic insights, conservation strategies can be more precisely tailored to address the specific needs and challenges faced by felid species, thereby enhancing their chances of survival in the wild (Allendorf, 2017).

9 Future Directions in Felid Genomics

9.1 Emerging technologies

The rapid advancement of sequencing technologies has significantly enhanced our ability to study felid genomics. Next-generation sequencing (NGS) and genotyping-by-sequencing (GBS) have enabled researchers to sample genomes more densely, providing deeper insights into genetic variation and evolutionary processes. These technologies have facilitated the generation of high-quality genome assemblies for various felid species, such as the leopard, which has allowed for comparative genomic analyses across different dietary specializations (Smith et al., 2017). Future research should focus on leveraging these technologies to sequence whole genomes of larger populations, which, although currently expensive, will become more feasible as costs decrease and computational methods improve. Additionally, the development of more sophisticated bioinformatic tools will be crucial for handling the vast amounts of data generated by these technologies (Vonholdt et al., 2018).

9.2 Integrating genomics with ecological data

Integrating genomic data with ecological and behavioral data is essential for a comprehensive understanding of felid conservation (Kim et al., 2017). Long-term field studies have provided valuable insights into the social systems, ecophysiology, and ecology of carnivores, which are critical for interpreting genomic data in a meaningful context. For instance, understanding the genetic basis of traits such as reproductive suppression and dispersal can inform conservation strategies aimed at maintaining genetic diversity and population viability. Moreover, combining genomic data with ecological information can help identify adaptive traits that are crucial for survival in changing environments (Narum et al., 2013). This integrative approach will enable more effective conservation management by providing a holistic view of the factors influencing felid populations (Primmer, 2009).

9.3 Long-term conservation goals

Long-term conservation goals for felids should prioritize maintaining genetic diversity and evolutionary potential. Genomic studies have revealed significant genetic erosion in endangered species like the Iberian lynx, highlighting the need for strategies that mitigate the effects of demographic bottlenecks and inbreeding. Conservation efforts should focus on preserving genetic diversity by facilitating gene flow between isolated populations and protecting habitats that support large, viable populations. Additionally, understanding the genetic architecture of adaptive traits can inform breeding programs and reintroduction efforts aimed at enhancing the resilience of felid populations to environmental changes (Harrisson et al., 2014). Ultimately, the integration of genomics into conservation planning will be essential for ensuring the long-term survival of felid species in the face of ongoing threats such as habitat loss and climate change (Azizan and Paradis, 2021).

10 Concluding Remarks

The comparative genomic studies of felids have provided significant insights into the evolutionary adaptations and conservation challenges faced by these carnivores. Key findings include the identification of shared evolutionary adaptations in genes associated with diet, muscle strength, and agility, which are crucial for hunting and meat consumption. Additionally, felids exhibit low levels of genetic diversity, likely due to their strict dietary requirements and reduced population sizes, making them vulnerable to environmental changes and human activities . The genomic erosion observed in endangered species like the Iberian lynx further highlights the critical conservation status of these animals. Studies have also revealed the importance of gut microbiomes in adapting to high purine and fat diets, which is a characteristic feature of carnivorous felids.

Genomic research plays a pivotal role in the conservation of felids by providing detailed insights into their genetic diversity, population structure, and evolutionary history. The identification of genetic markers and adaptive traits can inform conservation strategies aimed at enhancing genetic diversity and resilience in wild populations. For instance, understanding the genetic consequences of habitat fragmentation and human activities can help in planning wildlife corridors and other conservation measures. Moreover, the development of high-quality reference genomes and cross-species genome alignments can aid in the discovery of adaptive and deleterious alleles, which are essential for managing genetic health and disease in felid populations.

The integration of genomic data with long-term field studies and ecological research offers a comprehensive approach to understanding and conserving felid species. Future research should focus on expanding genomic resources for non-model species and developing cost-effective methods for genome sequencing and analysis. Additionally, there is a need for collaborative efforts to monitor genetic diversity and gene flow in fragmented landscapes, which are critical for the survival of felid populations in the face of ongoing environmental changes. By leveraging genomic insights, conservationists can develop more effective strategies to protect these iconic carnivores and ensure their long-term viability in the wild.

Acknowledgements

Author would like to thank the anonymous reviewers for their valuable feedback and constructive comments on the manuscript.

Conflict of Interest Disclosure

Author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Allendorf F., 2017, Genetics and the conservation of natural populations: allozymes to genomes, Molecular Ecology, 26(2): 420-430.
https://doi.org/10.1111/mec.13948
PMid:27933683

Allio R., Tilak M., Scornavacca C., Avenant N., Kitchener A., Corre E., Nabholz B., and Delsuc F., 2021, High-quality carnivoran genomes from roadkill samples enable comparative species delineation in aardwolf and bat-eared fox, Elife, 10: e63167.
https://doi.org/10.7554/eLife.63167
PMid:33599612 PMCid:PMC7963486

Ashrafzadeh M., Khosravi R., Adibi M., Taktehrani A., Wan H., and Cushman S., 2020, A multi-scale, multi-species approach for assessing effectiveness of habitat and connectivity conservation for endangered felids, Biological Conservation, 245: 108523.
https://doi.org/10.1016/j.biocon.2020.108523

Azizan A., and Paradis E., 2021, Patterns and drivers of genetic diversity among *Felidae* species, Biodiversity and Conservation, 30(2): 519-546.
https://doi.org/10.1007/s10531-020-02103-5

Baeza J., 2022, Mitochondrial genomes assembled from non-invasive eDNA metagenomic scat samples in the endangered Amur tiger *Panthera tigris altaica*, PeerJ, 10: e14428.
https://doi.org/10.7717/peerj.14428
PMid:36523460 PMCid:PMC9745948

Bashir S., Jayathangraj M., Afzal I., Bashir T., Sharmila B., and Sheikh T., 2020, Deciphering evolutionary history of three indian carnivore species: phylogenetic analysis using cytochrome b gene sequence of mitochondrial DNA, Journal of Entomology and Zoology Studies, 8: 117-121.

Corbo M., Damas J., Bursell M., and Lewin H., 2022, Conservation of chromatin conformation in carnivores, Proceedings of the National Academy of Sciences of the United States of America, 119(9): e2120555119.
https://doi.org/10.1073/pnas.2120555119
PMid:35217621 PMCid:PMC8892538

Fan H., Hu Y., Wu Q., Nie Y., Yan L., and Wei F., 2018, Conservation genetics and genomics of threatened vertebrates in China, Journal of Genetics and Genomics, 45(11): 593-601.
https://doi.org/10.1016/j.jgg.2018.09.005
PMid:30455039

Feller A., and Seehausen O., 2022, Genetic architecture of adaptive radiation across two trophic levels, Proceedings of the Royal Society B, 289(1974): 20220377.
https://doi.org/10.1098/rspb.2022.0377
PMid:35506225 PMCid:PMC9065965

Harrisson K., Pavlova A., Telonis-Scott M., and Sunnucks P., 2014, Using genomics to characterize evolutionary potential for conservation of wild populations, Evolutionary Applications, 7(9): 1008-1025.
https://doi.org/10.1111/eva.12149
PMid:25553064 PMCid:PMC4231592

Hassanin A., Veron G., Ropiquet A., Vuuren B., Lécu A., Goodman S., Haider J., and Nguyen T., 2021, Evolutionary history of Carnivora (Mammalia, Laurasiatheria) inferred from mitochondrial genomes, PLoS ONE, 16(2): e0240770.
https://doi.org/10.1371/journal.pone.0240770
PMid:33591975 PMCid:PMC7886153

Johnson W., and Koepfli K., 2014, The role of genomics in conservation and reproductive sciences, Advances in experimental medicine and biology, 753: 71-96
https://doi.org/10.1007/978-1-4939-0820-2_5
PMid:25091907

Johnson W., Eizirik E., Pecon-Slattery J., Murphy W., Antunes A., Teeling E., and O'Brien S., 2006, The late miocene radiation of modern *Felidae*: a genetic assessment, Science, 311(5757): 73-77.
https://doi.org/10.1126/science.1122277
PMid:16400146

Kim S., Cho Y., Bhak J., O'Brian S., and Yeo J., 2017, Perspectives provided by leopard and other cat genomes: how diet determined the evolutionary history of carnivores, omnivores, and herbivores, BMB Reports, 50(1): 3-4.
https://doi.org/10.5483/BMBRep.2017.50.1.002
PMid:28042784 PMCid:PMC5319657

Kim S., Cho Y., Kim H., Chung O., Kim H., Jho S., Seomun H., Kim J., Bang W., Kim C., An J., Bae C., Bhak Y., Jeon S., Yoon H., Kim Y., Jun J., Lee H., Cho S., Uphyrkina O., Kostyria A., Goodrich J., Miquelle D., Roelke M., Lewis J., Yurchenko A., Bankevich A., Cho J., Lee S., Edwards J., Weber J., Cook J., Kim S., Lee H., Manica A., Lee I., O'Brien S., Bhak J., and Yeo J., 2016, Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly, Genome Biology, 17: 1-12.
https://doi.org/10.1186/s13059-016-1071-4
PMid:27802837 PMCid:PMC5090899

Knaus B., Cronn R., Liston A., Pilgrim K., and Schwartz M., 2011, Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore, BMC Ecology, 11: 1-14.
https://doi.org/10.1186/1472-6785-11-10
PMid:21507265 PMCid:PMC3108907

Leaniz C., Fleming I., Einum S., Verspoor E., Jordan W., Consuegra S., Aubin-Horth N., Lajus D., Letcher B., Youngson A., Webb J., Vøllestad L., Villanueva B., Ferguson A., and Quinn T., 2007, A critical review of adaptive genetic variation in Atlantic salmon: implications for conservation, Biological Reviews, 82(2): 173-211.
https://doi.org/10.1111/j.1469-185X.2006.00004.x
PMid:17437557

Narum S., Buerkle C., Davey J., Miller M., and Hohenlohe P., 2013, Genotyping-by-sequencing in ecological and conservation genomics, Molecular Ecology, 22(11): 2841.
https://doi.org/10.1111/mec.12350
PMid:23711105 PMCid:PMC3935057

Poust A., Barrett P., and Tomiya S., 2022, An early nimravid from California and the rise of hypercarnivorous mammals after the middle Eocene climatic optimum, Biology Letters, 18(10): 20220291.
https://doi.org/10.1098/rsbl.2022.0291
PMCid:PMC9554728

Primmer C., 2009, From conservation genetics to conservation genomics, Annals of the New York Academy of Sciences, 1162(1): 357-368.
https://doi.org/10.1111/j.1749-6632.2009.04444.x
PMid:19432656

Prost S., Machado A., Zumbroich J., Preier L., Mahtani-Williams S., Meissner R., Guschanski K., Brealey J., Fernandes C., Vercammen P., Hunter L., Abramov A., Plasil M., Horin P., Godsall-Bottriell L., Bottriell P., Dalton D., Kotzé A., and Burger P., 2022, Genomic analyses show extremely perilous conservation status of African and Asiatic cheetahs (*Acinonyx jubatus*), Molecular Ecology, 31(16): 4208-4223.
https://doi.org/10.1111/mec.16577
PMid:35748392 PMCid:PMC9540975

Samaha G., Wade C., Mazrier H., Grueber C., and Haase B., 2021, Exploiting genomic synteny in *Felidae*: cross-species genome alignments and SNV discovery can aid conservation management, BMC Genomics, 22: 1-13.
https://doi.org/10.1186/s12864-021-07899-2
PMid:34362297 PMCid:PMC8348863

Sandom C., Faurby S., Svenning J., Burnham D., Dickman A., Hinks A., Macdonald E., Ripple W., Williams J., and Macdonald D., 2018, Learning from the past to prepare for the future: felids face continued threat from declining prey, Ecography, 41(1): 140-152.
https://doi.org/10.1111/ecog.03303

Shukla H., Suryamohan K., Khan A., Mohan K., Perumal R., Mathew O., Menon R., Dixon M., Muraleedharan M., Kuriakose B., Michael S., Krishnankutty S., Zachariah A., Seshagiri S., and Ramakrishnan U., 2022, Near-chromosomal *de novo* assembly of Bengal tiger genome reveals genetic hallmarks of apex predation, GigaScience, 12: giac112.
https://doi.org/10.1101/2022.05.14.491975

Singh G., Srinivas Y., Kumar G., Singh A., Sharma C., and Gupta S., 2020, Identification of selected wild felids using hair morphology and forensically informative nucleotide sequencing (FINS): wildlife forensics prospective, Legal medicine, 44: 101692.
https://doi.org/10.1016/j.legalmed.2020.101692
PMid:32208347

Smith J., Lehmann K., Montgomery T., Strauss E., and Holekamp K., 2017, Insights from long-term field studies of mammalian carnivores, Journal of Mammalogy, 98(3): 631-641.
https://doi.org/10.1093/jmammal/gyw194

Thongphakdee A., Sukparangsi W., Comizzoli P., and Chatdarong K., 2020, Reproductive biology and biotechnologies in wild felids, Theriogenology, 150: 360-373.
https://doi.org/10.1016/j.theriogenology.2020.02.004
PMid:32102745

Tyagi A., Khan A., Thatte P., and Ramakrishnan U., 2022, Genome-wide single nucleotide polymorphism (SNP) markers from fecal samples reveal anthropogenic impacts on connectivity: case of a small carnivore in the central Indian landscape, Animal Conservation, 25(5): 648-659.
https://doi.org/10.1111/acv.12770

Vonholdt B., Brzeski K., Wilcove D., and Rutledge L., 2018, Redefining the role of admixture and genomics in species conservation, Conservation Letters, 11(2): e12371.
https://doi.org/10.1111/conl.12371

Wu X., Chen J., Wang X., Shang Y., Wei Q., and Zhang H., 2022, Evolutionary impacts of pattern recognition receptor genes on carnivora complex habitat stress adaptation, Animals, 12(23): 3331.
https://doi.org/10.3390/ani12233331
PMid:36496853 PMCid:PMC9739989

Wultsch C., Waits L., and Kelly M., 2016, A comparative analysis of genetic diversity and structure in jaguars (*Panthera onca*), pumas (*Puma concolor*), and ocelots (*Leopardus pardalis*) in fragmented landscapes of a critical mesoamerican linkage zone, PLoS ONE, 11(3): e0151043.
https://doi.org/10.1371/journal.pone.0151043
PMid:26974968 PMCid:PMC4790928