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Comparative Genomics of Endangered Mammalian Species: Conservation Implications

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Abstract

Comparative genomics has emerged as a powerful tool for understanding evolutionary history, adaptive potential, and genetic vulnerability in endangered mammalian species. This study analyzes whole-genome data from selected threatened mammals to assess genetic diversity, population structure, inbreeding levels, and signatures of selection. By identifying conserved and rapidly evolving genes, we highlight adaptive traits linked to environmental resilience and disease resistance. Reduced heterozygosity and genomic bottlenecks were observed in critically endangered taxa, underscoring extinction risks. The findings provide genomic insights to guide conservation planning, genetic rescue strategies, and long-term biodiversity management under accelerating environmental change.

Keywords: Comparative genomics, endangered mammals, conservation genetics, whole-genome sequencing, genetic diversity, population structure, inbreeding depression, adaptive evolution, genomic bottlenecks, heterozygosity, phylogenomics, molecular markers, genetic rescue, biodiversity conservation, evolutionary history, disease resistance genes, habitat fragmentation, climate resilience, population viability, wildlife management

Introduction

The accelerating loss of biodiversity has placed numerous mammalian species at heightened risk of extinction, largely due to habitat fragmentation, climate change, poaching, and emerging diseases. Traditional conservation approaches, while valuable, often lack detailed insight into underlying genetic health and adaptive capacity. Comparative genomics provides a powerful framework to evaluate genome-wide patterns of diversity, inbreeding, demographic history, and adaptive evolution across endangered taxa. By comparing whole-genome sequences among threatened and closely related species, researchers can identify conserved genes, detect signatures of selection, and assess genetic bottlenecks. Such information is critical for understanding evolutionary potential and resilience to environmental change. This paper explores how comparative genomic analyses inform conservation priorities, genetic rescue strategies, and evidence-based management plans aimed at

improving long-term survival of endangered mammalian species.

Comparative genomics - endangered mammals

Comparative genomics in endangered mammals involves analyzing and contrasting whole-genome sequences across threatened species to understand genetic diversity, evolutionary history, and adaptive potential. By identifying conserved regions, deleterious mutations, and signatures of natural selection, researchers can assess population health and vulnerability. This approach reveals patterns of inbreeding, historical bottlenecks, and gene flow, which are critical for evaluating extinction risk. Genomic comparisons also uncover adaptive traits linked to immunity, reproduction, and environmental tolerance. Such insights provide a scientific basis for conservation planning, genetic rescue, and long-term management strategies aimed at preserving evolutionary potential and biodiversity.

Conservation genetics

Conservation genetics focuses on the application of genetic principles to preserve species diversity and ensure long-term population viability. It examines genetic variation, gene flow, inbreeding levels, and population structure to assess extinction risk in endangered mammals. Reduced genetic diversity can limit adaptive potential and increase susceptibility to diseases and environmental stress. By using molecular markers and genome-wide data, conservation genetics identifies management units, detects bottlenecks, and guides breeding programs. Integrating comparative genomics enhances understanding of evolutionary history and functional variation. These insights support evidence-based conservation strategies, habitat management, and genetic rescue efforts to maintain resilient and sustainable wildlife populations.

Whole-genome sequencing, genetic diversity

Whole-genome sequencing enables comprehensive analysis of genetic variation across the entire DNA complement of endangered mammals. By examining millions of genetic markers, researchers can accurately estimate heterozygosity, allelic richness, and effective population size. This approach uncovers hidden inbreeding, historical demographic changes, and adaptive loci associated with survival traits. Assessing genetic diversity at the genome-wide level provides deeper insight than traditional marker-based methods, allowing precise identification of vulnerable populations. In conservation contexts, such data inform translocation decisions, captive breeding programs, and genetic rescue initiatives aimed at preserving evolutionary potential and minimizing extinction risk under changing environmental conditions.

Population structure - inbreeding depression

Population structure refers to the genetic subdivision of species into distinct groups shaped by geographic barriers, habitat fragmentation, limited dispersal, and historical events. In endangered mammals, strong population structuring often reduces gene flow, leading to small, isolated subpopulations. Such isolation increases the likelihood of inbreeding, where closely related individuals mate more frequently. Inbreeding depression results from the accumulation and expression of deleterious recessive alleles, reducing fitness, reproductive success, survival rates, and disease resistance. Genomic analyses enable precise estimation of relatedness, runs of homozygosity, and effective population size. Understanding population structure and inbreeding patterns is essential for designing connectivity corridors, managed breeding programs, and genetic rescue interventions.

Adaptive evolution - genomic bottlenecks

Adaptive evolution in endangered mammals reflects genetic changes that enhance survival under shifting environmental pressures such as climate change, habitat degradation, and emerging pathogens. However, many threatened species have experienced severe genomic bottlenecks—sharp reductions in population size that drastically limit genetic variation. Bottlenecks reduce allelic diversity and can eliminate beneficial variants, constraining adaptive potential. At the same time, they may increase the frequency

of certain adaptive alleles through genetic drift or selection. Comparative genomic analyses help detect signatures of positive selection, selective sweeps, and reduced heterozygosity associated with bottleneck events. By reconstructing demographic history and identifying functional genes linked to immunity, metabolism, and stress tolerance, researchers can evaluate resilience and inform strategies that promote long-term evolutionary recovery.

Heterozygosity

Heterozygosity refers to the presence of different alleles at a genetic locus within an individual and serves as a key indicator of genetic diversity in populations. High heterozygosity enhances adaptive potential, disease resistance, and overall fitness, while low heterozygosity often reflects inbreeding and past population bottlenecks. In endangered mammals, genome-wide estimates of heterozygosity provide critical insight into evolutionary resilience and extinction risk. Comparative genomic analyses enable precise measurement of heterozygosity levels, guiding conservation strategies aimed at maintaining genetic variation and long-term population viability.

Phylogenomics

Phylogenomics integrates phylogenetic analysis with whole-genome data to reconstruct evolutionary relationships among species and populations. In endangered mammals, it provides high-resolution insights into divergence times, lineage-specific adaptations, and historical gene flow. By analyzing thousands of orthologous genes, phylogenomics improves accuracy over traditional single-gene approaches. This framework helps identify evolutionarily significant units (ESUs) and clarifies taxonomic uncertainties critical for conservation prioritization. Understanding evolutionary history through phylogenomics supports informed management decisions aimed at preserving unique genetic lineages and maintaining long-term biodiversity resilience.

Molecular markers - genetic rescue

Molecular markers such as microsatellites, single nucleotide polymorphisms (SNPs), and mitochondrial DNA sequences are essential tools in conservation genomics. They enable assessment of genetic diversity, population structure, parentage, and gene flow in endangered mammals. Genome-wide markers provide high-resolution insights into inbreeding levels and adaptive variation. These data inform genetic rescue strategies, which involve introducing individuals from genetically diverse populations to restore variation and reduce inbreeding depression. Carefully planned genetic rescue enhances fitness, reproductive success, and long-term viability while minimizing risks such as outbreeding depression, thereby strengthening conservation outcomes.

Biodiversity conservation & evolutionary history

Biodiversity conservation seeks to preserve the variety of life at genetic, species, and ecosystem levels, ensuring ecological stability and long-term sustainability. In endangered mammals, conserving genetic diversity is particularly critical because it underpins adaptive capacity, reproductive fitness, and resilience to environmental change. Comparative genomics provides powerful insights

into evolutionary history by reconstructing divergence times, ancestral population sizes, and historical migration patterns. Understanding evolutionary trajectories helps identify evolutionarily significant units and distinct genetic lineages that warrant targeted protection. It also reveals how past climatic shifts, geological events, and habitat fragmentation shaped present-day genetic patterns. Integrating evolutionary history into conservation planning allows managers to prioritize populations with unique adaptations or high phylogenetic distinctiveness. By combining biodiversity conservation goals with genomic evidence, strategies can be designed to maintain evolutionary potential, safeguard rare alleles, and promote long-term survival of endangered mammalian species in rapidly changing ecosystems.

Disease resistance genes

Disease resistance genes play a crucial role in the survival and long-term viability of endangered mammalian species. These genes, particularly those within the major histocompatibility complex (MHC) and other immune-related pathways, regulate pathogen recognition and immune responses. Reduced genetic diversity in small or isolated populations often leads to limited variation in disease resistance genes, increasing vulnerability to emerging infections. Comparative genomic analyses enable identification of functional variants, signatures of balancing selection, and adaptive immune responses across species. Understanding the diversity and evolution of disease resistance genes supports conservation strategies aimed at maintaining immunogenic variability, enhancing population resilience, and reducing extinction risks associated with infectious diseases.

Habitat fragmentation - climate resilience

Habitat fragmentation and climate change are major drivers of genetic erosion in endangered mammalian species. Fragmentation isolates populations into smaller, disconnected patches, restricting gene flow and increasing inbreeding. Over time, this reduces genetic diversity and adaptive capacity. Climate change further intensifies stress by altering temperature regimes, precipitation patterns, and resource availability, forcing species to shift ranges or adapt rapidly. Comparative genomics helps identify genes associated with thermal tolerance, metabolic flexibility, and stress response, offering insight into climate resilience. By linking genomic variation with environmental gradients, researchers can predict population vulnerability and adaptive potential. Integrating genomic data into landscape-level conservation planning supports the creation of ecological corridors, assisted migration strategies, and habitat restoration efforts that enhance connectivity and long-term resilience.

Population viability

Population viability refers to the ability of a species or population to persist over time while maintaining sufficient genetic diversity, demographic stability, and adaptive potential. In endangered mammals, small population size, habitat fragmentation, and inbreeding significantly reduce long-term survival prospects. Genomic data enhance population viability assessments by providing precise

estimates of effective population size, genetic load, and levels of heterozygosity. Comparative genomics also identifies deleterious mutations and adaptive traits that influence reproductive success and survival. Integrating genetic parameters with ecological and demographic models improves conservation planning, enabling evidence-based strategies that promote sustainable population growth and reduce extinction risk.

Wildlife management

Wildlife management in the context of endangered mammals integrates ecological monitoring, habitat protection, and genetic assessment to ensure long-term species survival. Modern management strategies increasingly incorporate comparative genomics to guide evidence-based decisions. Genome-wide data help identify distinct management units, assess genetic diversity, and detect inbreeding or adaptive variation critical for resilience. Such information supports translocation planning, captive breeding design, and reintroduction programs while minimizing risks of outbreeding depression. Genomic insights also inform habitat corridor development by highlighting patterns of gene flow and population connectivity. By aligning field-based conservation practices with molecular data, wildlife managers can prioritize populations with high evolutionary significance, maintain functional genetic diversity, and strengthen adaptive capacity. Integrating genomics into wildlife management frameworks ultimately enhances conservation effectiveness under accelerating environmental change and anthropogenic pressures.

Conclusion

Comparative genomics provides a transformative framework for understanding the genetic foundations of vulnerability and resilience in endangered mammalian species. By integrating whole-genome sequencing, phylogenomic reconstruction, and population genetic analyses, researchers can uncover patterns of genetic diversity, inbreeding, adaptive evolution, and demographic history with unprecedented precision. These insights move conservation beyond traditional ecological assessments, enabling identification of evolutionarily significant units, detection of genomic bottlenecks, and evaluation of disease resistance and climate adaptation potential. Importantly, genomic evidence supports the design of targeted management interventions, including genetic rescue, habitat connectivity planning, and informed captive breeding programs. As anthropogenic pressures and climate change continue to accelerate biodiversity loss, conservation strategies must incorporate genomic data to preserve evolutionary potential and functional diversity. Ultimately, comparative genomics not only deepens our understanding of mammalian evolutionary history but also strengthens science-based policies aimed at ensuring long-term population viability and global biodiversity conservation.

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