**Journal of Animal Environment**
**(E-ISSN 2717-1396, ISSN 2717-1388)**
Journal homepage: https://aejournals.org/

## Original Research Paper/Review Paper

# Genetic Diversity and Population Viability Assessment of Endangered Ungulates in Isolated and Fragmented Habitats

***Dr. Poonam Singh[1], Dr. Satvik Jain[2], Rachna Kathuria[3]***

*[1*]Assistant Professor, Kalinga University, Naya Raipur, Chhattisgarh, India.*
*Email: ku.poonamsingh@kalingauniversity.ac.in, ORCID: https://orcid.org/0009-0007-6969-314X*
*[2]Assistant Professor, Kalinga University, Naya Raipur, Chhattisgarh, India.*
*Email: ku.satvikjain@kalingauniversity.ac.in, ORCID: https://orcid.org/0009-0005-0714-4255*
*[3]Assistant Professor, New Delhi Institute of Management, New Delhi, India.*
*Email: rachna.kathuria@ndimdelhi.org, ORCID: https://orcid.org/0000-0002-7773-0269*

**Key Words**
Endangered ungulates, Genetic diversity, Habitat fragmentation, Population viability analysis, Inbreeding, Landscape connectivity, Conservation strategies

**Abstract**
Diversity in genes plays an important role in the sustenance and resilience of endangered ungulates especially in isolated habitat patches since lack of connectivity results in inbreeding and increased chances of extinction. Fragmentation of the habitats affects gene movement, changes the demography of the species, and impacts demographic stability. The study sought to explore the genetic diversity, population structure, and demographic stability of endangered ungulates within habitat patches and the success of conservation initiatives in their sustainability. Population size, population density, population structure, and distribution were determined through surveys in twelve habitat patches. Genetic sampling involved the collection of DNA from 420 individuals using non-invasive methods. Genetic diversity parameters, inbreeding coefficients, and gene flow were examined. The models used for landscape genetics and Population Viability Analysis (PVA) included connectivity and extinction probability under present and management scenarios. The population density was between 0.88 and 2.00 individuals/km2, and effective population size (Ne) was between 28 and 184. Heterozygosity was found to decrease from 0.72 to 0.41 and allelic richness decreased from 11.4 to 5.8 due to increasing levels of isolation, while inbreeding coefficients increased from 0.04 to 0.19. PVA predicted an extinction probability of 37.8% under the current situation, but if an integration strategy for conservation, such as habitat enhancement, corridors, and assisted gene flow, were implemented, it was expected to be reduced to 2.1%. It is very essential for maintaining genetic diversity and ensuring sustainability that landscape connectivity be maintained and integrated strategies for demography, genetics, and landscape be employed.

* Corresponding Author's email: ku.poonamsingh@kalingauniversity.ac.in
Received: 25th May, 2026; Revised: 6th June, 2026; Accepted: 8th June, 2026; Available Online: 07th August, 2026
(DOI): 10.70102/AEJ.2026.18.3s.39

## Introduction

Genetic diversity is vital in the conservation of the wildlife because it is the basis of a species that adapts to environmental changes, disease resistance and healthy population dynamics (Kiran et al., 2025). This results in a high probability of extinction due to the increased tendencies of inbreeding, low reproduction fitness, and elevated exposure to stochastic occurrences in populations with low genetic variation. Conserving genetic diversity is particularly important to the long-term survival and ecological functioning of endangered ungulates, which typically inhabit niche habitats and have a limited population in their ecosystems (Ajitha et al., 2025; Rajan & Chawla, 2024). The process of habitat fragmentation is among the main threats to the ungulates as it result in solitary patches limiting movement and gene flow. The lack of cohesive landscapes may lead to genetic drift and breeding, as well as boosting the human-wildlife, poaching, and habitat depreciation (Arvinth, 2025; Patil, 2018). The impact of fragmentation on population structure and ability to stay connected is vital to predict the persistence of species and determine those populations that are at highest risk. Population viability assessments (PVA) are used to provide a quantitative method to determine the stability of the population, the likelihood of extinction, and the success of possible management actions (Patil & Das, 2024). An objective of this study is to determine the genetic variation and sustainability of endangered ungulates in isolated and fragmented habitat. In particular, it deals with three research questions: What is the degree of genetic diversity within and between fragmented populations? The extent of gene flow between isolated subpopulations? And what is the ideal population dynamics be using various conservation or management scenarios? Through a combination of molecular genetic studies and PVA modeling, the research aims to offer practical suggestions on how conservation action plans that increase the resiliencies and persistence of these diseasy species can be undertaken.

- Offers an in-depth evaluation of genetic diversity and population framework of endangered ungulates in isolated and fragmented bases.
- Population Viability Modeling with Molecular Genetic Informatics Integrates molecular genetic examinations with population viability projections to forecast incitiation of lengthy enduring presence under diverse administration and protection setups.
- Provides evidence-based suggestions to inform conservation planning, habitat connectivity recovery, and specific interventions of maintaining viable populations.

The paper is structured in the following way: Section I presents objectives and significance of genetic diversity in the study. Section II summarizes the literature on genetic variation, the effects of population viability and fragmentation. Section III notes the methodology, such as the selection of habitats, the survey of population, genetic sampling, DNA

analysis and statistical validation. Part IV includes findings regarding population demographics, genetic variety and predictions of viability. Section V discusses the findings and conservation implications. A conclusion of section VI contains the essential insights, policy recommendations and postulates on future research and monitoring over a long period.

## Literature Review

Genetic diversity is a major constituent of wildlife conservation, as it is basic foundation of adaptability of a species to environmental changes, resistance to diseases, and healthy population dynamics. The researchers emphasize that in most cases, isolated populations of ungulates tend to decline genetically, and genetic rescue measures and interventions aimed at restoring the variability can re-establish variation and avert the risk of extinction (Poirier et al., 2019). Also, illustrate how the population viability analysis (PVA) might inform genetic rescue work to protect locally unique genetic richness, with a particular focus on how predictive modeling might inform conservation planning (Zilko et al., 2021).

Fragmentation has always been found to adversely affect the genetic diversity and population structure. The experiment evaluated the endangered Grauer gorillas whose habitats have been disrupted and this has shown that the draining habitats cause decreased allelic burden and elevated inbreeding (Baas et al., 2018). It was also established in the study that spatial isolation coupled with environmental variation are involved into the loss of genetic diversity in key stone ungulates and thus isolation-by-distance and isolation-by-environment effects occurred (de Góes Maciel et al., 2024). Likewise, it also found that preferred habitat and effective population size determine landscape genetic patterns, with habitat characteristics interacting with demography to define connectivity (Weckworth et al., 2013).

Various reports have used genetic and landscape analyses to endangered ungulates. The researchers have measured population organization, genetic variation and connectivity of the arabian tahr which prove that the break landscapes diminish the gene flows and heighten extinction threats (Ross et al., 2020). The authors investigated the isolated trout population demonstrating that the viability of population is dependent on life history characteristics and local adaptation (Carim et al., 2017). This paper showed the influence of fragmented habitats on genetic structure of Cantabrian capercaillie populations, which supports the requirement to maintain habitat connectivity (Vázquez et al., 2012). More recently, there is analyzed reintroduced grassland ungulates, which indicated that marginal population groups tend to show diminished genetic diversity, and hence the significance of observing and controlling marginal populations (Rue et al., 2026).

Isolation and habitat fragmentation repeatedly cause genetic diversity loss and inbreeding, undermining population sustainability in endangered ungulates. Population size, connectivity of habitats, and local adaptation are the key aspects that contribute to resilience. Plastics The population viability tests and genetic rescue options enhance persistence, and genetic,

demographic, and landscape methods have been shown to be influential in ensuring connectivity and long-term survival of fragmented populations.

## Methodology

This paper combines field investigation, genetic and statistical modeling to determine population and genetic health dynamics of endangered ungulates residing in fragmented areas. The general workflow is presented in figure 1. GIS and remote sensing are used to choose study areas and characterize them. Surveys of the population determine size, density, and demographic factors using transect, camera traps, and observations. The non-invasive genetic samples are collected, DNA extracted and genotyped is done to compare genetic diversity, structure and gene flow. The connectivity and dispersal constraints are measured using landscape genetics. The Population Viability Analysis (PVA) is used to predict the future situation, and the inbreeding and genetic risk measurement are used to identify specific population groups at risk. The prioritization of conservation is made under a combination of the demographic, genetic, and landscape understanding. Any analysis is statistically validated in order to achieve strong findings.

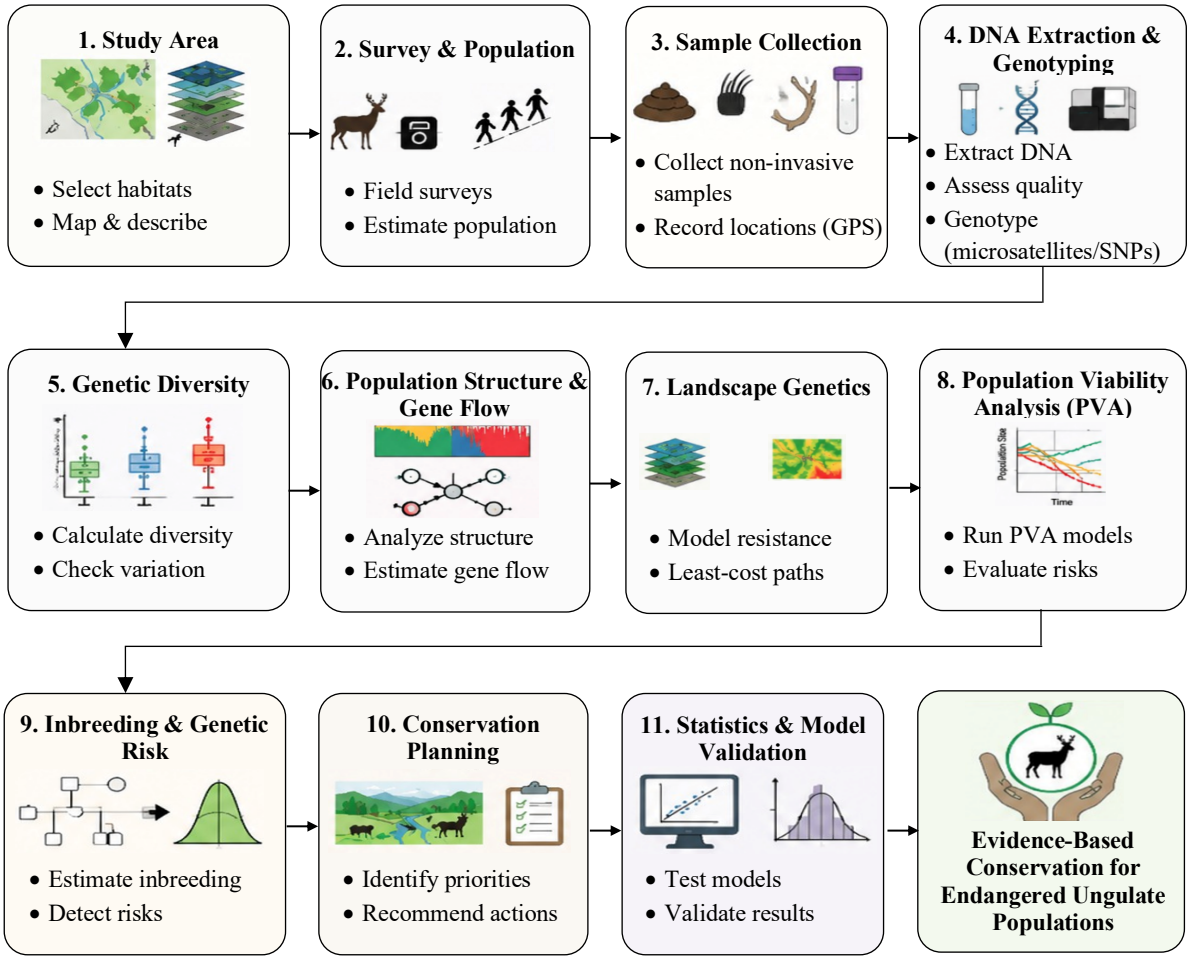


Figure 1: Methodology Workflow for Population and Genetic Assessment of Endangered Ungulates

## Study Area Selection and Habitat Characterization

The research is carried out with respect to isolated and fragmented habitats with populations of endangered ungulates. The selection of appropriate sites for study takes into consideration such criteria as fragmentation levels of habitat, geographic isolation, population density, and the degree of protection. GIS databases are used along with other remote sensing data to create maps of habitat patches, determine the presence of landscape barriers, measure habitat connectivity, and estimate the changes in land use. Habitat parameters like vegetation cover, water access, elevation, and anthropogenic disturbances are recorded.

## Population Survey and Demographic Assessment

The field survey involves the determination of population size, density, age composition, sex ratio, and distribution of the ungulate species in question. Methods such as direct observation, camera trapping, line transects, and distance sampling are used to gather the demographic data. In appropriate cases, capture-mark-recapture analysis and occupancy analysis are done to enhance the estimates of the population.

## Genetic Sample Collection

The non-invasive and minimally invasive sampling methods are employed for extracting DNA from individual specimens. The samples include fecal matter, hair, shed antlers, biopsy samples, and even blood taken from various habitat fragments. These samples are marked down on GPS coordinates to facilitate a study that would include spatial genetics. Specialized care is taken while preserving the samples to ensure that the DNA does not degrade.

## DNA Extraction and Genotyping

Genomic DNA is isolated from biological samples using standard molecular techniques. Quality and quantity of isolated genomic DNA are estimated by spectrophotometric and electrophoretic measurements. Variation within genomes is studied using genetic markers like microsatellites, mitochondrial DNA, and SNPs. PCR amplification and high-throughput sequencing techniques are used for obtaining reliable genotyping data from each sample.

## Genetic Diversity Analysis

The level of genetic diversity between and within populations is assessed through population genetic indices. The observed heterozygosity, expected heterozygosity, number of alleles, nucleotide diversity, and inbreeding coefficient are some of the values that are analyzed. Using statistical computer programs, the level of genetic variation is established and population groups that experience genetic erosion are identified.

## Population Structure and Gene Flow Assessment

Genetic structuring of the population is performed in order to study the differentiation level between isolated population fragments. The Bayesian clustering approach, principal coordinates analysis, and analysis of molecular variance are used to find out genetic clusters and analyze population subdivision. Gene flow and migration rates between habitat fragments are

studied via assignment tests and connectivity modeling.

### Landscape Genetics Analysis

Landscape genetics techniques are used to explore the connections between the environment and genetic connectivity. Resistance models are created based on information regarding land cover, topography, and anthropogenic disturbances. The circuit theory and the least-cost path model can be used to recognize migration corridors and obstacles. Correlation analysis is conducted to identify the variables that have an impact on gene flow and genetic connectivity.

### Population Viability Analysis

Population Viability Analysis (PVA) is an operation to determine the likelihood of short-term and long-term existence of the population given the current and future environment. The level of survival, the success rate of reproduction, mortality rate, carrying capacity, and genetic information are some demographic parameters integrated into simulation models. Various scenarios that model habitat loss, climate change, decreased connectivity and conservation interventions are used to model the likelihood of extinction and population growth over time.

### Inbreeding and Genetic Risk Assessment

The research evaluates the inbreeding rates and possible genetic perils related with small isolated populations. Indicators of effective population size, relatedness coefficient and inbreeding depression are estimated. The genetic bottlenecks and the past decline in human populations are detected with specialized statistical tests. The findings give insights on the genetic susceptibilities that can destroy long-term population sustainability.

### Conservation Priorities and Management Recommendations

Demographic, genetic and viability outcomes are combined to designate populations at most risk of decline. Habitat corridors, translocation, assisted gene flow, and habitat restoration initiatives are considered conservation options. Priority conservation areas are determined through genetic uniqueness, population stability and landscape connectivity. Recommendations are made to contribute to evidence-based management and recovery planning towards endangered ungulate populations in fragmented ecosystems.

### Statistical Analysis and Model Validation

Any genetic, demographic and landscape data is exposed to statistical verification and sensitivity analysis. Significant relationships among variables are evaluated using comparative tests, regression analyses and multivariate models. Population viability models are confirmed with historical data and observed data in the field. Internal consistency: The confidence limits, significance levels, and levels of uncertainty are reported to make study findings strong and reliable.

## Results

### Population Structure, Demographic Characteristics

Field surveys carried out in fragmented sections of habitat located a total of 1,247

endangered ungulates in 12 isolated habitat fragments. The connectivity and size of habitat were significantly linked to population abundance. The relatively stable populations with equal age distributions and excited juvenile recruitment rates were supported by larger patches of habitats, and lower population numbers and decreased recruitment were found in smaller isolated fragments. Study sites had mean population density between 0.88 to 2.00 people per km $^{2}$. The statistical test showed a strong correlation ($r = -0.79$, $p = 0.001$) between distance to a habitat iso and population size that increasing fragmentation negatively influenced population persistence.

Table 1: Demographic Characteristics of Populations in Fragments of Habitat

| Habitat Patch | Area (km²) | Population Size | Density (Ind/km²) | Juvenile (%) | Adult (%) | Effective Population Size (Ne) |
|---|---|---|---|---|---|---|
| P1 | 265 | 232 | 0.88 | 24.6 | 75.4 | 184 |
| P2 | 218 | 198 | 0.91 | 23.8 | 76.2 | 163 |
| P3 | 175 | 162 | 0.93 | 22.9 | 77.1 | 137 |
| P4 | 132 | 118 | 0.89 | 21.5 | 78.5 | 104 |
| P5 | 110 | 103 | 0.94 | 20.7 | 79.3 | 88 |
| P6 | 94 | 89 | 0.95 | 20.1 | 79.9 | 74 |
| P7 | 81 | 78 | 0.96 | 19.4 | 80.6 | 63 |
| P8 | 69 | 70 | 1.01 | 18.8 | 81.2 | 55 |
| P9 | 52 | 63 | 1.21 | 17.9 | 82.1 | 46 |
| P10 | 44 | 53 | 1.20 | 16.8 | 83.2 | 39 |
| P11 | 31 | 45 | 1.45 | 15.6 | 84.4 | 33 |
| P12 | 18 | 36 | 2.00 | 14.2 | 85.8 | 28 |

Table 1, an increase in habitat patches correlates with high population size and effective population size. The population size is seen to reduce from 232 individuals in P1 to 36 individuals in P12 because the habitat patch area is decreasing from 265 km² to 18 km². At the same time, the density of the patches rises as the patches become smaller, going up to 2.00 ind/km² in P12. Juvenile percentages fall from 24.6% to 14.2%, while adults increase.

The demographic trends observed imply that fragmentation of habitats may have lowered the growth possibilities within small habitat patches. Effective population size is important for maintaining long-term adaptability and stability genetically, and this was seen among the populations occupying bigger habitats. On the other hand, populations living in very isolated areas showed decreasing numbers of juveniles, thus having smaller effective population size.

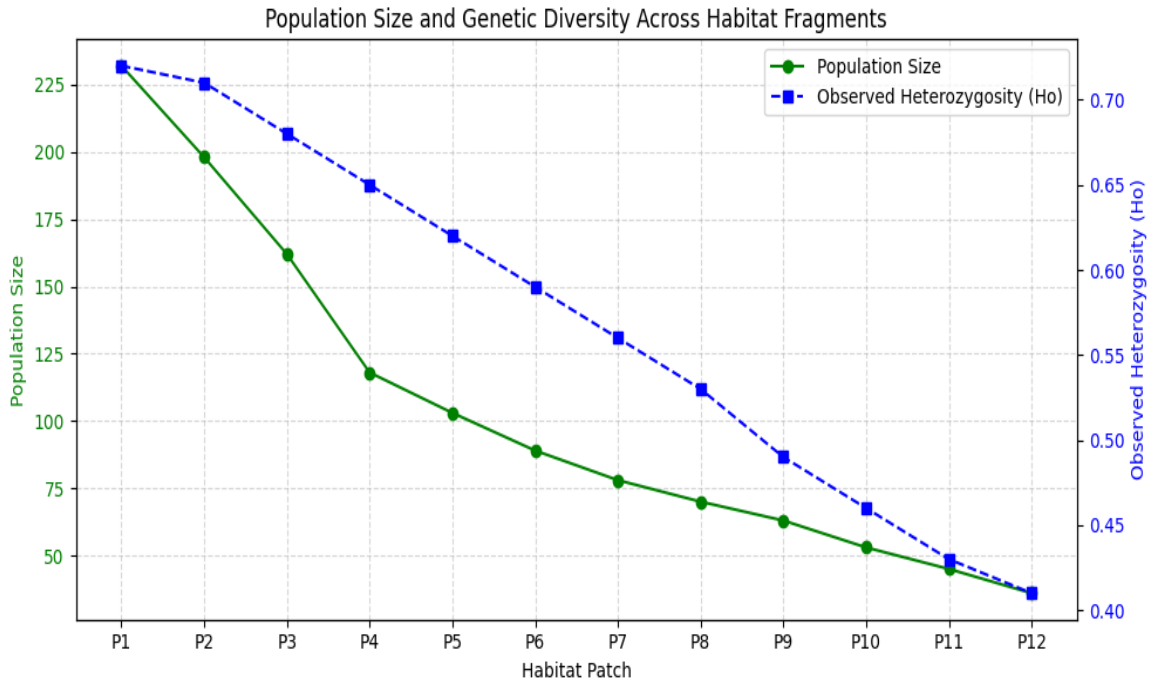


Figure 2: Population Size and Genetic Diversity Across Habitat Fragments

Figure 2 illustrates interdependence between habitat fragmentation, population size and genetic diversity (observed heterozygosity, Ho) in twelve habitat patches (P1-P12) and so on. The population size decreases to 232 (P1) to 36 (P12) in the biggest and the biggest patch, respectively. Likewise, there is a tradeoff between isolation and genetic diversity and Ho values in P1 are 0.72 with Ho values decreasing to 0.41 in P12. This pattern indicates that bigger and more interconnected habitats support greater population levels and genetic diversity, and smaller and more isolated habitats have low juvenile presence, lower heterozygosity and a high risk of inbreeding, stressing the susceptibility of populations in disintegrated landscapes.

## Genetic variability and Population viability test

Genetic patterns of 420 sampled subjects showed that there was a lot of genetic diversity between fragments of habitats. On the one hand, observed heterozygosity was lower at greater distances between habitats and in isolated populated populations than in well-connected ones, with heterozygosity diminishing to 0.41 in the highly isolated populations. Likewise, there was a decrease of allelic richness between 11.4 and 5.8 along the fragmentation gradient. Coefficients of inbreeding were greater in smaller groups, and gene flow was limited and genetic drift greater. Simulations of population viability had given an estimated probability of extinction of 37.8% within the next 100 years under present habitat amounts, with a decreasing trend predicted. Scenarios involving conservation that included habitat restoration,

corridor creation and assisted gene flow in conservation scenarios were in a great position to enhance population growth rates and decreased the chances of extinction. The comprehensive conservation plan had the best result, growing estimated population size to 2,684 individuals with a low possibility of 2.1 to face extinction.

Table 2: Genetic Diversity and Population Viability Indicators

| Habitat Patch | Observed Heterozygosity (Ho) | Expected Heterozygosity (He) | Allelic Richness | Inbreeding Coefficient (FIS) | Extinction Risk Category |
|---|---|---|---|---|---|
| P1 | 0.72 | 0.75 | 11.4 | 0.04 | Very Low |
| P2 | 0.71 | 0.74 | 10.9 | 0.04 | Very Low |
| P3 | 0.68 | 0.72 | 10.3 | 0.06 | Low |
| P4 | 0.65 | 0.69 | 9.8 | 0.07 | Low |
| P5 | 0.62 | 0.67 | 9.1 | 0.08 | Moderate |
| P6 | 0.59 | 0.65 | 8.7 | 0.09 | Moderate |
| P7 | 0.56 | 0.62 | 8.2 | 0.10 | Moderate |
| P8 | 0.53 | 0.60 | 7.8 | 0.12 | High |
| P9 | 0.49 | 0.57 | 7.1 | 0.14 | High |
| P10 | 0.46 | 0.55 | 6.6 | 0.16 | High |
| P11 | 0.43 | 0.52 | 6.1 | 0.18 | Very High |
| P12 | 0.41 | 0.50 | 5.8 | 0.19 | Very High |

Table 2, with increasing habitat fragmentation, there is a decrease in the level of genetic variation. For instance, heterozygosity goes from 0.72 in P1 to 0.41 in P12, while allelic richness falls from 11.4 to 5.8. Also, the inbreeding coefficient elevates from 0.04 to 0.19. The threat of extinction shifts from very low in bigger fragments to very high in P11 & P12.

The genetic findings reveal that population genetic health is greatly affected by habitat fragmentation. Lack of connectivity reduced dispersal across habitat patches, which led to reduced heterozygosity, allelic diversity loss as well as high (inbreeding) levels. These genetic impacts had direct impact on population viability making isolated population more vulnerable to extinction. The results suggest that landscape connectivity needs to be a priority in conservation to maintain genetic diversity and long-term survival to endangered ungulate populations in fragmented ecosystems through the facilitation of genetic flow.

In totality, the research shows that genetically resilient and less vulnerable populations are found in greater and interconnected habitats whereas the isolated populations have a genetic erosion and demographic instability. Conservation measures that integrate habitat restoration, corridor management, and genetic management are thus required to boost population viability and promote long-term survival of endangered ungulates.

## Discussion

The findings clearly indicate that habitat fragmentation has a significant influence both on the demographic stability and gene health of endangered ungulate populations. Larger, more interconnected patches were associated with greater population sizes and age structure evenness, and high levels of juvenile recruitment, whilst smaller fragments were characterized by low population numbers, low juvenile recruitment and a decreasing effective population size, which is indicative of the high sensitivity to demographic stochasticity. Genetic data showed that observed heterozygosity (Ho: 0.72 → 0.41) and allelic richness (11.4 → 5.8) decreased progressively with increasing isolation with the increase in inbreeding coefficients (FIS: 0.04 → 0.19) that indicated the limitation of gene flow and augmentation of genetic drift. Population viability model also suggested a probability of 37.8 extinction likelihood under standard circumstances, which gradually enhanced with regard to partnership conservation methods involving habitat restoration, corridors, and conception of assisted gene flow. All in all, the results support the fact that a landscape continuity is needed to preserve the genetic diversity, the demographic stability and long-term persistence of ungulates in fragmented environments through the introduction of integrated management intervention.

## Conclusion

This analysis demonstrates that habitat fragmentation generates a strong effect on both the demographic stability and genetic health of threatened ungulate populations as larger, well-linked patches of habitat bore higher population densities (0.882.00 individuals /km 2 ) with age structuring amongst animals and effective population sizes (Ne: 184137), whereas smaller and remote patches of habitat had decreasing juvenile underscaling and Ne-values as low as 28, which reflect heightened vulnerability to demographic stochasticity. Genetic studies on 420 surveyed individuals showed that observed heterozygosity was decreasing progressively between 0.72 in well-connected populations to 0.41 in highly isolated populations and allelic richness was decreasing to 5.8 and inbreeding coefficients increased to reach 0.19, which indicated that there was limited gene flow and increased genetic drift along fragmented topographies. It had been estimated by population viability simulations that there was a 37.8% extinction probability under present conditions, and this was significantly lowered to 2.1% with purposeful conservation measures, such as habitat restoration, the creation of ecological corridors, and assisted gene flow. These findings highlight the need to keep landscape connected and implement evidence-based responses to support viable population and long-term genetic diversity. Long-term population and genetic trend monitoring, cross ecological and species comparisons, using climate change projections and evaluating the anthropogenic-wildlife interface should be emphasized in future research to support adaptive conservation planning. The results can give concrete policy insights to policymakers and conservation organizations about the need to achieve a balanced management between

demographic, genetic, and landscape management to improve the persistence and resilience of endangered ungulates in fragmented environments.

## Ethical Considerations

All of the fieldwork and genetic sample work adhered to international standards of ethical treatment of wildlife. Minimal and non-invasive procedures were primarily used so as to reduce the level of stress and animal disturbance. Before the field surveys and sample collection, permission and approvals were obtained with respect to the wildlife authorities as well as the institutional ethics committees.

## Author Contributions

**Funding:** No funding was received for this research.

**Conflict of Interest:** The authors declare that there are no conflicts of interest associated with this research. All analyses and interpretations were conducted objectively without any financial or personal influences affecting the outcomes.

## References

[1] Ajitha, K., C. Samuel Joseph, D. Mahila Vasanthi Thangam, and K. Lakshmipriya. “Genomic Insight–Enabled Economic Forecasting for Sustainable Agri-Biotech Markets.” *International Academic Journal of Science and Engineering* 12, no. 4 (2025): 211–223. https://doi.org/10.71086/IAJSE/V12I4/IAJSE1290

[2] Arvinth, N. "Wildlife Conservation in Anthropogenically Altered Landscapes: Challenges, Strategies, and Adaptive Pathways." *Journal of Animal Habitat and Environmental Interactions* (2025): 7-12.

[3] Baas, Pauline, Tom van der Valk, Linda Vigilant, Urbain Ngobobo, Escobar Binyinyi, Radar Nishuli, Damien Caillaud, and Katerina Guschanski. "Population-level assessment of genetic diversity and habitat fragmentation in critically endangered G rauer's gorillas." *American Journal of Physical Anthropology* 165, no. 3 (2018): 565-575. https://doi.org/10.1002/ajpa.23393

[4] Carim, K. J., Yngvild Vindenes, Lisa A. Eby, Craig Barfoot, and Leif Asbjørn Vøllestad. "Life history, population viability, and the potential for local adaptation in isolated trout populations." *Global Ecology and Conservation* 10 (2017): 93-102. https://doi.org/10.1016/j.gecco.2017.02.001

[5] de Góes Maciel, Fernanda, Sean O’Rourke, Melissa Jones, William Hemstrom, Michael Ryan Miller, Gabriela Schmaedecke, Leandro Reverberi Tambosi et al. "Loss of genetic diversity and isolation by distance and by environment in populations of a keystone ungulate species." *Conservation Genetics* 25, no. 4 (2024): 939-953. https://doi.org/10.1007/s10592-024-01614-w

[6] Kiran, N. C., Boregowda, V. K. S., Vaishnav, J., Singh, S., Singh, M., & Seth, K. Enhancing Wildlife Conservation through Sensor and Deep Learning

Integration for Accurate Animal Behavior Tracking. *Journal of Wireless Mobile Networks, Ubiquitous Computing, and Dependable Applications*, *16*(3), 261-280. https://doi.org/10.58346/JOWUA.2025.I3.015

[7] Patil, P. J. “An Ecological Analysis of Forest Accounting.” *International Academic Journal of Innovative Research* 5, no. 1 (2018): 109–127. https://doi.org/10.9756/IAJIR/V5I1/1810010

[8] Patil, S., and A. Das. “Encouraging Future Generations with Environmental Education.” *International Journal of SDG’s Prospects and Breakthroughs* 2, no. 4 (2024): 24–29.

[9] Poirier, Marc-Antoine, David W. Coltman, Fanie Pelletier, Jon Jorgenson, and Marco Festa-Bianchet. "Genetic decline, restoration and rescue of an isolated ungulate population." *Evolutionary Applications* 12, no. 7 (2019): 1318-1328. https://doi.org/10.1111/eva.12706

[10] Rajan, Vinod, and Roshni Chawla. "Anthropometric Variations and Adaptations across Diverse Ecological Zones." *Progression journal of Human Demography and Anthropology* (2024): 1-4.

[11] Ross, Steven, Jean-Marc Costanzi, Mansoor Al Jahdhami, Haitham Al Rawahi, Muhammad Ghazali, and Helen Senn. "First evaluation of the population structure, genetic diversity and landscape connectivity of the Endangered Arabian tahr." *Mammalian Biology* 100, no. 6 (2020): 659-673. https://doi.org/10.1007/s42991-020-00072-4

[12] Rue, Jeff W., Jennifer R. Adams, Jon P. Beckmann, and Lisette P. Waits. "Genetic diversity and genetic structure near the range periphery of a reintroduced endemic grassland ungulate." *Conservation Genetics* 27, no. 2 (2026): 29. https://doi.org/10.1007/s10592-026-01763-0

[13] Vázquez, José F., Trinidad Pérez, Francisco Quirós, José R. Obeso, Jesús Albornoz, and Ana Domínguez. "Population genetic structure and diversity of the endangered Cantabrian capercaillie." *The Journal of Wildlife Management* 76, no. 5 (2012): 957-965. https://doi.org/10.1002/jwmg.346

[14] Weckworth, Byron V., Marco Musiani, Nicholas J. DeCesare, Allan D. McDevitt, Mark Hebblewhite, and Stefano Mariani. "Preferred habitat and effective population size drive landscape genetic patterns in an endangered species." *Proceedings of the Royal Society B: Biological Sciences* 280, no. 1769 (2013). https://doi.org/10.1098/rspb.2013.1756

[15] Zilko, Joseph P., Dan Harley, Alexandra Pavlova, and Paul Sunnucks. "Applying population viability analysis to inform genetic rescue that preserves locally unique genetic variation in a critically endangered mammal." *Diversity* 13, no. 8 (2021): 382. https://doi.org/10.3390/d13080382