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Original Research Paper

Synergizing Ecological Modelling and Genetic Conservation Strategies for Species Reintroduction and Habitat Restoration

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Key Words
Wildlife reintroduction, Habitat restoration, Ecological modelling, Conservation genetics, Genetic diversity, Population viability.

Abstract

Reintroduction and restoration of habitats are popular methods of restoring threatened animal species and reintroduction is a success that has not been consistently successful because of the lack of integration of ecological and genetic factors. This work will bring forward a combined framework that will integrate ecological modelling and genetic conservation approaches to aid in the evidence-based animal reintroduction planning. An assessment of habitat suitability and landscape connectivity was done among candidate reintroduction sites, and values of Habitat Suitability Index (HSI) were 0.48 to 0.82, and a landscape connectivity index of 0.31-0.76. Genetic analyses of candidate source populations showed that there was an anticipated heterozygosity range of 0.54-0.71 and inbreeding coefficients of 0.04-0.18, which is a wide range of variation in genetic viability. A combination of ecological and genetic measures gave composite scores of viabilities between 0.32 and 0.84 among site-population interactions. The scenarios that incorporated high habitat and connectivity with genetically strong source populations were always found to score high viability (>0.75), and the ones that incorporated fragmented habitats and genetically weak populations were found to score low viability (<0.50). The results show that ecological suitability and genetic quality are not sufficient factors to guarantee the success of reintroduction. The suggested framework offers a clear and quantitative methodology for setting priorities in reintroduction sites, source population selection, and habitat restoration to increase long-term population survival.

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Introduction

The reintroduction of species and habitat restoration are becoming common methods in reversing the changes of animal populations caused by habitat loss, fragmentation, and environmental alteration. Nonetheless, the success of reintroduction over time is still unreliable because not all reintroduction initiatives can lead to self-sufficient populations, even after a significant conservation investment has been made (Fischer & Lindenmayer, 2000). Initial syntheses in reintroduction biology highlighted that failure is commonly caused by poor planning structures that lack adequacy to combine ecological, demographic, and biological limitations (Armstrong & Seddon, 2008; Seddon et al., 2007).

Ecological modeling has become a focal point in the contemporary restoration of wildlife as it has been used to perform strategic assessment of the habitat, population endurance, and landscape structure. Innovations in reintroduction models have shown that a combination of various ecological models can enhance accurate predictions and aid in making decisions in a state of uncertainty (Hunter-Ayad et al., 2020). Analysis: Population viability and reserve selection algorithms have further enhanced conservation planning by providing a relationship between the availability of a habitat and the extinction risk at a spatial scale (Carroll et al., 2003). Behavioral population models further emphasize the importance of animal movement, habitat choice, and dispersal in population growth and achievement of establishment success (Sutherland & Norris, 2002).

Simultaneously, hereditary factors have been identified as important determiners of the reintroduction results. Small numbers used in reintroduced populations tend to create a weakened genetic diversity, depression of inbreeding, and poor adaptations, especially in varying environmental conditions (Weeks et al., 2011; Sindhu, 2024). Conservation genetics is thus now a viable management science, and some of the paradigms are well supported and are used to inform genetic monitoring, genetic rescue, and adaptive potential management of threatened species (Willi et al., 2022). It has been shown that, given a careful selection of the source population based on genetic composition, a significant degree of success can be achieved in reintroduction (Houde et al., 2015). The merging of evolution with demographics is one of the important developments in conservation science. By including genetic dynamics into the population viability models, it is now possible to consider long-term persistence on a more realistic footing by integrating demography and genetics (Pierson et al., 2015). Research on reintroduction

At larger scales, increasing rates of land-use transformation have driven terrestrial biodiversity to unsafe levels on Earth, highlighting the urgency of conservation efforts based on restoration (Newbold et al., 2016). International evaluations have determined areas of priority in which the restoration of the ecosystem can maximize the recovery of biodiversity and the resilience of the ecological environment (Strassburg et al., 2020). The application of wildlife restoration has been increasingly focusing on integrated habitat analysis, animal surveillance, and adaptive management to aid in long-term conservation outcomes (Morrison, 2013). Community-based conservation is another issue that has become a key facilitating factor, enhancing the sustainability of wildlife management by engaging the locals in management and as custodians (Dash et al., 2025). Other environmental stressors, such as the effects of climatic changes on freshwater and on land ecosystems, add further reinforcement to the need for holistic and ecosystem-based restoration strategies (Godefroid et al., 2011). It is against this context that this research contributes to a unified framework of ecological modeling and genetic conservation measures to steer the process of species reintroduction and habitat restoration (Lawrence & Kaye, 2011). The approach will enhance the reintroduction planning and the long-term persistence of restored animal populations in complex landscapes by integrating habitat suitability, landscape connectivity, and genetic viability into one decision-support system (Mishra, 2024).

The research contributes to the science of reintroduction and restoration in three aspects. First, it suggests an integrated ecological-genetic model that clearly combines the habitat suitability, landscape connectivity, and population genetic viability in one decision support model. Second, it illustrates the use of this framework with the help of quantitative ecological and genetic indicators to assess the candidate reintroduction sites and source populations. Third, it offers a value-based, open approach of prioritizing habitat restoration and reintroduction conditions, evidence-based conservation planning in environmentally changing conditions.

The rest of the paper is structured in the following way. Section 2 outlines the methodological framework and analytical approach by integrating the ecological and genetic approaches. In section 3, the findings of habitat suitability, genetic assessment, and integrated viability evaluation are offered. Section 4 explains how the framework has implications for reintroducing a species and restoring its habitat. Then it concludes by giving some important findings and future perspectives on the integrated conservation planning.

Materials and Methods

Methodological Framework

In this research, a conceptual synthesis method is used that involves the combination of ecological modeling and genetic conservation principles into a single concept to be used in the reintroduction of the species and restoration of the habitat. The framework is set to influence evidence-based decision-making through a systematic provision of connections between the environmental suitability, landscape connectivity, and genetic viability. Figure 1 illustrates the general working process and the analysis relationships between the components, which is a conceptual representation of the methodological approach.

Figure 1 demonstrates the proposed Integrated ecological-genetic methodological approach to species reintroduction and habitat restoration. This is a theoretical model of the procedures, explaining the interrelationship between ecological and genetic parts, and is not an empirical finding. The figure provides a summary of the input data, ecological modelling and connectivity analysis, genetic assessment and management, a combination of ecological and genetic data, and decision-making processes outlined in the Methods section. It is a conceptual figure and is not the result of empirical findings.

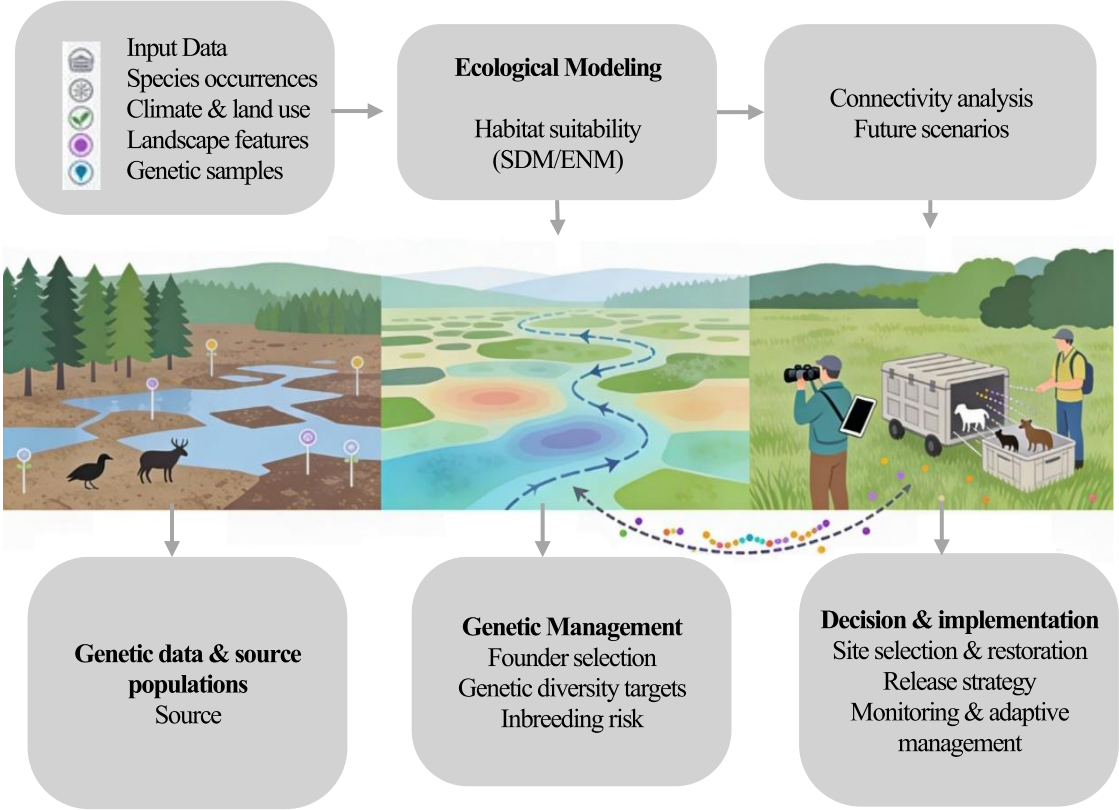

Figure 1: Integrated Ecological–Genetic Methodological Framework for Species Reintroduction and Habitat Restoration

Ecological Data and Modeling

The ecological modeling is concerned with determining landscapes that can sustain possible animal populations. The habitat suitability is measured using species distribution or ecological niche modeling methods using species occurrence records, climatic variables, land-use data, and landscape features (Saidova et al., 2024). To analyze key landscape-scale connectivity metrics, such as landscape fragmentation, dispersal routes, and permeability in the long term, these models are supported by landscape-level connectivity analyses to analyze alternative future scenarios.

Population Viability and Restoration Planning

Population viability is also put in place to assess the stability of the population and the risk of extinction of different populations given different management conditions. The results of the ecological model are inferred within a framework of population viability to determine the ability of ecological candidate reintroduction sites to sustain populations in the long run. The restoration planning also takes into consideration the habitat quality and ecological similarity of the source and release sites that have been found to contribute to the establishment success.

Genetic Data and Source Population Evaluation

Genetic assessment is aimed at defining the proper source populations and reducing the genetic risks of reintroduction. Genetic information is utilized to measure diversity, an effective population size, and a risk of inbreeding, among others, and assist in the selection of founders and genetic management. Selection of source populations is done according to their genetic compatibility and demographic factors so as to minimize chances of inbreeding or maladaptation. The evaluation of genetic risks due to translocations in fluctuating or changing environments is conducted in accordance with the well-known conservation genetics principles (Weeks et al., 2011).

Integration and Management Implementation

Ecological and genetic products are combined in a multi-criteria state of evaluation that is synthesized with the suitability of the habitat and its connectivity to the genetic viability. Specifically, evolutionary mechanisms are directly taken into account in demographic evaluations in order to model the interaction between genetic diversity and population persistence. The integrated framework helps in practical management decision-making, such as site selection, priorities of the restoration of the habitat, release strategy design, and post-release monitoring (Morrison, 2013). The broader restoration aims are linked to the international ecosystem restoration needs and biodiversity conservation models to sustain the long-term sustainability (Strassburg et al., 2020; Newbold et al., 2016). There is inclusion of community-based conservation principles to support stakeholder involvement and promote long-term conservation results (Swaisgood, 2010). To facilitate analytical clarity, the site of reintroduction of the candidates, as defined by ecological modeling, was later given an anonymous name

Results

Habitat Suitability and Landscape Connectivity

Table 1 shows that ecological modeling indicated a high rate of spatial heterogeneity of habitat suitability and landscape connectivity across the candidate reintroduction area. The value of Habitat Suitability Index (HSI) varies, that is, between low and high, which implies that the environment and restoration potential are heterogeneous. High-priority sites had high suitability and strong connectivity, implying that they were good at supporting viable animal populations. Conversely, less suitable sites were also found to have a low degree of connectivity and high anthropogenic disturbance, potentially constraining dispersal and long-term persistence.

Table 1: Habitat Suitability and Restoration Potential Across Candidate Reintroduction Sites

Site ID	Habitat Suitability Index (HSI)	Landscape Connectivity Index	Human Disturbance Score	Restoration Priority
Site A	0.82	0.76	0.21	High
Site B	0.74	0.61	0.35	Moderate
Site C	0.69	0.58	0.42	Moderate
Site D	0.56	0.39	0.63	Low
Site E	0.48	0.31	0.71	Low

Genetic Diversity and Source Population Assessment

Table 2 shows genetic measures of genetic diversity and risk of inbreeding difference between candidate source populations through genetic assessment. The heterozygosity and allelic richness were expected to differ among populations, and this showed the variation in the potential for evolution. Genetically diverse populations were found to have smaller inbreeding coefficients, meaning that they are more suitable as source populations in reintroduction. Conversely, less diverse populations exhibited increased risk of inbreeding phenomena, which indicate possible genetic limitations in the long term, if it is not utilized with management control.

Table 2: Genetic Diversity Metrics for Candidate Source Populations

Population	Expected Heterozygosity (He)	Allelic Richness	Inbreeding Coefficient (FIS)	Genetic Status
Pop 1	0.71	6.4	0.04	Genetically robust
Pop 2	0.68	5.9	0.06	Stable
Pop 3	0.63	5.2	0.09	Moderate risk
Pop 4	0.58	4.6	0.14	High risk
Pop 5	0.54	4.1	0.18	High risk

Integrated Ecological–Genetic Evaluation

Table 3 presents the results of ecological and genetic indicators integration to give composite viability scores of site-population pairings. The groups that responded with high habitat suitability and connection with genetically robust source populations were always the ones with high viability scores and were defined as the most viable to be reintroduced. In between combinations were relatively viable and were categorized as conditional, which implied that directed habitat restoration or genetic enrichment may be necessary to enhance performance. Matings between low suitability locations and genetically impaired populations produced low viability values and were considered inappropriate.

Generally, the findings prove that reintroduction is feasible when there is a match in habitat suitability, landscape connectivity, and genetic viability. High predicted viability that was based solely on ecological appropriateness was inadequate where genetic diversity was low, whilst genetically robust populations did not work well in pairs with inappropriate or disjointed environments. The unified framework will allow to observe alternative scenarios transparently and prioritize the efforts to restore habitats and reintroduce species based on the evidence.

Table 3: Integrated Ecological–Genetic Evaluation of Reintroduction Scenarios

Site–Population Pair	Habitat Suitability	Genetic Diversity	Predicted Viability Score	Reintroduction Recommendation
Site A – Pop 1	High	High	0.84	Recommended
Site A – Pop 2	High	Moderate	0.78	Recommended
Site B – Pop 2	Moderate	Moderate	0.66	Conditional
Site B – Pop 3	Moderate	Moderate	0.61	Conditional
Site C – Pop 4	Moderate	Low	0.48	Not recommended
Site D – Pop 5	Low	Low	0.32	Not recommended

Conclusion

This paper shows that successful reintroduction of species and habitat restoration should be explicitly integrated to give consideration to ecological appropriateness and landscape connectivity, as well as genetic feasibility. Quantitative assessment of candidate reintroduction sites indicated that more suitable habitats (HSI 0.74 and higher) and better-connected ones (0.61 and higher) have significantly higher potential of supporting a viable population of animals. Genetic data also indicated that the source groups with greater heterozygosity (He 0.68) and lower inbreeding coefficients (FIS 0.06) are more appropriate for reintroduction with fewer genetic risks in the long run. Under ecological and genetic integration, composite viability scores were diverse (0.32084) with a clear distinction of optimal, conditional, and inappropriate reintroduction scenarios. The high-viability (>0.75) pairings were always associated with the combination of favorable habitats and the genetically robust populations, but the low-viability (<0.50) situations were associated with the combination of fragmented habitats and genetically weak sources. Such findings numerically verify that the success of reintroduction is limited by the poorest part of the ecological-genetic network. Due to its structured value-based framework, the current study facilitates transparent decision-making in wildlife conservation and restoration planning. The methodology allows practitioners to give primary focus to habitat restoration, choose the right source populations, and develop reintroduction plans that can be as long-term persistent as possible. With increased loss of biodiversity and environmental change, unified models that integrate ecological modeling with genetic conservation indices will be necessary towards the realization of sustainable wildlife recovery throughout most of the restored landscapes.

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