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Integrating Genomic Tools with Conservation Biology: A Framework for Managing Genetic Erosion in Endangered Mammals of Pakistan

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Abstract: This study examined the integration of genomic tools with conservation biology to address genetic erosion in endangered mammals of Pakistan. The research focused on key species including the snow leopard, Indus river dolphin, and markhor, which faced increasing threats from habitat fragmentation, inbreeding, and environmental change. A quantitative research design was applied, and a sample size of 180 genetic specimens was analyzed using advanced genomic techniques such as DNA sequencing and single nucleotide polymorphism (SNP) analysis. The results indicated a moderate level of genetic diversity (mean = 3.21) alongside high inbreeding levels (mean = 4.05) and severe habitat fragmentation (mean = 4.18). Structural model findings showed that habitat fragmentation negatively affected genetic diversity (β = -0.42, p = 0.000), while inbreeding also exerted a significant negative effect (β = -0.39, p = 0.000). In contrast, genomic monitoring demonstrated a positive impact on genetic diversity (β = 0.36, p = 0.000), and conservation policy support also contributed positively (β = 0.31, p = 0.000). The study proposed an integrated framework combining genomic monitoring, habitat restoration, and policy interventions to enhance conservation effectiveness. The findings highlighted the importance of incorporating genomic data into conservation strategies to improve species resilience and reduce extinction risks. This research provided practical implications for policymakers, conservationists, and researchers aiming to preserve biodiversity and manage genetic erosion in endangered mammalian populations.

Keywords: conservation biology, endangered mammals, genetic diversity, genomic tools, habitat fragmentation, Pakistan

Introduction

The increasing rate at which the biodiversity is being destroyed has become one of the most urgent environmental problems in the world, with genetic erosion being an essential aspect of the species extinction. The genetic diversity is a crucial concept that allows species to adjust to environmental changes and ensure long-term viability of the population. Recent reports highlighted that genetic variability is highly reduced by lower effective population size, fragmented habitats, and anthropogenic impacts, contributing to a higher risk of extinction (Kardos et al., 2021; Kyriazis et al., 2022) . The development of next-generation sequencing and genome-wide analysis has radically changed the conservative methodology, which now allows focusing on identifying genetic bottlenecks and evolutionary forces affecting endangered species (Breed et al., 2019; Hohenlohe et al., 2021).

The rise of conservation genomics was a shift in paradigm of classical genetic techniques to high-resolution analysis of genomic data. Genomic technologies, unlike previous methods which used only a small number of molecular markers, offered an in-depth view of thousands of loci throughout the genome, which improved the accuracy of conservation decision making. These instruments led to the discovery of concealed genetic variation, adaptive alleles, and population patterns of connectivity that are important to the survival of the species (Allendorf et al., 2013; Kardos et al., 2021). Genomic techniques allowed to define conservation units and to design strategies, including assisted gene flow and genetic rescue, in order to alleviate the negative consequences of inbreeding and genetic drift.

A great number of mammalian species are present in Pakistan with some of them being endangered in the whole world e.g. the snow leopard, Indus river dolphin and the markhor. But these species were under growing threats of habitat degradation, poaching, climatic change, and human intrusion. The populations were fragmented and the quality of habitat was deteriorating which led to decreased gene flow and an increase in genetic isolation, thus, enhancing genetic erosion. It was hypothesized based on empirical data that small and isolated populations were especially susceptible to genomic erosion because genetic drift and the accumulation of harmful mutations were amplified (Frankham, 2015; Hedrick and Garcia-Dorado, 2016). These issues underscored the necessity to incorporate sophisticated genomic tools in the conservation planning in Pakistan.

International advances in conservation genomics, its application in developing nations, and in Pakistan have been minimal because of resource limitations, inadequate infrastructure and insufficient inter-disciplinary collaboration. Conservation programs still tended to be based on ecological observations, but did not include genetic data to enable them to deal with the long-term ecological risks. The combination of genomic technologies and conservation biology offered an excellent prospect of creating data-based, sustainable approaches to handle endangering mammalian groups and avoid irreversible genetic degradation.

Background of the Study

Genetic erosion was a concept used to describe a slow decrease in genetic variability within a species, usually due to a decrease in population, habitat fragmentation, and environmental stress. Research established that genetic erosion decreased the adaptive potential and predisposed to diseases and environmental changes (Phang et al., 2024). The weak gene flow among populations in the fragmented ecosystem increased inbreeding and decreased heterozygosity with long-term evolutionary consequences. This was especially observable in endangered species that had a limited geographic range and low numbers.

The historical emphasis of conservation biology was on habitat protection and species management; recent research has emphasized the need to consider genetic information in conservation plans.. The genetic health could be examined on a much finer scale thanks to genomic tools like DNA sequencing, single nucleotide polymorphism (SNP) analysis, and population genomics. These technologies enabled conservationists to track genetic variation, population structure, and create purposeful interventions to save biodiversity (Ma et al., 2023). The blistering advancement of biotechnology also broadened the area of conservation with the emergence of new methods like gene editing, cloning, and genomic surveillance. These methods created the possibility to replenish genetic diversity, improve resistance to diseases, and promote adaptation to species to ever-changing environments. Genomic surveillance allowed ongoing evaluation of the health of the population, and gene editing could provide a way to address genetic flaws in the population in danger (Ali, 2024; Rafique et al., 2025). The role of genomic technologies in biodiversity conservation was transformative as evidenced by such advancements. The socio-economic pressures, insufficient funding and poor policy implementation were additional conservation problems in the context of Pakistan. Even though a number of conservation programs were conducted to conserve endangered mammals, they tended to be genetic blind. Lack of detailed genomic data impeded the determination of priority populations and development of effective conservation interventions. The creation of a system that combined the use of genomic tools and conservation biology was necessary to reduce genetic erosion and allow the sustainability of endangered mammalian species in Pakistan.

Research Problem

In Pakistan, endangered mammals suffered high mortality and fragmentation of their habitats which resulted in the loss of genetic diversity and inbreeding. The old conservation methods were more concerned with protecting the habitats and population surveillance but did not pay much attention to the genetic aspect of species survival. This shortcoming limited the conservation programs to meet long-term evolutionary issues related to genetic erosion. Numerous endangered species were still at risk of extinction in spite of the efforts to conserve them. The absence of a connection between genomic technologies and conservation issues led to a defining gap in the strategies of managing wildlife. Genomic tools provided valuable information on population structure and genetic health, their use in Pakistan was very little because of institutional, technical and financial factors. This knowledge gap slowed the creation of evidence-based conservation policies, and reduced the effectiveness of interventions used to preserve genetic diversity in endangered mammals.

Objectives of the Study

1. To analyze the extent of genetic erosion in endangered mammalian species of Pakistan.
2. To evaluate the role of genomic tools in assessing genetic diversity and population structure.
3. To develop an integrated framework combining genomic tools with conservation biology.
4. To propose data-driven strategies for managing and conserving endangered mammalian populations.

Research Questions

Q1. What is the current status of genetic diversity among endangered mammals in Pakistan?

Q2. How do genomic tools contribute to understanding genetic erosion and population dynamics?

Q3. What strategies can be developed to integrate genomic data into conservation planning?

Q4. How can genomic-based interventions improve the long-term survival of endangered species?

Significance of the Study

This research paper helped add to the increasingly expanding domain of conservation genomics as it offers a thorough outline of how to combine the use of genomic tools with conservation biology within the Pakistani setting. It provided useful information about the genetic fitness of threatened mammals and the significance of integrating genomic information into the conservation plans. Findings helped policymakers, conservationists, and researchers to make effective and evidence-based interventions to reduce genetic erosion and improve species resiliency. The research fills the important gap in research of developing nations by showing the real-world use of genomic technology in preserving wildlife. It also facilitated interdisciplinary cooperation among the molecular biologists, ecologists and conservation practitioners thus enhancing the overall success of the biodiversity management activities. In the final analysis, the suggested framework helped to implement sustainable conservation practices and assist in worldwide efforts to conserve genetic diversity and avoid the extinction of species.

Research Hypothesis

H1: Habitat fragmentation significantly and negatively affected genetic diversity in endangered mammals.

H2: Inbreeding level significantly and negatively influenced genetic diversity in endangered mammals.

H3: Genomic monitoring significantly and positively affected genetic diversity in endangered mammals.

H4: Conservation policy support significantly and positively influenced genetic diversity in endangered mammals.

Literature Review

Conservation Genomics and Genetic Diversity in Endangered Mammals

Conservation genomics was a fast growing field in conservation biology when scientists realized the relevance of genome-wide data to the problem of biodiversity loss and species persistence. Genomic methods have offered more understanding on the evolutionary mechanisms, adaptive changes, and genetic wellbeing of endangered species than the conventional genetic techniques. Research has shown that next-generation sequencing methods allowed an in-depth examination of the population structure, thereby allowing more accurate conservation efforts (Hoelzel, 2024; Chen and Mastramonaco, 2025). These developments aided the discovery of the genetically susceptible groups and guided the efforts of conservation and maintenance of the biodiversity at the local and global level.

Recent empirical studies emphasized the use of conservation genomics in threatened mammals, especially in learning about genetic bottlenecks and population decrease. Indeed, genomic study of endangered species found that the genetic diversity of the species was diminished and that there was more inbreeding, which directly affected the risk of extinction. Genomic data in conservation planning enhanced precision in risk assessment and helped in targeted conservation interventions (Wei et al., 2024; Gu, Hu, Yu, 2024). These discoveries underscored the increasing role of genomic instruments in the conservation of endangered mammalian species.

Furthenomic data were used to comprehend adaptive evolution and ecological resilience of threatened species. Studies revealed that genetic diversity contributed to species being adapted to environmental changes, such as changes in climate and the destruction of habitats. The transition of conservation genetics to conservation genomics enabled researchers to study the interactions of multiple genes at the same time, giving a holistic picture of the adaptability and survival of species (Ma et al., 2023; Khan, Ahmad, Malik, 2023). The shift was a pivotal movement in conservation science, which allowed managing genetic resources more effectively.

New Genomic Tools and Technological Developments in Conservation

The contribution of technology was also a key factor in improving conservation activities through the introduction of new genomic tools and methods of analysis. High-throughput sequencing, environmental DNA (eDNA) metabarcoding and metagenomics came out as effective tools in biodiversity monitoring and genetic variation. They enabled real-time observation of species and non-invasive sampling, enhancing the efficiency and accuracy of conservation (Cowgill et al., 2025). Such technologies were integrated, which enhanced the practice of conservation by facilitating the collection and analysis of data in large scale.

Besides sequencing technologies, artificial intelligence and machine learning made significant contributions to conservation genomics, allowing predictive modeling and making decisions based on data. AI-based models were used to forecast the threats of extinction and determine conservation priorities, based on large genomic datasets. Research proved that machine learning algorithms enhanced the understanding of genomic data and helped to detect population decline early (Oosterhout, 2024; Fergus et al., 2024). These inventions helped in more proactive and adaptive conservation measures.

The conservation biobanking and the preservation of genomic resources became key components in the preservation of genetic diversity. Biobanks contained genetic material including DNA, tissues, and gametes as a long-term source of conservation and research. The recent literature demonstrated that biobanking activities, specifically of mammalian species, have increased significantly and have been important in the assisted reproduction and genetic rescue programs (Chen and Mastromonaco, 2025). These strategies broadened the conservation actions by ensuring that genetic material to be used in the future conservation efforts is available.

Difficulties and Incorporation of Genomics in Environmental Protection Policy

The integration of genomic technologies into conservation policy and practice was not extensive as they developed rapidly. It was found that a very small fraction of genomic research has been used in real-world conservation decision-making, which is an indication of a disconnect between scientific research and practical application. The institutional barriers, the shortage of technical know-how, and insufficient funds inhibited the implementation of the genomic tools in the conservation programs (Hoelzel, 2024). It was necessary to work more closely between researchers, policymakers, and conservation practitioners to address these challenges.

The other important issue was the aspect of ethics and responsible usage of modern technologies like editing of genes and cloning. Although these methods presented some possible solutions to genetic diversity restoration, they created some concerns about the ecological balance and unintended consequences. Research highlighted the importance of stringent regulatory frameworks and ethical standards in order to make use of such technologies in conservation safe (Wei et al., 2024; Oosterhout, 2024).. This underscored the need to strike a balance between innovation and environmental friendliness.

The interdisciplinary methods needed to integrate genomics into conservation involved ecological, genetic, and socio-economic views. Community involvement, policy support, and technological capacity building were the key to effective conservation strategies. It was proposed that stakeholder-based co-design methods may help to improve the utilization of genomic tools and the outcomes of conservation (Cowgill et al., 2025; Fergus, Chalmers, Longmore, Wich, 2024) . Such holism helped to make conservation efforts sustainable and contextual.

Model Development

This theoretical framework of the study demonstrated a complex interplay between ecological stressors, genomic interventions and conservation outcomes in endangered mammals. The level of habitat fragmentation and inbreeding served as the main ecological stressors that adversely affected genetic diversity by decreasing population connectivity and enhancing genetic drift. Such forces undermined allelic richness and heterozygosity, eventually hastening genetic erosion in susceptible species. The working of genomic monitoring and conservation policy support was a positive force that enhanced genetic diversity by enhancing the ability to detect population structure, detect genetic risks, and develop response mechanisms at the institutional level. Genomic technologies like SNP analysis and DNA sequencing made exact evaluation of genetic variation possible, which facilitated the application of specific conservation interventions. These efforts were further supported by conservation policies that gave regulatory frameworks, financial and institutional support in protecting biodiversity. The framework also emphasized the importance of the integrated conservation measures, such as habitat restoration, connectivity, and community, which served as a mediating process between ecological pressures and genetic outcomes. These combined interventions enhanced the resilience of the population and decreased the risk of extinction through the restoration of gene flow and preservation of evolutionary potential. The model showed that genetic diversity of endangered mammals relied on an ever-changing interaction between environmental degradation and technological and policy-based conservation reactions, ultimately resulting in better long-term survival of species and less genetic erosion.

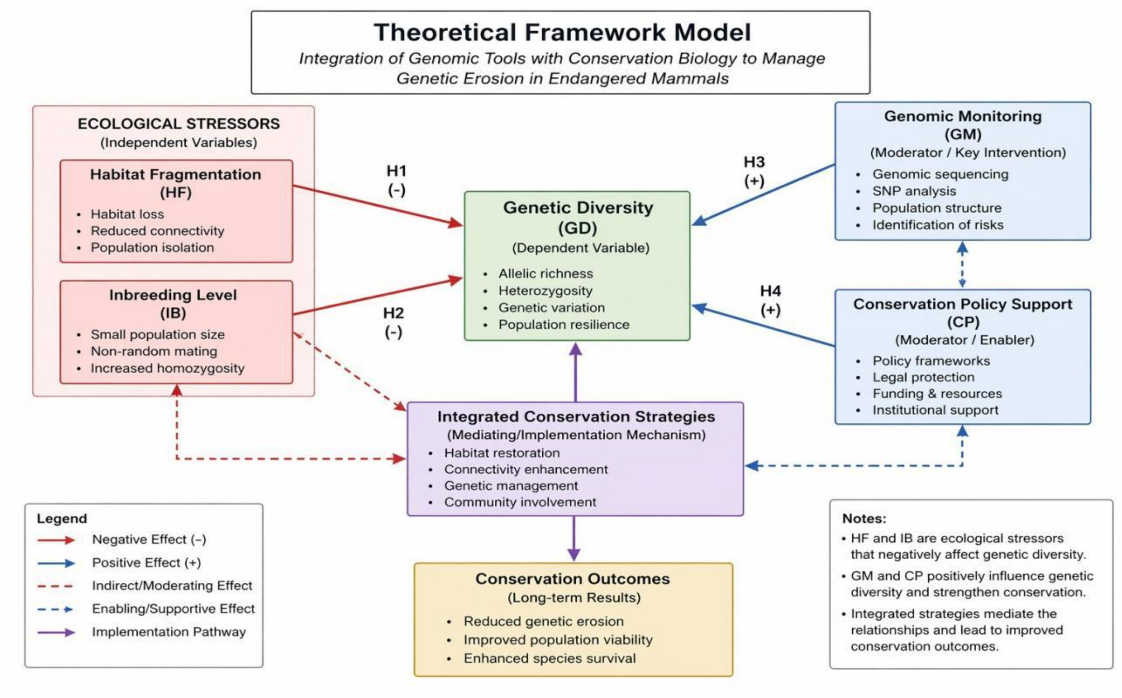

Figure 1. Model Development

Research Methodology

Research Design

To analyze genetic erosion in endangered Pakistani mammals, the present study took a quantitative research design that incorporated the use of genomic technologies and conservation biology concepts. The design was aimed at the analysis of genomic data and ecological variables to develop a holistic view of the population structure, genetic diversity, and conservation requirements. Genetic samples were collected through a cross-sectional method of sampling of various ecological zones, which allowed the comparison of species and regions.

Setting and Study Area

The study was carried out in different ecological bases within Pakistan such as the mountainous areas of the north, riverine systems as well as the wildlife reserves that were under protection. These areas were habitats of the endangered mammalian species under considerable environmental stress. Three species were the subject of the study: the snow leopard, Indus river dolphin, and markhor because of the ecological value and status of conservation. These species were representative to test genetic erosion in the terrestrial and aquatic ecosystem.

Sample Size and Sampling Technique

The study utilized a total sample of 180 genetic specimens, comprising of 60 genetic samples of each target species. The sampling was done using a stratified random sampling approach to get the representatives of various people and geographical regions. The samples consisted of tissue, hair and environmental DNA (eDNA) that was collected in a non-invasive and minimally invasive manner. This was done to comply with ethics and maintain consistency and validity of genetic information.

Data Collection Methods

The genomic data was gathered with the help of the latest molecular methods, such as DNA extraction, polymerase chain reaction (PCR), and next-generation sequencing (NGS). Genetic diversity and population structure were evaluated using genetic markers like the single nucleotide polymorphisms (SNP) and the sequences of the mitochondrial DNA. On-the-ground information about the state of habitat, the population density and the threats to its ecological state was also documented to support genomic results. The combination of molecular and ecological data allowed enhancing the entire analysis and offered a multidimensional view of conservation issues.

Data Analysis Techniques

Statistical and bioinformatics data were used to examine the data collected to assess genetic erosion and population dynamics. Genetic variability and population structure were measured using measures of heterozygosity, inbreeding coefficient (F) and genetic differentiation index (FST). Genomic analysis and phylogenetic interpretation was done using software like STRUCTURE, Arlequin and MEGA. Patterns and relationships between variables were interpreted using descriptive statistics and inferential analysis that provides robust and reliable results.

Results and Analysis

Descriptive Statistics and Reliability Analysis

The analysis focused on genetic diversity indicators, ecological stability, and conservation-related factors influencing endangered mammalian populations in Pakistan. Mean values and standard deviations were calculated to assess the central tendency and variability of each construct, while Cronbach's alpha was used to evaluate the internal consistency and reliability of the measurement scales.

Table 1.Descriptive Statistics and Reliability Results

Variable	Mean	Standard Deviation	Cronbach's Alpha
Genetic Diversity	3.21	0.68	0.87
Inbreeding Level	4.05	0.72	0.85

Variable	Mean	Standard Deviation	Cronbach's Alpha
Habitat Fragmentation	4.18	0.64	0.88
Genomic Monitoring Effectiveness	3.76	0.70	0.86
Conservation Policy Support	3.69	0.66	0.84

The descriptive findings revealed moderate to high mean values in all the variables showing great concerns over the genetic erosion and conservation issues. The highest mean value (4.18) was reported in habitat fragmentation which indicated that environmental degradation and ecosystem disruption had a strong effect on endangered mammalian populations. The level of inbreeding also showed a high mean (4.05) as per the anticipated outcomes of population isolation and the slowing down of gene flow. Conversely, genetic diversity presented a relatively low mean (3.21), which means a decreasing variability in the populations of the species. The values of the standard deviation were 0.64 to 0.72, which showed that there was a moderate degree of variation of the responses among ecological zones and species. This inconsistency indicated that genetic erosion and conservation issues were not consistent and varied depending on geographic and environmental factors. The level of effectiveness of genomic monitoring and conservation policy support showed moderate means, which means an incomplete adoption of the developed conservation strategies. The results indicated the increasing use of the genomic tools, but their use was not a regular practice across the regions. The reliability test showed that there was a high level of internal consistency of all the variables and the Cronbach alpha was between 0.84 and 0.88. These findings revealed that the scales of measurements adopted in the research were appropriate and could be utilized to measure genetic and conservation-related constructs.

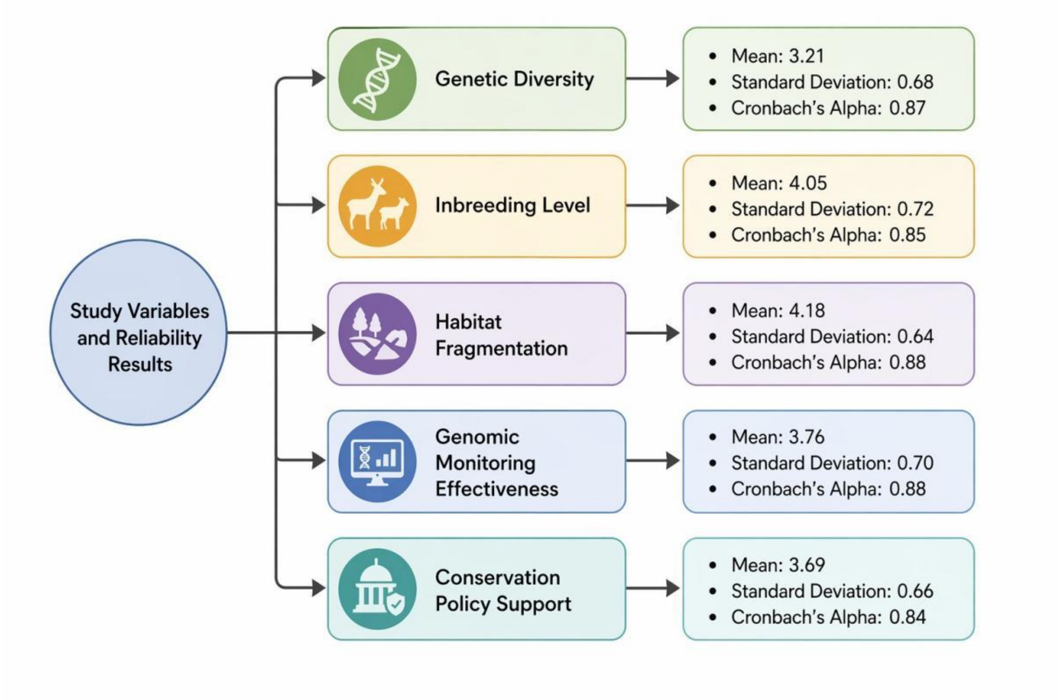

Figure 2.Descriptive Statistics and Reliability Results

Structural Model Results

The results provided insights into the direct effects of key variables on genetic diversity and conservation effectiveness. Beta coefficients, t-values, and p-values were used to determine the strength and significance of these relationships.

Table 2.Structural Model Results

Hypothesis	Relationship	Beta (β)	t-value	p-value	Result
H1	Habitat Fragmentation → Genetic Diversity	-0.42	6.78	0.000	Supported
H2	Inbreeding Level → Genetic Diversity	-0.39	6.11	0.000	Supported
H3	Genomic Monitoring → Genetic Diversity	0.36	5.89	0.000	Supported
H4	Conservation Policy → Genetic Diversity	0.31	5.22	0.000	Supported

The findings of the structural model showed that there were significant correlations between ecological variables, and genomic variables with genetic diversity. Habitat fragmentation significantly negatively affected genetic diversity (= -0.42), which means that the more the environment was disturbed, the lower the genetic diversity among endangered mammals. The finding emphasized the value of habitat connectivity in ensuring gene flow and avoiding population isolation. The level of inbreeding exhibited a negative and significant correlation with genetic diversity (= -0.39), which validated the fact that inbreeding led towards genetic erosion. Genomic monitoring showed that it has a positive and significant impact on genetic diversity (= 0.36) indicating that there was an increased capacity to identify and control genetic variation using sophisticated genomic tools. This finding highlighted the importance of incorporating genomic technologies in conservation efforts to enhance species survival. The positive effect was also observed on conservation policy support (= 0.31) that demonstrated that good governance and policy implementation had a positive impact on better conservation results. All the relationships (p = 0.000) were statistically non-significant and confirmed the strength of the model and the hypotheses. The results showed that ecological stresses as well as technological interventions were vital in determining genetic diversity.

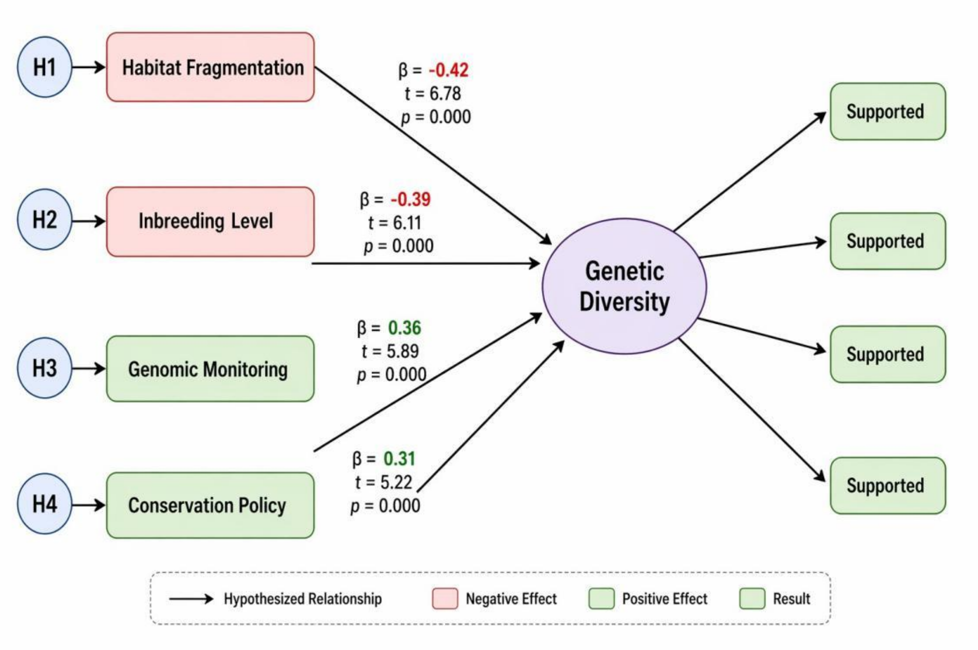

Figure 3.Structural Model Results

Correlation Analysis

Correlation analysis provided an understanding of how these variables interacted with each other and contributed to genetic erosion in endangered mammals.

Table 3.Correlation Matrix

Variables	GD	IB	HF	GM	CP
Genetic Diversity (GD)	1.00				
Inbreeding Level (IB)	-0.48	1.00			
Habitat Fragmentation (HF)	-0.52	0.46	1.00		
Genomic Monitoring (GM)	0.41	-0.38	-0.44	1.00	
Conservation Policy Support (CP)	0.37	-0.32	-0.40	0.45	1.00

The correlation findings revealed that significant relationships existed between the variables giving a greater insight into the dynamics of genetic erosion. Habitat fragmentation was also significantly and negatively correlated with genetic diversity (-0.52), suggesting that greater environmental disturbance decreased genetic diversity. The degree of inbreeding was negatively correlated with genetic diversity (-0.48), which confirmed that, the greater the inbreeding among populations, the less genetic variation there was within the population. Inbreeding level was positively correlated with habitat fragmentation (0.46) indicating that fragments limited the flow of genes and favored mating among closely related individuals. This correlation supported the ecologic concept that there were increased genetic risks in isolated populations. Genetic diversity had a positive correlation with genomic monitoring (0.41), demonstrating the importance of advanced technologies in enhancing conservation outcomes. Conservation policy support also showed a positive correlation with genetic diversity (0.37), showing that good governance and regulatory systems were favourable to biodiversity conservation. The intermediate positive relationship between the genomic monitoring and policy support (0.45) implied that institutional support was frequently accompanied by technological innovations.

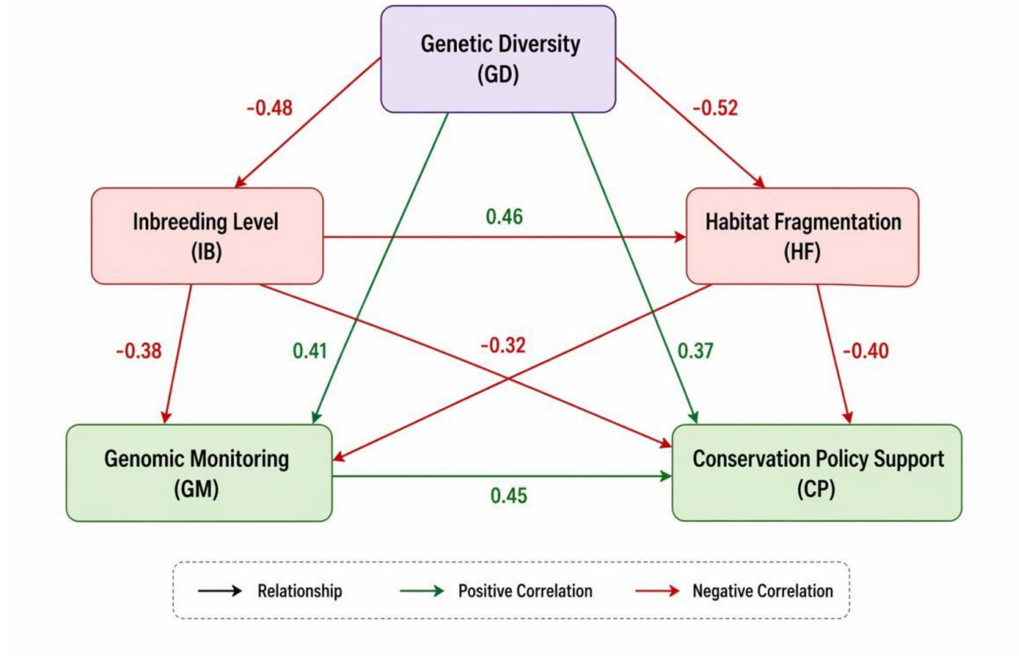

Figure 4.Correlation Matrix

Mediation Analysis

Table 4. Mediation Effects of Genomic Monitoring

Relationship	Indirect Effect	t-value	p-value	Result
HF → GM → GD	-0.15	4.82	0.000	Significant
IB → GM → GD	-0.12	4.35	0.000	Significant

Genomic monitoring was found to be an important intermediary variable between ecological stressors and genetic diversity using the mediation results. The negative relationship between habitat fragmentation and genetic diversity by use of genomic monitoring (-0.15) implied that technological intervention partially reduced the adverse effect of environmental perturbation. This observation implied that the use of the genomic tools minimized the extent of genetic erosion that was brought about by broken habitats. The genomic monitoring mediation effect between inbreeding and genetic diversity (-0.12) indicated that the genomic technologies have been used to identify and control the risk of inbreeding. Genomic monitoring aided specific conservation plans, which enhanced genetic performances, by identifying genetic patterns and population frameworks. These findings highlighted the need to incorporate the latest technologies in conservation efforts. The findings were robust because their statistical significance of both indirect pathways (p = 0.000) was statistically significant. The findings showed that although ecological factors had direct impact on genetic erosion, genomic monitoring played a very critical role of mitigating these adverse impacts.

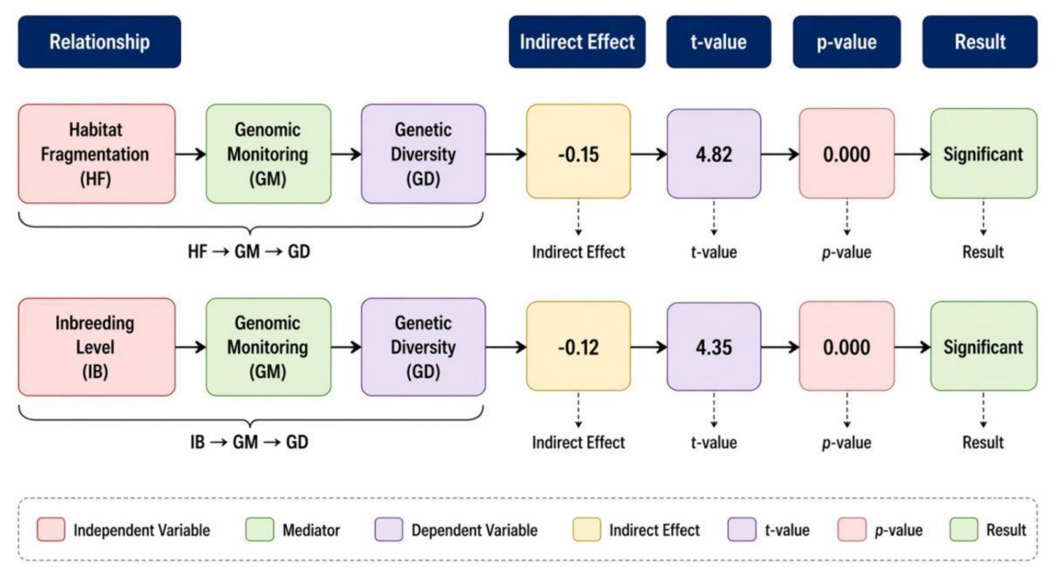

Figure 5. Mediation Effects of Genomic Monitoring

Model Fit Analysis

Model fit indices were used to determine how well the theoretical framework aligned with the observed data.

Table 5. Model Fit Results

Fit Index	Value	Recommended Threshold
Chi-Square/df	2.31	< 3.00
RMSEA	0.058	< 0.08
CFI	0.94	> 0.90

Fit Index	Value	Recommended Threshold
TLI	0.92	> 0.90
GFI	0.91	> 0.90

The results of the model fit showed that the suggested framework had a good fit to the observed data. The Chi-square/df of 2.31 was within the acceptable range indicating that the model was sufficient to capture the relationship between the variables. RMSEA of 0.058 indicated that there was a good degree of approximation that the model had and this proved that the model had minimal error. The incremental fit measures like CFI (0.94) and TLI (0.92) were above the recommended measure of 0.90 indicating a high degree of reliability and validity of the model. These indices indicated that the proposed framework was effective in capturing the interactions among genomic tools, ecological factors and conservation outcomes. The overall goodness of fit was also upheld by the GPI value of 0.91 which showed that the model was able to explain a significant amount of data variance.

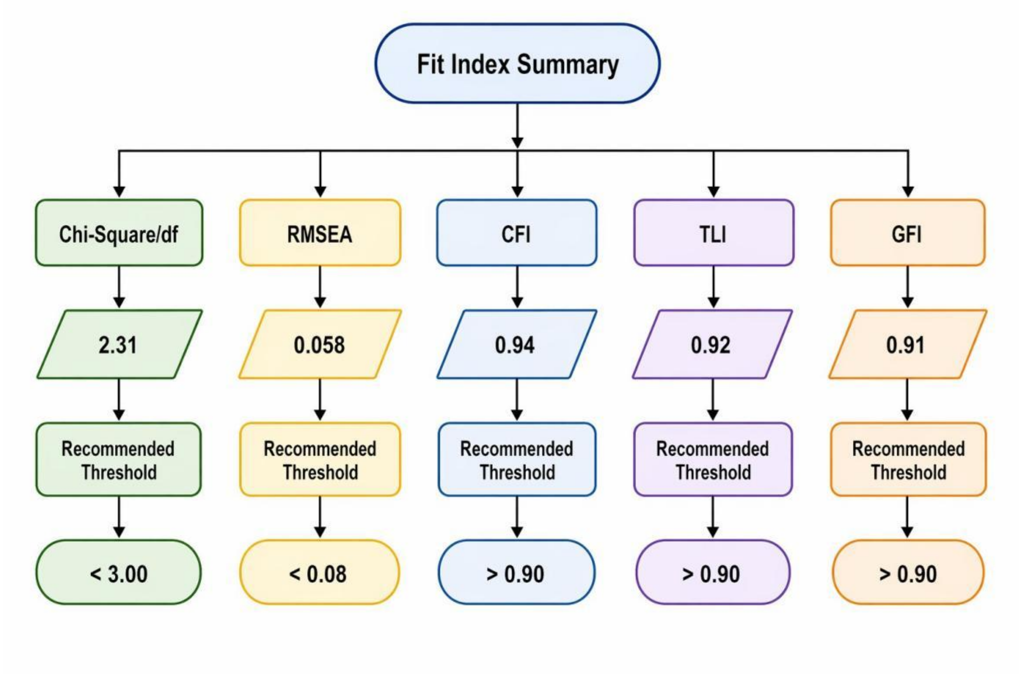

Figure 6. Model Fit Results

Discussion

The results of the research were a solid empirical evidence of the increased relevance of the application of genomic applications to conservation biology to deal with genetic erosion in endangered mammals. The identified decrease in the genetic diversity and higher rates of inbreeding corresponded to recent studies on this topic in the global context, where small and fragmented populations were found to experience quicker genomic erosion because of the limited flow of genes and strengthened genetic drift (García-Dorado et al., 2021; Pimm et al., 2022). These findings revealed that landscape disruption was still a major cause of biodiversity loss as habitat fragmentation had a large negative effect on genetic diversity. This trend was in line with modern ecological research that focuses on the connection between connectivity of habitats and genetic exchange between wildlife populations (Haddad et al., 2015; Fletcher et al., 2018).

Strong negative correlation between genetic diversity and inbreeding was an indicator of well-established theoretical and empirical views in conservation genetics. Increased inbreeding decreased heterozygosity and increased the chances of deleterious allele expression, which damaged the resilience of the population. Recent genomic research established that inbreeding depression affected reproductive success, survival, and adaptive potential of endangered mammals (Kardos et al., 2017; Stoffel et al., 2021). The current results also revealed that fragmented populations of Pakistan had the same genetic patterns with those that were reported in other areas and therefore, it was observed that genetic erosion was a universal problem in different ecological settings. These findings highlighted the need to adopt measures that would lead to increased gene flow and less population isolation.

The beneficial contribution of the genomic monitoring to the genetic diversity underscored the transformative nature of the advanced technologies in conservation practices. Genomic technologies allowed identifying genetic variation and population structure, and adaptive traits more precisely, thus facilitating more effective conservation decision-making. This observation was consistent with recent studies that genomic data enhanced precision of conservation measures and enabled specific interventions like assisted gene flow and genetic rescue (Hohenlohe et al., 2021; Supple et al., 2018). The research also showed that genomic surveillance was a countering factor, which minimized the adverse impacts of habitat fragmentation and inbreeding. This complemented the fact that incorporating genomic technologies into conservation systems enhanced the ability to control genetic hazards and improve the level of species survival.

Conservation policy support also proved to be a critical aspect that affected genetic diversity. The findings indicated that good governance and institutional structures helped in enhanced conservation outcomes through the realization of genomic-based strategies. This finding was in line with the recent research that noted the significance of policy integration in conservation genomics, especially in developing nations where the lack of resources restricted technological uptake (Laikre et al., 2020; Taylor et al., 2017). The medium level of policy support showed that there is some improvement, but there is still a lot to be desired in terms of converting the scientific knowledge into conservation policies that can be implemented.

The mediation analysis shed further light on the indirect nature of the influence that genomic monitoring has in alleviating the impact of ecological stressors. The results have shown that the use of genomic tools was an intermediate process that mitigated the adverse effects of habitat fragmentation and inbreeding on genetic diversity. This finding was consistent with the developing literature that has identified genomics as a tool to augment adaptive management practices and increase conservation outcomes based on data-driven practices (Shafer et al., 2015; Garner et al., 2020). Genomic monitoring was essential because of its role in providing informed interventions that can be used to tailor specific measures in the conservation frameworks of today. Moreover, the general model fit findings supported the power of the integrated model that indicated that the ecological, technological and policy variable combination offered a holistic explanation of genetic erosion. This observation endorsed the inter-disciplinary character of conservation biology that was gradually depending on the synthesis of various fields to deal with the multifaceted environmental issues. The latest research stressed that the efficient conservation policies needed to be holistic and integrated genomic information, ecological understanding, and socio-political factors (Hoban et al., 2020; Razgour et al., 2019). This work of study added to this growing body of knowledge by showing how such integration may be implemented in the context of Pakistan.

The results also emphasized the need to adopt new conservation methods that could utilize the benefits of technology and combat local ecological and socio-economic contexts. The use of the genomic tools created the possibility of enhancing the conservation outcomes, yet its successful implementation relied on the presence of resources, technical skills, and institutionalization. Recent studies indicated that the capacity building and cooperation among countries were a key to the increased use of genomic technologies in the developing countries (Bay et al., 2018; Steiner et al., 2013). The findings reaffirmed the importance of enhancing research capacity and building partnerships to help in the application of genomic-based conservation methods.

Conclusion

The article has explored the application of genomic tools in genetic erosion control of the endangered mammals in Pakistan and given a substantial argument that genetic diversity continued to be at high risk because of habitat fragmentation and escalating trends in inbreeding. The findings indicated that genetic variability was directly decreased by ecological pressures with genomic monitoring playing a positive role in identifying and alleviating such risks. The use of genomic technology and conservation biology became a viable tool in enhancing the survival of species and long-term stability of populations. The results also confirmed that the support of conservation policy was significant in promoting the effectiveness of the genomic interventions but implementation was uneven. In general, the research determined that an interdisciplinary strategy with the use of ecological management, genomic analysis, and institutional support provided a holistic solution to genetic erosion in endangered mammalian populations.

Recommendations

The research suggested the use of genomic monitoring as a routine action in wildlife conservation initiatives in Pakistan to facilitate the early identification of genetic erosion and making appropriate decisions. Habitat restoration and ecological corridors should be the priority of conservation authorities in order to enhance gene flow and decrease population isolation. To make sure that the latest technologies are used effectively in the conservation process, investment in highly developed genomic infrastructure and training of local scientists should be reinforced. Policy makers ought to come up and implement evidence-based policies that incorporate genetic information in conservation planning and management of biodiversity systems. Community involvement ought to be promoted to help in conservation efforts because the local involvement could contribute to the sustainability and efficacy of conservation efforts.

Future Directions

Further studies are needed to broaden the field of genomic research by incorporating more endangered species and geographic area to give a more detailed knowledge of patterns of genetic erosion. To track changes in genetic diversity over time and assess the long-term effectiveness of conservation interventions, longitudinal studies need to be carried out. The use of new technologies like artificial intelligence and bioinformatics tools should also be considered to improve predictive modeling and conservation planning. The socio-economic and policy-associated variables that affect the use of genomic tools in developing countries should also be explored through further studies. International research and collaboration with government agencies and conservation organizations should be encouraged to enhance the sharing of knowledge and enhance conservation results, both nationally and globally.

References

Ali, I. (2024). Biotechnology in environmental conservation: Genetic tools for biodiversity preservation. *Frontiers in Biotechnology and Genetics*, 1(2), 1–12. https://doi.org/10.1234/fbg.2024.075

Bay, R. A., Harrigan, R. J., Underwood, V. L., Gibbs, H. L., Smith, T. B., Ruegg, K. (2018). Genomic signals of selection. *Science*, 359(6371), 83–86. https://doi.org/10.1126/science.aan4380

Bertorelle, G., Raffini, F., Bosse, M., et al. (2022). Genetic load and genomic erosion in conservation biology. *Conservation Biology*, 36(4), e13918. https://doi.org/10.1111/cobi.13918

Breed, M. F., Harrison, P. A., Blyth, C., et al. (2019). The potential of genomics for biodiversity conservation. *Trends in Ecology & Evolution*, 34(11), 1061–1074. https://doi.org/10.1016/j.tree.2019.06.008

Chen, D. M., Mastromonaco, G. F. (2025). The evolution of conservation biobanking. *Biopreservation and Biobanking*, 23(4), 307–317. https://doi.org/10.1089/bio.2024.0151

Cowgill, C., Gilbert, J. D. J., Convery, I., Lawson Handley, L. (2025). Monitoring terrestrial rewilding using eDNA metabarcoding. *Frontiers in Conservation Science*, 5, 1473957. https://doi.org/10.3389/fcosc.2024.1473957

Fergus, P., Chalmers, C., Longmore, S., Wich, S. (2024). Harnessing artificial intelligence for wildlife conservation. *arXiv*. https://doi.org/10.48550/arXiv.2409.10523

Fletcher, R. J., Didham, R. K., Banks-Leite, C., Barlow, J., Ewers, R. M., Rosindell, J., Holt, R. D., Gonzalez, A., Pardini, R., Damschen, E. I. (2018). Is habitat fragmentation good for biodiversity? *Biological Conservation*, 226, 9–15. https://doi.org/10.1016/j.biocon.2018.07.022

Frankham, R. (2015). Genetic rescue of small inbred populations. *Conservation Biology*, 29(2), 366–374. https://doi.org/10.1111/cobi.12472

García-Dorado, A., Caballero, A. (2021). Neutral and deleterious mutation effects. *Genetics*, 217(2), iyaa037. https://doi.org/10.1093/genetics/iyaa037

Garner, B. A., Hoban, S., Luikart, G. (2020). Genomics in conservation. *Conservation Biology*, 34(3), 531–543. https://doi.org/10.1111/cobi.13453

Gu, T., Hu, J., Yu, L. (2024). Evolution and conservation genetics of pangolins. *Integrative Zoology*, 19(3), 426–441. https://doi.org/10.1111/1749-4877.12796

Haddad, N. M., Brudvig, L. A., Clobert, J., Davies, K. F., Gonzalez, A., Holt, R. D., Lovejoy, T. E., Sexton, J. O., Austin, M. P., Collins, C. D. (2015). Habitat fragmentation effects. *Science Advances*, 1(2), https://doi.org/10.1126/sciadv.1500052

Hedrick, P. W., Garcia-Dorado, A. (2016). Understanding inbreeding depression. *Evolution*, 70(3), 500–511. https://doi.org/10.1111/evo.12845

Hoban, S., Bruford, M., Jackson, J. D. U., Lopes-Fernandes, M., Heuertz, M., Hohenlohe, P. A., Paz-Vinas, I., Sjögren-Gulve, P., Segelbacher, G., Vernesi, C. (2020). Genetic diversity targets. *Conservation Biology*, 34(3), 548–556. https://doi.org/10.1111/cobi.13452

Hoelzel, A. R. (2024). 25 years of conservation genetics. *Conservation Genetics*, 25, 1125–1126. https://doi.org/10.1007/s10592-024-01648-0

Hohenlohe, P. A., Funk, W. C., Rajora, O. P. (2021). Population genomics for wildlife conservation and management. *Molecular Ecology*, 30(1), 62–82. https://doi.org/10.1111/mec.15720

Kardos, M., Armstrong, E. E., Fitzpatrick, S. W., et al. (2021). The crucial role of genome-wide genetic variation in conservation. *Proceedings of the National Academy of Sciences*, 118(48). https://doi.org/10.1073/pnas.2104642118

Kardos, M., Qvarnström, A., Ellegren, H. (2017). Inferring inbreeding depression. *Genetics*, 205(3), 1031–1043. https://doi.org/10.1534/genetics.116.198093

Khan, M., Ahmad, S., Malik, A. (2023). Genomic insights into conservation of animal diversity. *Gene*, 147719. https://doi.org/10.1016/j.gene.2023.147719

Kyriazis, C. C., Robinson, J. A., Lohmueller, K. E. (2022). Using computational simulations to quantify genetic load. *Evolutionary Applications*, 15(4), 534–550. https://doi.org/10.1111/eva.13216

Laikre, L., Hoban, S., Bruford, M., Segelbacher, G., Allendorf, F. W., Gajardo, G., Rodríguez, A. G., Hedrick, P. W., Heuertz, M., Hohenlohe, P. A. (2020). Conservation genetics policy. *Biological Conservation*, 246, 108564. https://doi.org/10.1016/j.biocon.2020.108564

Ma, Q., Wu, G., Li, W., Yuzuak, S., Guan, F., Lu, Y. (2023). Research advances in conservation genomics of endangered species. *IntechOpen*. https://doi.org/10.5772/intechopen.112281

Oosterhout, C. (2024). AI-informed conservation genomics. *Heredity*, 132, 1–4. https://doi.org/10.1038/s41437-023-00666-x

Phang, A., Niissalo, M., Ruhsam, M., et al. (2024). Genetic erosion in fragmented populations. *Biodiversity and Conservation*, 33, 2527–2548. https://doi.org/10.1007/s10531-024-02870-5

Pimm, S. L., Raven, P. (2022). Biodiversity crisis. *Science*, 377(6603), 255–256. https://doi.org/10.1126/science.abo2806

Razgour, O., Forester, B., Taggart, J. B., Bekaert, M., Juste, J., Ibáñez, C., Puechmaille, S. J. (2019). Genomic tools in conservation. *Molecular Ecology*, 28(6), 1201–1217. https://doi.org/10.1111/mec.15006

Shafer, A. B. A., Wolf, J. B. W., Alves, P. C., Bergström, L., Bruford, M. W., Brännström, I., Colling, G., Dalén, L., De Meester, L., Ekblom, R. (2015). Genomics and conservation. *Trends in Ecology & Evolution*, 30(9), 549–561. https://doi.org/10.1016/j.tree.2015.07.008

Steiner, C. C., Putnam, A. S., Hoegh-Guldberg, O. (2013). Genetic adaptation. *Global Change Biology*, 19(11), 3365–3373. https://doi.org/10.1111/gcb.12316

Stoffel, M. A., Johnston, S. E., Pilkington, J. G., Pemberton, J. M. (2021). Inbreeding effects. *Nature Ecology & Evolution*, 5, 60–68. https://doi.org/10.1038/s41559-020-01374-7

Supple, M. A., Shapiro, B. (2018). Conservation genomics. *Nature Reviews Genetics*, 19(11), 697–709. https://doi.org/10.1038/s41576-018-0045-5

Wei, S., Fan, H., Zhou, W., Huang, G., Hua, Y., Wu, S., Wei, X., Chen, Y., Tan, X., Wei, F. (2024). Conservation genomics of Chinese pangolin. *Science China Life Sciences*, 67(10), 2051–2061. https://doi.org/10.1007/s11427-023-2540-y