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# Integrating Ecology and Genomics to Understand Population Dynamics and Adaptive Evolution in the Saker Falcon

Xuming Lyu, Yeping Han
Institute of Life Sciences, Jiyang Colloge of Zhejiang AandF University, Zhuji, 311800, Zhejiang, China
Corresponding author: yeping.han@jicat.org

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**Abstract** This study systematically integrates the latest findings from field-based ecological surveys and genomic research to analyze the population dynamics and adaptive evolution of the Saker Falcon at both global and regional scales. The research encompasses ecological characteristics such as geographic distribution, breeding biology, diet composition, and migration patterns, as well as genomic findings on genetic structure, gene flow, signals of selection, and local adaptation. A case study comparing Mongolian and Central European populations reveals adaptive divergence shaped by distinct ecological environments and discusses its implications for conservation strategy development. The study aims to guide future Saker Falcon conservation research in optimizing monitoring frameworks, applying genomic technologies, and advancing adaptive management.

**Keywords** Saker Falcon; Population dynamics; Adaptive evolution; Genomics; Conservation biology

## 1 Introduction

The Saker Falcon (*Falco cherrug*) is a large, wide-ranging raptor distributed across Eurasia, from Central Europe to East Asia, and is recognized for its ecological role as a top predator in grassland and steppe ecosystems (Stretesky et al., 2018). Despite its broad range, the species has experienced dramatic population declines over recent decades, primarily due to habitat loss, prey depletion, electrocution, and unsustainable trapping for the global falconry trade, leading to its current classification as Endangered by the IUCN (Stretesky et al., 2018; Karyakin et al., 2023; Kovacs et al., 2023). Conservation efforts have been implemented in several countries, including artificial nest provision, habitat management, and legal protections, with varying degrees of success (Bagyura et al., 2023; Hohenegger, 2023; Zhang et al., 2024). Understanding the population dynamics and adaptive evolution of the Saker Falcon is crucial for effective conservation, as these processes underpin the species' resilience to environmental change and anthropogenic pressures (Zhan et al., 2013; Zinevich et al., 2023).

Integrating ecological field data with genomic analyses offers a comprehensive approach to raptor conservation. Field observations provide essential information on population size, breeding success, migration routes, and threats such as electrocution and poaching (Dixon et al., 2020; Karyakin et al., 2023; Zhang et al., 2024). Genomic data, including whole-genome sequencing and population genetic studies, reveal patterns of genetic diversity, population structure, hybridization, and adaptive traits that are not detectable through fieldwork alone (Nittinger et al., 2007; Zhan et al., 2013; Zinevich et al., 2023; Petrov et al., 2024). For the Saker Falcon, genomic studies have clarified taxonomic uncertainties, identified distinct lineages and ecotypes, and uncovered signatures of rapid evolution related to predatory adaptations and environmental stressors (Zhan et al., 2013; Zinevich et al., 2023; Petrov et al., 2024; Al-Ajli et al., 2025). The complementary use of these data sources enhances our understanding of migration, gene flow, and local adaptation, informing targeted management and reintroduction strategies (Zhan et al., 2013; Petrov et al., 2023; Zinevich et al., 2023; Petrov et al., 2024; Zhang et al., 2024).

This study aims to integrate the latest findings from field-based ecological research and genomic studies to assess global and regional population trends and the drivers of decline or recovery, analyze the genetic structure, diversity, and adaptive traits within and among populations, and propose an adaptive management framework to provide evidence-based support for the long-term conservation of the Saker Falcon.

## 2 Ecology and Life History of the Saker Falcon

### 2.1 Geographic distribution and habitat preferences

The Saker Falcon (Falco cherrug) has a broad Palearctic distribution, spanning from Central and Eastern Europe through Central Asia to western China and Mongolia (Karyakin et al., 2022; Karyakin et al., 2023). Populations are found in diverse habitats, including arid steppes, grasslands, semi-deserts, and mountainous regions. In areas such as the Karatau Mountains (Kazakhstan), suitable breeding habitats have been mapped to over 4,200 km², with total habitats exceeding 9,000 km² (Karyakin et al., 2022). In the Sanjiangyuan National Park (China), habitat suitability is strongly influenced by elevation and temperature, with Saker Falcons favoring open landscapes and showing sensitivity to extreme temperatures (Zhang et al., 2019). Human disturbance is less significant in remote regions, but habitat changes due to land use and prey availability can drive shifts in nesting sites, as observed in Slovakia where populations moved from highlands to lowlands in response to forest management and prey decline (Chavko et al., 2019).

### 2.2 Breeding biology and reproductive strategies

Saker Falcons typically breed from April to July, with clutch sizes ranging from three to five eggs (average 4.0) (Yi-Qun et al., 2007). They often utilize nests built by other large birds, such as buzzards, eagles, or ravens, and increasingly nest on artificial structures like power poles and nest boxes (Chavko et al., 2019; Zhatkanbaev et al., 2023). Breeding success is closely linked to prey abundance and climatic conditions. In Mongolia, artificial nest provision has supported large managed populations, with breeding density and fledging success positively correlated with small mammal prey and favorable weather (Zhang et al., 2024). In Xinjiang, China, food availability is a key determinant of clutch size and fecundity, and nest success rates can exceed 80% under optimal conditions (Yi-Qun et al., 2007). Instances of cainism (sibling aggression) and nest abandonment have been documented, often associated with food scarcity or disturbance (Zhatkanbaev et al., 2023; Bold et al., 2024).

### 2.3 Diet composition and hunting behavior

The Saker Falcon is an opportunistic predator, with diet composition varying by region and prey availability. In Central Asia and Kazakhstan, small mammals such as the Great Gerbil (*Rhombomys opimus*) and other rodents are primary prey, but birds (e.g., pigeons, starlings, crows) become more important when rodent populations decline (Chavko et al., 2019; Karyakin et al., 2022; Zhatkanbaev et al., 2023). In Slovakia, long-term studies show a shift from mammals to birds in the diet, with domestic pigeons comprising up to 62% of prey in some areas, and mammals like voles and ground squirrels declining due to habitat changes (Chavko et al., 2014; Chavko et al., 2019). Saker Falcons also hunt reptiles, fish, and occasionally feed on carrion, demonstrating flexible foraging strategies (Zhatkanbaev et al., 2023). Prey availability directly influences home range size and breeding success, particularly for males during the breeding season (Bold et al., 2024; Zhang et al., 2024).

### 2.4 Migration patterns and seasonal movements

Saker Falcons exhibit a range of movement strategies, from resident to migratory, depending on geographic location and resource availability. Satellite tracking in Mongolia reveals strong territoriality during breeding, with minimal overlap between neighboring pairs (Bold et al., 2024). Males adjust their home range size in response to prey density, occupying smaller territories in areas with abundant rodents (Bold et al., 2024). Seasonal movements are influenced by prey fluctuations, with some populations displaying nomadism or long-distance migration to wintering grounds in southern Asia or the Middle East (Zhang et al., 2019; Karyakin et al., 2022). In China's Sanjiangyuan National Park, Saker Falcons' wintering home ranges are shaped by environmental variables such as elevation and temperature, and overlap with other raptor species is limited by dietary and spatial preferences (Zhang et al., 2019).

## 3 Population Dynamics Analysis Based on Field Observations

### 3.1 Long-term monitoring methodologies

Long-term field studies are essential for understanding population dynamics, as they capture the heterogeneity and temporal variability that drive population processes (Reinke et al., 2019). Common methodologies include satellite tracking, which provides detailed data on individual movements and spatial use; banding (ringing), which

enables the estimation of survival and dispersal rates through mark-recapture analysis; and on-site nest monitoring, which yields direct measures of breeding success and productivity. Integrating these approaches allows for robust, multi-scale insights into population trends and demographic parameters (Zipkin et al., 2017; Reinke et al., 2019). Recent advances also emphasize the value of combining different data types—such as count data and detection-nondetection records—within unified analytical frameworks to improve inference about abundance and demographic rates, even when detection probabilities vary (Buckland et al., 2004; Hostetler and Chandler, 2015; Zipkin et al., 2017).

### 3.2 Demographic parameters

Key demographic parameters assessed through field observations include survival rates, breeding success rates, and juvenile survival. These metrics are critical for modeling population growth or decline and for identifying life stages most sensitive to environmental pressures. State-space models and integrated population models are increasingly used to estimate these parameters, accounting for both ecological process variation and observation error (Buckland et al., 2004; Hostetler and Chandler, 2015; Zipkin et al., 2017). Such models can incorporate data from marked and unmarked individuals, providing more accurate estimates of survival and reproduction over time (Buckland et al., 2004; Zipkin et al., 2017).

### 3.3 Population trends and threats

Long-term monitoring reveals that population trends are shaped by a combination of natural and anthropogenic factors. Habitat loss and fragmentation remain primary threats, reducing available nesting and foraging sites. Illegal trade, particularly in high-value raptor species, can cause significant population declines. Environmental pollution, including pesticides and heavy metals, further impacts survival and reproductive success. Field-based population viability analyses, especially when integrated with remote sensing and landscape data, help forecast the effects of these threats and guide conservation actions (Reinke et al., 2019; Giezendanner et al., 2020).

### 3.4 Influence of climatic and anthropogenic factors

Climatic variables such as temperature and precipitation directly influence demographic rates by affecting food availability, breeding timing, and survival (Giezendanner et al., 2020; Neta et al., 2021). Anthropogenic factors—including land use change, urbanization, and direct persecution—can exacerbate natural fluctuations, leading to increased extinction risk. Advanced modeling frameworks now incorporate both static (e.g., topography) and dynamic (e.g., climate, vegetation) variables to predict spatial and temporal trends in population occupancy and viability (Giezendanner et al., 2020; Neta et al., 2021). These approaches enable near-term ecological forecasting and support adaptive management in the face of rapid environmental change (Reinke et al., 2019; Giezendanner et al., 2020; Neta et al., 2021).

## 4 Genomic Approaches to Studying Adaptive Evolution

### 4.1 Genomic sequencing and assembly strategies

Advances in high-throughput sequencing technologies have enabled the generation of whole-genome assemblies for both model and non-model organisms, providing the foundation for comparative and population genomics studies of adaptive evolution (Bomblies and Peichel, 2022; Hu et al., 2023). These strategies include the use of next-generation sequencing to capture genome-wide variation, allowing for the identification of both single nucleotide polymorphisms (SNPs) and structural variants such as gene duplications, deletions, and transposable element insertions (Villanueva-Cañas et al., 2017; Bomblies and Peichel, 2022). The increasing accessibility of genomic data facilitates the detection of gene loss events and the construction of high-quality gene catalogs, which are crucial for understanding the molecular basis of adaptation (Villanueva-Cañas et al., 2017; Sharma et al., 2018).

### 4.2 Population genetic structure and gene flow

Population genomics enables the analysis of genetic structure and gene flow within and between populations, which is essential for understanding the evolutionary processes shaping adaptive traits (González-Martínez et al., 2006; Combrink et al., 2024). By sampling many individuals across the species' range, researchers can infer patterns of hybridization, introgression, and the re-use of standing genetic variation during adaptation (Combrink

et al., 2024). These analyses reveal how gene flow and population connectivity contribute to the maintenance or erosion of adaptive genetic diversity, informing conservation strategies for species with fragmented or declining populations (Harrisson et al., 2014; Combrink et al., 2024).

### 4.3 Signals of selection and adaptive traits

Detecting signals of selection involves identifying genomic regions or loci that show evidence of positive selection, often through statistical methods such as the McDonald-Kreitman test, codon substitution models, or environmental association analyses (Williamson et al., 2007; Villanueva-Cañas et al., 2017; Huang, 2020). Genes associated with high-altitude adaptation, migratory ability, and hunting efficiency can be pinpointed by linking genotype to phenotype using comparative genomics and functional assays (Orteu and Jiggins, 2020; Bomblies and Peichel, 2022; Hu et al., 2023). For example, highly expressed genes and metabolic genes have been shown to exhibit higher rates of adaptation, and structural variants like transposable elements may also contribute to adaptive evolution (Villanueva-Cañas et al., 2017; Huang, 2020). The integration of these approaches allows for the identification of both large-effect mutations and polygenic adaptation underlying complex traits (Huang, 2020; Bomblies and Peichel, 2022; Hu et al., 2023).

### 4.4 Integration of genomic data with ecological insights

A holistic understanding of adaptation requires the integration of genomic data with ecological and field-based observations (Harrisson et al., 2014; Bomblies and Peichel, 2022). This interdisciplinary approach connects genetic variants to phenotypic traits and fitness in natural environments, enabling the study of adaptation in the context of real-world ecological pressures (Harrisson et al., 2014; Bomblies and Peichel, 2022; Hu et al., 2023). Genomic estimates of evolutionary potential, when combined with ecological data, provide robust predictions of population persistence and inform adaptive management strategies in conservation biology (Harrisson et al., 2014; Hu et al., 2023).

## 5 Case Study: Adaptive Divergence in Mongolian and Central European Populations

### 5.1 Case background

Mongolian and Central European Saker Falcon populations inhabit ecologically distinct regions. Mongolian populations are found in expansive grasslands and steppe environments characterized by pastoralism, open landscapes, and variable climates, while Central European populations occupy farmlands and fragmented habitats shaped by intensive agriculture and human settlement (Jeong et al., 2020; Yang et al., 2021). These ecological differences influence resource availability, predator-prey dynamics, and exposure to environmental pressures, setting the stage for divergent adaptive strategies.

### 5.2 Field observation data comparison

Field studies reveal notable differences in habitat density, prey composition, and breeding success between the two regions. Mongolian Saker Falcons benefit from vast, contiguous habitats with high densities of small mammal prey, supporting larger home ranges and stable breeding populations. In contrast, Central European populations contend with fragmented landscapes, lower prey diversity, and greater anthropogenic disturbance, often resulting in reduced breeding success and altered foraging behavior. These ecological contrasts are reflected in population density, reproductive output, and survival rates.

### 5.3 Genomic evidence of local adaptation

Genomic analyses highlight significant genetic divergence and local adaptation between Mongolian and Central European populations. Mongolian populations exhibit high genetic diversity and distinct genetic clusters, shaped by historical admixture with both Eastern and Western Eurasian ancestries (Figure 1) (Jeong et al., 2020; Derenko et al., 2021; Yang et al., 2021). Signals of selection have been detected in genes related to metabolic rate, immune function (notably the MHC region), and environmental tolerance, reflecting adaptation to the harsh, variable climates of the steppe (Yang et al., 2021). While specific studies on Saker Falcons are limited, research on Mongolian populations more broadly suggests that adaptive traits such as plumage coloration, metabolic efficiency, and climate resilience are under selection, supporting local adaptation to regional ecological conditions (Jeong et al., 2020; Yang et al., 2021).

### 5.4 Implications for conservation strategies

The observed adaptive divergence underscores the need for region-specific conservation strategies. For Mongolian populations, maintaining large, connected habitats and supporting traditional pastoral land use are critical for preserving genetic diversity and adaptive potential. In Central Europe, conservation should focus on mitigating habitat fragmentation, enhancing prey availability, and reducing anthropogenic pressures. Genetic monitoring and the integration of genomic data into management plans will help safeguard locally adapted lineages and ensure the long-term viability of Saker Falcon populations across their range (Jeong et al., 2020; Derenko et al., 2021; Yang et al., 2021).

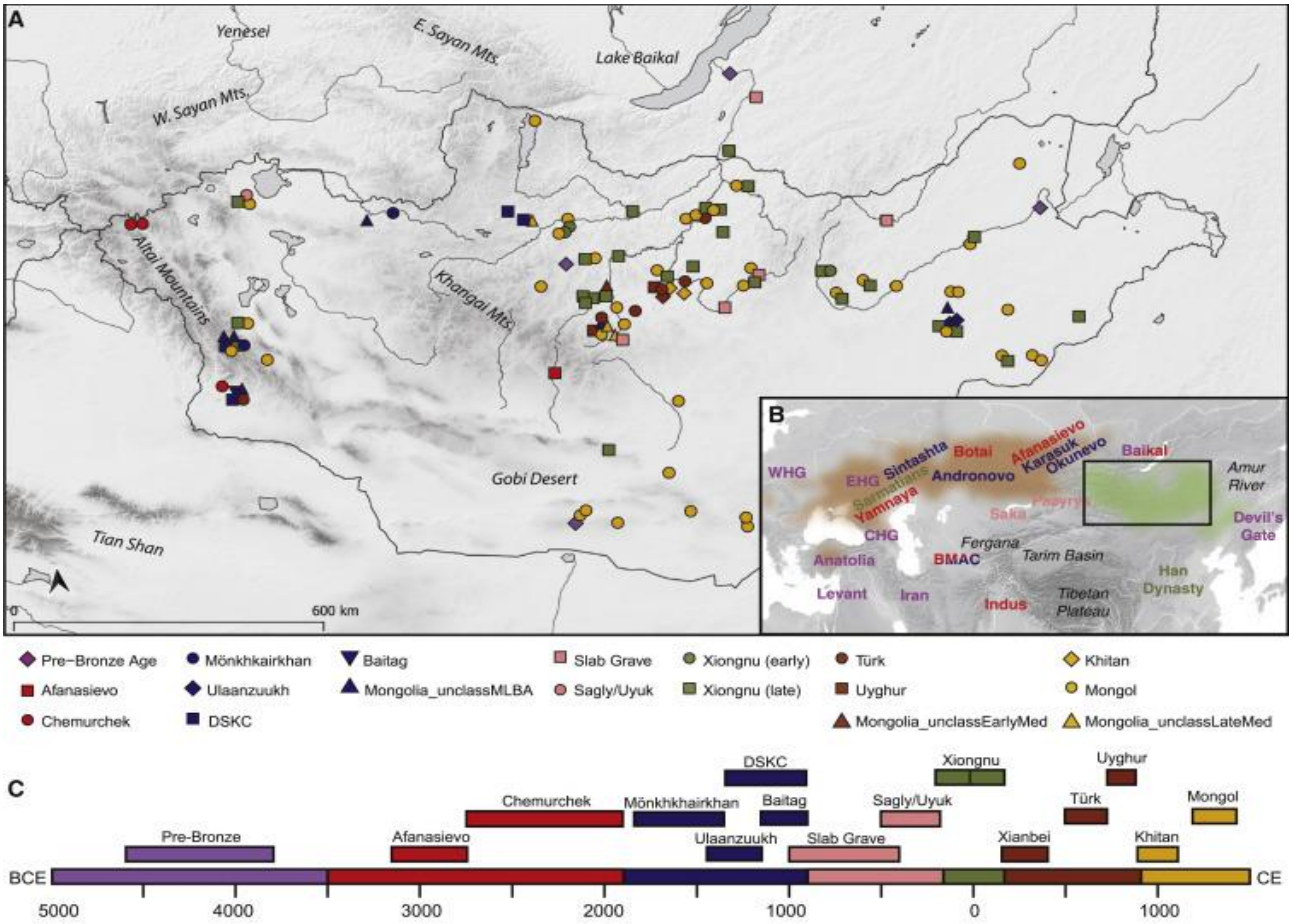


Figure 1 Overview of ancient populations and time periods (adopted from Jeong et al., 2020)

Image caption: (A) Distribution of sites with their associated culture and time period indicated by color: Pre-Bronze, purple; Early Bronze, red; Middle/Late Bronze, blue; Early Iron, pink; Xiongnu, green; Early Medieval, brown; Late Medieval, gold (see STAR Methods). See Figure S1A and Table S1B for site codes and labels; (B) Inset map of Eurasia indicating area of present study (box) and the locations of other ancient populations referenced in the text, colored by time period. The geographic extent of the Western/Central Steppe is indicated in light brown, and the Eastern Steppe is indicated in light green; (C) Timeline of major temporal periods and archaeological cultures in Mongolia. Site locations have been jittered to improve visibility of overlapping sites (Adopted from Jeong et al., 2020)

## 6 Integrative Analysis: Linking Ecology and Genomics

### 6.1 Correlating environmental variables with genetic markers

Ecological genomics leverages functional genomic approaches to identify genes and genomic regions associated with responses to specific environmental variables, such as temperature, habitat type, or resource availability (Ungerer et al., 2008; Katsikis et al., 2014). By analyzing correlations between environmental gradients and genetic markers, researchers can uncover the genetic basis of ecologically relevant phenotypic variation and adaptive traits (Ungerer et al., 2008; Katsikis et al., 2014). Statistical methods, such as multivariate analyses and environmental association studies, are commonly used to link environmental metadata with genomic data,

allowing for the detection of loci under selection in response to ecological pressures (Pérez-Cobas et al., 2020; Ozerov et al., 2025). This integrative approach enhances the understanding of how natural selection operates in heterogeneous environments and informs the identification of adaptive genetic variation.

### 6.2 Identifying eco-genomic units for management

Defining eco-genomic units—populations or lineages characterized by distinct ecological and genomic profiles—enables more precise conservation management (Katsikis et al., 2014; Guevara-Escudero et al., 2021). Integrative studies that combine ecological, phylogeographic, and genomic data can map the geographic distribution of genealogical lineages and adaptive traits across landscapes (Guevara-Escudero et al., 2021). This process helps identify locally adapted populations and informs the delineation of management units that reflect both genetic diversity and ecological function, which is critical for maintaining evolutionary potential and ecosystem resilience (Katsikis et al., 2014; Guevara-Escudero et al., 2021).

### 6.3 Predictive models for population viability

The integration of ecological and genomic data supports the development of predictive models for population viability under changing environmental conditions (Richardson et al., 2016; Matthews et al., 2018). By incorporating genomic estimates of adaptive capacity and ecological variables, these models can forecast population responses to threats such as habitat loss, climate change, and disease (Richardson et al., 2016; Matthews et al., 2018). Such models are essential for adaptive management, as they allow conservationists to anticipate future challenges and prioritize actions that enhance the persistence of genetically and ecologically important populations (Richardson et al., 2016; Matthews et al., 2018).

## 7 Conservation and Management Implications

### 7.1 Conservation priorities based on integrated data

Effective conservation of the Saker Falcon requires integrating ecological, genomic, and social data to set priorities that address both species persistence and ecosystem health. Area-based conservation remains foundational, but its effectiveness depends on adaptive management, robust monitoring, and the use of open data infrastructures to track population trends and threats (Maxwell et al., 2020; Hoffmann, 2021). Conservation actions—such as habitat protection, invasive species control, and restoration—have been shown to improve or slow declines in biodiversity in most cases, but require scaling up and continuous evaluation to meet global targets (Maxwell et al., 2020; Langhammer et al., 2024). Prioritizing conservation actions should also consider the evolutionary impacts of management, ensuring that strategies maintain genetic diversity and adaptive potential (Shefferson et al., 2018).

### 7.2 Transboundary cooperation in falcon protection

Given the Saker Falcon's wide range across multiple countries, transboundary cooperation is essential for effective conservation. International agreements, shared monitoring protocols, and coordinated management of protected areas can help address threats such as habitat loss, illegal trade, and environmental change that cross national borders (Van Kerkhoff et al., 2018; Maxwell et al., 2020). Collaborative frameworks should secure adequate financing, harmonize biodiversity policies, and mainstream conservation into broader land, water, and sea management to ensure long-term success (Van Kerkhoff et al., 2018; Maxwell et al., 2020). The "One Conservation" approach, which integrates in situ and ex situ efforts and involves multiple sectors, further highlights the need for joint action across regions and disciplines (Pizzutto et al., 2021).

### 7.3 Role of citizen science and local communities

Engaging local communities and citizen scientists is critical for the long-term success of conservation initiatives. Community-based conservation, co-management, and biocultural approaches that integrate local knowledge and address social, economic, and cultural needs can reduce conflicts and increase support for protected areas (Bennett, 2016; He et al., 2020; Hoffmann, 2021). Positive perceptions and active participation by local people enhance compliance, monitoring, and adaptive management, while also ensuring that conservation benefits are equitably shared (Bennett, 2016; He et al., 2020; Mubalama et al., 2020). Citizen science initiatives can fill data gaps, improve monitoring efficiency, and foster stewardship, making them valuable tools for both research and management (Bennett, 2016; Hoffmann, 2021).

## 8 Challenges and Future Directions in Saker Falcon Research

### 8.1 Data integration limitations and biases

Integrating field observations with genomic data presents significant challenges, including inconsistencies in data collection methods, spatial and temporal mismatches, and varying data quality. These limitations can introduce biases that affect the reliability of ecological-genomic analyses. For example, differences in monitoring intensity or technology adoption across regions may lead to uneven data coverage, while the integration of heterogeneous datasets requires robust frameworks to ensure comparability and minimize error propagation. Addressing these challenges will require standardized protocols, improved data sharing infrastructures, and interdisciplinary collaboration to harmonize methodologies and reduce integration biases.

### 8.2 Emerging genomic technologies in wildlife conservation

Rapid advances in genomic technologies—such as next-generation sequencing, environmental DNA (eDNA) analysis, and portable sequencing platforms—are transforming wildlife conservation. These tools enable high-resolution population genetic studies, real-time monitoring of genetic diversity, and the detection of adaptive genetic variation even in non-model species. However, the adoption of these technologies also brings challenges, including the need for specialized expertise, high costs, and the management of large, complex datasets. Future directions should focus on making genomic tools more accessible, developing user-friendly analytical pipelines, and integrating genomic insights into practical conservation management.

### 8.3 Long-term monitoring and climate change adaptation

Long-term ecological monitoring remains essential for understanding population trends and adaptive responses to climate change. However, sustaining such efforts is challenged by funding limitations, logistical constraints, and the need for consistent methodologies over time. Climate change introduces additional complexity, as shifting environmental baselines may alter species distributions, phenology, and adaptive pressures. Future research should prioritize the development of adaptive monitoring frameworks that can respond to changing conditions, leverage remote sensing and automated data collection, and incorporate predictive modeling to inform proactive conservation strategies.

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## Conflict of Interest Disclosure

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

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