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Perspective

Management Pathways for Fragmented Populations: From Habitat Restoration to Genetic Intervention

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Abstract

Habitat fragmentation is reshaping ecosystems worldwide, reducing connectivity, eroding genetic diversity, and limiting species' capacity to adapt to rapid environmental change. Conservation management responses to fragmentation generally follow three pathways: restoring habitats to rebuild connectivity, translocating individuals to bolster declining populations, and, more recently, directly managing adaptive genetic variation. We synthesize the ecological and genetic consequences of fragmentation and evaluate these management pathways along a continuum from landscape-scale interventions to genome-level strategies. Habitat restoration can reconnect patches and improve demo-graphic stability, but its genetic outcomes remain uncertain without baseline and post-restoration monitoring. Translocation offers a more immediate means of restoring gene flow but introduces demographic risks, potential impacts on source populations, and uncertainties in establishment and long-term fitness. Emerging genomic technologies now support a third approach: Targeted Genetic Intervention (TGI), which aims to accelerate the spread of beneficial genetic variants or enhance adaptive potential directly. Although promising, TGI faces significant challenges, including polygenic trait architecture, risks to genome-wide diversity, and the need for robust ethical and governance frameworks. Across all pathways, genetic data are essential for prioritizing actions, diagnosing vulnerable species and populations, and restoring the evolutionary potential necessary for long-term persistence in increasingly fragmented landscapes.

Keywords: habitat fragmentation; genetic diversity; gene flow; translocation; restoration; genetic rescue; conservation genomics; targeted genetic intervention

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1. Overview

Habitat alteration, including destruction and fragmentation, is now one of the dominant forces shaping global biodiversity [1]. It is widely recognized as a leading driver of species loss [2] and has contributed to declines of up to 75% in some regions [3]. Human activities have altered nearly 80% of terrestrial environments [4], 90% of oceans [5], and 50% of rivers [6].

Herein, habitat fragmentation refers to the division of once continuous habitat, not the total loss of habitat, although fragmentation can contribute to habitat loss. While the ecological consequences of fragmentation, including reduced habitat area, increased edge effects, and disrupted organismal movement, are well established [7,8], its genetic and evolutionary impacts remain inconsistently acknowledged in conservation planning [9–11].

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Genetic diversity underpins a population's capacity to persist and adapt over time. Fragmentation restricts movement among populations [12], reducing gene flow and effective population sizes. In turn, this elevates inbreeding, genetic drift [13], and the stochastic loss of genetic variation [14]. Even populations that appear demographically stable may experience hidden erosion of their adaptive potential, increasing the risk of extirpation under environmental change [15]. Fragmentation can also prevent the spread of beneficial genetic variation, limiting isolated populations' ability to respond to changing environments.

Because fragmentation is largely human-driven, conservation management interventions seek to counter its ecological, demographic, and genetic consequences. We outline three primary pathways through which managers can maintain or restore genetic diversity in fragmented systems below (Table 1).

Table 1. Highlighting the main goals, challenges, and risks of the three management pathways for fragmented habitats. The essential genetic information required for each is indicated at the bottom of each column.

Feature	Habitat Restoration	Translocation	Targeted Genetic Intervention (TGI)
Primary Goal	Re-establish ecological connectivity to facilitate natural demographic recovery.	Deliberate movement of organisms to facilitate gene flow, provide demographic support, and genetic rescue of imperiled populations.	Directly alter allele frequencies through synthetic biology to increase fitness against specific threats or restore lost diversity.
Spatial and temporal Scales	Landscape level, long-term (decades to centuries).	Population level, medium-term (years to decades).	Individual/gene level, potentially rapid intergenerational change.
Relative Cost	Very high (land acquisition, earthworks, long-term maintenance).	Moderate to high (capture, transport, monitoring, disease screening).	High initial R&D, potentially lower long-term cost if self-sustaining.
Key Feasibility Challenges	Land ownership, political will, conflicts of interest, scale mismatch due to fragmentation, and a long time lag for genetic effects.	Finding suitable and sufficient source populations, logistical complexity of capture/transport.	Lack of genomic resources for non-model species, technical difficulty, regulatory hurdles, and public acceptance.
Primary Risks	Ineffective if populations are already genetically depauperate; may facilitate the spread of invasive species.	Outbreeding depression, disease transmission, genetic swamping, and demographic impact on the source population.	Off-target effects, unintended ecological consequences (pleiotropy), escape of modified genes, and ethical concerns.
Essential Genetic Information	Landscape genomics to prioritize corridors; pre- and post-monitoring of genetic diversity and connectivity.	Genomic assessment of divergence and local adaptation (GEA) to mitigate outbreeding depression risk.	Whole-genome sequencing, identification of adaptive loci (GEA), functional validation, and off-target analysis.

I. Habitat restoration: rebuilding ecological connectivity to allow natural movement and gene flow to resume.
II. Translocation: moving individuals to support demographic stability and bolster genetic variation.
III. Targeted Genetic Intervention: directly facilitating the spread of genetic variants, including through emerging synthetic biology tools.

These strategies are not mutually exclusive and may be most effective when used in combination. In Figure 1, we present a concise decision tree to guide practitioners on which strategies should be considered; see a complementary practitioner guide based on the Restoration Gene Pool concept for sourcing plant material [16]. In the sections that follow, we examine habitat fragmentation, its effects on genetic diversity and evolutionary potential, and highlight each management pathway in detail, emphasizing how explicit consideration of genetic diversity can improve restoration outcomes, guide translocation and genetic rescue efforts, and inform the emerging role of targeted genetic intervention in conservation management.

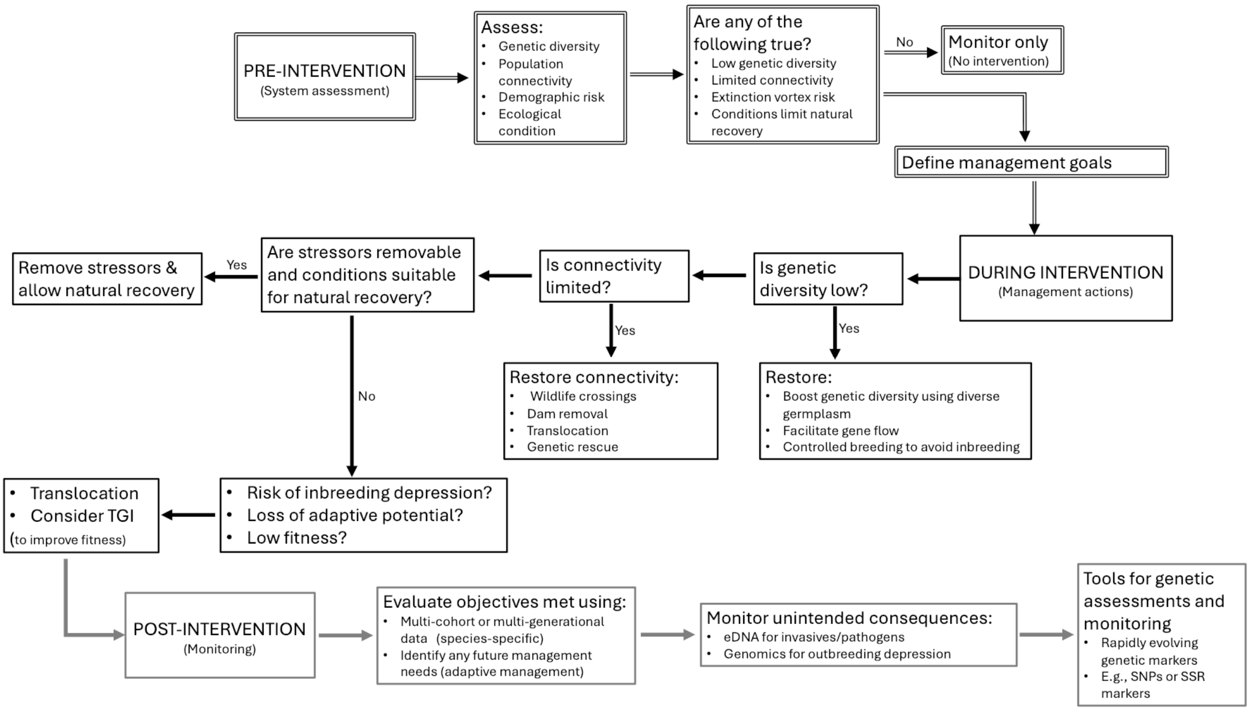

Figure 1. Concise decision tree for determining what management strategies may be considered by practitioners. Double-lined arrows connect steps to consider prior to any management intervention; simple solid black arrows connect steps to consider during the management phase; while simple solid gray-lined arrows connect steps to consider for monitoring, after management interventions are complete.

2. Habitat Fragmentation

Habitats in most ecosystems are naturally fragmented to some degree. This “patchiness” arises from spatial heterogeneity in resources, abiotic conditions, and species-specific niche requirements. Natural fragmentation structures biodiversity and promotes species coexistence [17]. Major landscape features such as mountains and rivers restrict dispersal and contribute to lineage diversification [18–20]. At the land–sea interface, shoreline geomorphology, coastal dynamics, and ocean currents generate natural patchiness in organisms such as mangroves [21–23]. Submerged aquatic vegetation similarly forms shifting mosaics of patches influenced by local environmental conditions in coastal and estuarine systems [24,25]. In riverine networks, hierarchical drainage structures naturally isolate fish populations across catchments [26,27]. In marine environments, biogeochemical provinces, nutrient dynamics, and other physical and biological processes similarly determine natural species patchiness and patch size [28–30].

In contrast, anthropogenic habitat fragmentation results from human activities that subdivide formerly continuous habitats into smaller, isolated patches. This process is typically more rapid and severe than natural fragmentation, driving habitat loss, degradation, and separation. In aquatic systems, structures such as weirs and dams disrupt connectivity [27,31], while bridge construction and culverts can also impede dispersal [32]. Although less conspicuous resistance created by chemical pollution can create “soft” barriers that also reduce habitat continuity [33]. Terrestrial landscapes are further subdivided through deforestation, agriculture, urban expansion, roads, and railways. All species experience the effects of fragmentation, but those most at risk include short-range endemics [34], species with limited dispersal ability [35], and taxa already listed as critically endangered by the IUCN [36]. Across ecosystems, fragmentation affects biodiversity at multiple spatial scales, shaping ecological and evolutionary processes both within and among habitat patches.

2.1. Within-Patch Impacts of Habitat Fragmentation

By breaking large, contiguous habitats into smaller, isolated patches, fragmentation reduces the overall extent of hospitable space within a landscape. This loss and rearrangement of usable habitat lowers population carrying capacity by limiting resources, restricting movement, and forcing patches to function in isolation. The resulting within-patch effects consistently depress local population sizes, often with cascading consequences. For example, shrinking mangrove patches greatly diminish global carbon sequestration capacity [37], with millions of tons of carbon released annually as mangroves are destroyed. Fragmentation of dense aquatic vegetation beds leads to smaller, more structurally complex patches during recovery [38], and these changes occur alongside increasingly frequent extreme weather events that can eliminate entire beds [39–41].

Smaller, isolated patches also support fewer species interactions due to reduced resource availability and species diversity [42–44]. Because habitat size is strongly correlated with species richness, fragmentation-driven reductions in patch size can trigger “ecosystem decay” or the progressive decline in ecosystem health and the continued loss of species in small, isolated habitats [45]; although other mechanisms, such as distance-decay, environmental heterogeneity, and sampling effort, are also associated in fragmented landscapes [46]. In such populations, mate limitation becomes common, reducing sexual reproduction [47–49]. This isolation may favor selfing and increase inbreeding [50], reducing overall fitness and survival. Combined with limited resources and fewer species interactions, these demographic and ecological pressures increase the risk of extirpation [51,52]. Without intervention, these within-patch challenges often worsen or persist [35,53], with the smallest and most isolated fragments typically experiencing the most severe effects [3].

Beyond reducing patch size, fragmentation intensifies edge effects, thereby degrading resource availability and altering microclimates [53]. Such shifts can influence population processes (e.g., phenology) and community interactions [48,49,54], driving changes in selective pressures and compromising patch-level fitness [55]. Notably, approximately 70% of the world’s remaining forests lie within 1 km of an edge [3]. Although edge severity varies with forest age, affected forests tend to be drier, warmer, windier, more light-exposed, and more disturbance-prone [56]. These conditions contribute to an estimated 9% global loss of above-ground forest biomass due to edge effects [53]. In other systems, such as seagrass beds, edges show reduced shoot densities but elevated densities of invertebrates and benthic fishes [57], illustrating how edge effects can differentially influence community members.

2.2. Among Patch Impacts of Habitat Fragmentation

Habitat permeability and connectivity are central drivers of landscape-scale community dynamics. High permeability across space promotes functional diversity, facilitates species interactions, and supports long-term population persistence [58]. Fragmentation reduces this permeability by degrading habitat quality [33,59], increasing movement costs [33,44], and altering individual fitness [60]. In plants, fragmentation disrupts pollination by altering wind regimes, reducing pollinator abundance, and weakening plant–pollinator interactions [49,61,62]. Seed dispersal is also restricted by fragmentation, reducing effective dispersal among patches [43]. These constraints reshape natural metapopulation dynamics as unsuitable habitat increasingly surrounds and isolates smaller suitable patches [35]. The surrounding habitat matrix, including agricultural land, roads, and urban development, can impede dispersal [63].

In aquatic systems, fragmentation caused by dams has variable impacts depending on species' dispersal abilities [64]. Yet, the consequences are broadly consistent: reduced habitat quality, lower reproductive success [65,66], and increased population isolation [27,36,66,67]. Altered movement pathways can also drive turnover in community composition, as observed in stream fish assemblages [68].

Although both natural and anthropogenic processes can isolate populations, anthropogenic fragmentation generally produces stronger and faster population divergence [69]. These heightened effects stem from the rapid pace of habitat alteration, the abrupt formation of barriers, and the broad spatial scale of human impacts. Anthropogenic fragmentation also imposes novel selection pressures [70], yet many species cannot adapt quickly enough to keep pace with these changes. Even when adaptive responses arise, they may exacerbate rather than mitigate the impacts of fragmentation because evolutionary adjustments rarely compensate for the magnitude of environmental change associated with human-driven habitat alteration [70].

3. Genetic Diversity and Evolutionary Potential

Gene flow, mediated by the movement of individuals, spores, or gametes among populations, is fundamental to maintaining genetic diversity [71,72]. Habitat fragmentation restricts dispersal and gene flow, isolating patches and creating small, evolutionarily independent populations [14]. These patches effectively function as habitat "islands" surrounded by a less favorable matrix of habitat [73]. When populations remain well connected, gene flow provides substantial genetic benefits within a metapopulation [74–76]. Gene flow counters the random fixation of alleles due to genetic drift [77,78] and increases genetic variation by replenishing rare alleles that might otherwise be lost [79]. In fragmented and isolated populations, these advantages diminish as dispersal and gene flow decline [80].

Isolation of mates and changes in habitat quality associated with fragmentation may alter fitness by lowering fecundity in birds [3] and by shifting reproductive strategy toward asexual reproduction in plants [70], thereby reducing seed production. Lower fecundity negatively affects populations by decreasing population size and the number of effective breeders, and by reducing total allelic diversity within the gene pool [81,82]. As inbreeding increases, deleterious recessive alleles become homozygous and accumulate [83,84]. Because drift is stronger in smaller populations, both census size (Nc) and effective population size (Ne) decline [85]. Long-term persistence typically requires $Ne \geq 500$ to retain adaptive potential, while $Ne \geq 50$ may suffice only in the short term [82]. Yet many disturbed or isolated populations fall well below these thresholds and suffer a disproportionately high stochastic loss of genetic variation each generation [34,41,86]. Low-diversity, inbred populations with fixed deleterious alleles exhibit reduced fitness and diminished resilience to environmental change [80,87]. In extreme cases, mate limitation can exacerbate inbreeding in self-compatible species or prevent reproduction entirely in dioecious species [88,89]. With fewer individuals, net mutation rates effectively decline, and new genetic variants arise more slowly than they are lost [90,91]. The Florida panther (*Puma concolor coryi*) illustrates these consequences: habitat loss isolated the population, driving declines in genetic diversity and increases in inbreeding, resulting in reduced fitness and harmful phenotypes [92].

Together, the reduced gene flow, elevated drift, and increased inbreeding caused by fragmentation increase genetic divergence among patches while eroding standing genetic variation—the substrate on which natural selection acts [93,94]. Without gene flow, adaptive alleles cannot spread among populations, and genetic drift accelerates the loss of variation [87,95]. Populations subject to drift-driven allele loss (i.e., small isolated populations) may be less resistant or resilient to disease, environmental change, and other stressors [14,96,97]. Fragmentation also unfolds alongside other anthropogenic pressures and increasing extreme weather events [98,99], which can cause additional genetic bottlenecks and further reduce the diversity retained by surviving individuals [100]. Small, genetically depauperate populations respond less robustly to stochastic and environmental challenges than larger, more variable populations [101]. Collectively, these processes diminish evolutionary potential and the likelihood of population persistence.

4. Habitat Restoration

Accelerated extinction rates in increasingly patchy habitats call for urgent efforts to mitigate landscape degradation and other human-driven pressures on biodiversity [102]. To counter fragmentation, managers have implemented a range of connectivity-focused interventions. Habitat corridors link isolated terrestrial patches [103], while dam removal and fish bypass structures restore movement pathways in river systems [67,104]. Additionally, constructing artificial habitats or refuge pools has been proposed to maintain in-stream connectivity during drought and reduce fragmentation impacts [65,105].

Most interventions occur at local scales, but ambitious large-scale restoration targets have been established across ecosystems. Examples include global initiatives for mangrove recovery [106], submerged aquatic vegetation [107–109], fish population restoration [110], and terrestrial reforestation efforts [111]. Many of these programs have been designated as United Nations World Restoration Flagships [112]. Ecological restoration encompasses diverse approaches, but combining protection of intact habitat with the restoration of degraded areas increases the likelihood of preventing biodiversity loss linked to fragmentation [107,108].

Despite global momentum, restoration outcomes remain mixed [109]. Many projects fail or fall short of expectations [110,113,114]. High failure rates often reflect an emphasis on the number or size of projects rather than on rigorous planning, design, implementation, and monitoring [106,115,116]. Scaling up restoration also requires broader adoption of technological innovations and meaningful involvement of local stakeholders [117]. Local engagement is essential, as resistance frequently arises when landowner priorities conflict with restoration objectives, limiting access to restorable areas [115]. Efforts to align habitat needs with societal benefits and foster community buy-in can improve long-term engagement and accessibility [118,119].

Large-scale restoration programs typically require extensive transdisciplinary collaboration and sustained political support [118]. However, political will remains a significant barrier, in part due to the complexity and high costs associated with restoration. Global estimates place median costs at up to USD3012/ha for terrestrial projects [120] and USD80,000/ha for marine coastal habitats [121]. Such costs can constrain restoration to smaller local initiatives [122], underscoring the challenge of implementing restoration at scales commensurate with global biodiversity loss.

4.1. Realism Versus Scale in Habitat Restoration

Successful restoration requires overcoming numerous ecological, logistical, and social challenges. Although meeting ambitious restoration targets could yield benefits at local to global scales [122,123], the scale of restoration remains small compared to that of habitat loss and fragmentation. For example, Indonesia is planting 600,000 mangrove trees by 2024 [106], but the country has lost about 1 million hectares of mangroves since the 1800s [123], which implies that the restoration target represents roughly 0.06% of the total mangrove loss, assuming a planting density of 1000 trees per ha. Similarly, the Chesapeake Bay Program's goal of restoring 130,000 acres of submerged aquatic vegetation by 2025 has not been met, and even if achieved, would remain well below historical estimates of 200,000–600,000 acres [124].

Shortfalls in meeting ambitious targets stem from multiple factors. A key challenge is the mismatch between restoration pragmatism and the scale of degradation. Project goals are often unrealistic, infeasible, or insufficiently defined [111,125]. Strategies that work locally may not scale to broader landscapes because site-specific conditions rarely translate across regions. Moreover, failures often arise from an inability to anticipate or plan for stochastic weather events, climatic variability, or other environmental uncertainties [123]. These uncertainties require flexible frameworks, making adaptive management essential [125,126].

The tension between realistic scale and ecological ambition, combined with broader restoration challenges, underscores the need to prioritize sites based on expected ecological and evolutionary outcomes. Genetic surveys can be used both to prioritize restoration sites and to measure the success of restoration activities [127]. Nevertheless, many restoration efforts still rely on feasibility and accessibility rather than scientific evidence. For instance, germplasm sourcing often emphasizes short-term practicality over long-term resilience [128]. Poor site selection driven by accessibility, as well as mismatches between species' biology and selected sites, contribute substantially to mangrove restoration failures [129,130]. Ultimately, ecological restoration aims to establish systems capable of persisting under future environmental change without continual human intervention [115,131,132]. Achieving this goal requires accounting for species biology and for locally relevant within-species genetic variation, both of which are critical for building resilient restored landscapes [133]. Restoring habitat without restoring the inhabitants is bound to fail.

4.2. The Value of Genetic Assessments in Ecological Restoration

Understanding the amount and spatial distribution of genetic diversity is fundamental to managing degraded landscapes, and although still underutilized, genetic diversity is increasingly considered in restoration research [127]. Yet for most species and regions, such data are still lacking. By quantifying levels and patterns of genetic variation, genetic assessments can identify vulnerable or at-risk populations that appear demographically stable but are genetically compromised, helping to determine the interventions needed to mitigate fragmentation impacts [134]. Assignment tests, mating-system analyses, and estimates of genetic connectivity can guide germplasm source population designation for minimizing risks associated with moving individuals or propagules [133,135]. Connectivity analyses can further highlight sites with strong potential for natural colonization [136], which may require only minimal intervention to support recruitment. These analyses also reveal dispersal barriers and population ancestries and can delineate management units or genetic neighborhoods [21,27,34].

Monitoring with genetic data can additionally illuminate the consequences of past restoration interventions and can refine future management strategies [134]. Such monitoring enables evaluation of whether restored populations retain diversity and integrate successfully into surrounding metapopulations [134]. Environmental DNA (eDNA) has expanded the capacity to monitor biodiversity non-invasively, providing crucial information on how fragmentation and other anthropogenic pressures reshape community composition in degraded habitats. eDNA can detect invasive species before they become problematic [137,138] and illuminate the status of rare or imperiled species, particularly where baseline community data from pre-disturbance conditions do not exist.

Genetic tools can also be paired with machine-learning approaches to optimize restoration design for landscape function, recovery, and resilience [139,140]. Despite their broad utility, genetic data remain underused in restoration planning—especially in low-resource settings [11]. Their omission often reflects the limited availability of baseline genetic information, making it difficult to distinguish natural patterns of variation from those driven by anthropogenic disturbance. This distinction is critical because genetic variation is the substrate on which natural selection acts and is fundamental to population viability.

Even when management aims to maximize genetic diversity for long-term resilience, restoration is not a rapid solution. Restored populations require time to establish, recruit, and meaningfully contribute to local gene pools. The timeline for genetic recovery depends on generation time, reproductive systems, and turnover rates. Locally sourced propagules are typically considered low-risk, high-reward for maintaining adaptation to local conditions [11,141]. However, in severely fragmented landscapes where local populations have experienced bottlenecks and are genetically depauperate, exclusive reliance on local germplasm may limit resilience [11,142]. In such cases, genetic rescue through assisted migration or targeted translocations may be necessary to restore viability [11,143,144].

5. Translocation

The human-mediated movement of individuals from one site to another via translocation can serve as an artificial means of facilitating gene flow in populations threatened by fragmentation and low genetic diversity. Translocations may support assisted colonization into suitable environments under global change, recolonize extirpated sites, or demographically and genetically bolster declining populations [145–147]. Effective use of translocation requires consideration of the source and number of individuals, the frequency and timing of releases, and the criteria used to evaluate success [146]. Individuals may be sourced from other wild populations or from captive-breeding and hatchery programs [148–150]. The number of individuals matters, as moving 50 versus 100 can have substantially different demographic and genetic consequences for the recipient population [151–153]. Frequency of translocation is also essential, as single versus repeated introductions may differ in their ability to meet project goals [148,151]. Success further depends on seasonal and phenological timing, release location, and the ability of individuals to disperse among viable habitat patches [145,146]. Ultimately, outcomes hinge on the interplay between translocated individuals and the biotic and abiotic conditions of the recipient environment [146,154].

The ecological results of translocation can be varied and occasionally unintended. First, introduced individuals must recover from transport stress and survive release [155,156]. Beyond survival, successful establishment requires that translocated individuals mature, enter the effective breeding population, and reproduce [154,157]. They must interbreed not only among themselves (assortative mating) but also with local individuals [154,158]. Concerns include increased competition for resources and the introduction of novel pathogens that could reduce fitness in recipient populations [159,160].

Nevertheless, when implemented in biological restoration and conservation contexts, translocations are generally successful and rarely result in adverse ecosystem-wide effects [161]. Beyond concerns about the recipient population, the effects of removing individuals from source populations are often left unassessed, including changes in demographic stability over time [149]. However, the demographic consequences for source populations are frequently overlooked, and these populations may experience long-term declines after donating individuals—an especially critical issue for vulnerable or critically endangered species [162,163].

When translocations result in interbreeding between introduced and local populations, genetic benefits can be substantial. Facilitated or assisted gene flow can reverse genetic erosion, temporarily increase connectivity during periods when natural dispersal is unlikely, and restore genetic variation lost to drift [155,157]. Through genetic rescue [164], translocated individuals can enhance adaptive potential by replenishing the genetic variation available to natural selection [164,165]. Although outbreeding depression resulting in low fitness of offspring from adaptively divergent parents remains a concern [166], recent evidence suggests it is less common than previously thought [1,167]. Nonetheless, understanding population structure, divergence, and local adaptation remains essential when selecting donor populations to both preserve genetic identity and spread beneficial variation across landscapes [34,154,168]. It is also important to note that genetic benefits often unfold over many generations, potentially limiting the utility of translocation under rapid climate or land-use change [169].

Genetic Surveys to Guide Translocation

Facilitating gene flow through translocation to achieve genetic rescue requires a detailed understanding of population structure, standing genetic diversity, and patterns of adaptive differentiation across the landscape [170]. Genetic surveys provide the foundation for identifying the number of biologically meaningful populations, their boundaries, and the magnitude and direction of migration among them [27,34,63]. Population structure analyses, therefore, allow managers to move beyond arbitrary geographic units and instead define management units that reflect underlying evolutionary and demographic processes [170]. Quantifying within-population genetic diversity, inbreeding, and effective population size further enables managers to prioritize populations for intervention [34]. Populations with large effective sizes and high diversity may serve as robust donor sources. In contrast, small, isolated, or highly inbred populations can be identified as recipients most likely to benefit from assisted gene flow [164].

Although outbreeding depression appears to be less common than once feared [1,167], it remains prudent to evaluate adaptive differentiation among populations, particularly when translocations involve environmentally heterogeneous landscapes [170]. Genetic surveys can identify signals of local adaptation using genotype–environment association analyses, outlier scans, and clustering or assignment tests based on putatively adaptive genomic regions [34,171]. These approaches help managers avoid mixing individuals that are strongly adapted to contrasting environments, while still allowing movement among populations that share similar selective regimes. Models of contemporary landscape-level adaptation can also be projected into the future to estimate the potential maladaptation of populations and to prioritize donor and recipient populations [140]. Together, genetic surveys transform translocation from a largely demographic exercise into a genetically informed management strategy. By explicitly linking donor–recipient selection to population structure, diversity, and adaptive context, managers can maximize the likelihood that translocations enhance genetic variation and adaptive potential while minimizing the risks of maladaptation or unintended genetic consequences.

6. Targeted Genetic Intervention

The progression from managing landscapes (restoration) to managing populations (translocation) culminates in an emerging frontier: directly managing adaptive genetic variation within genomes [172,173]. Targeted Genetic Intervention (TGI) is broadly defined as a suite of approaches that seek to "change adaptive allele frequencies to increase population fitness," using tools such as artificial selection, gene editing, synthetic biology, and targeted gene flow [174]. This definition encompasses a range of related concepts—including "assisted evolution" [173], "facilitated adaptation" [175], and "gene-targeted conservation" [176]—all aimed at promoting adaptation in species for which traditional conservation measures are inadequate [174].

Historically, conservation genetics emphasized minimizing genetic erosion and inbreeding to preserve existing evolutionary potential [177]. TGI departs from this preservation-oriented paradigm. For challenges such as infectious diseases, climate change, and toxic pollutants—where eliminating the threat is often not feasible—long-term persistence may depend on the species' ability to adapt. TGI seeks to accelerate this adaptive process, shifting conservation from maintaining genetic variation to actively managing the genes themselves [174]. For species already reliant on intensive management (e.g., Conservation Breeding Programs), TGI offers a potential shift from maintaining perpetual "ark" populations to establishing resilient, self-sustaining wild populations.

Conservation breeding programs, often viewed as a last resort for critically endangered species, are in fact the indispensable platform for developing and implementing TGI. Controlled, ex situ environments provide access to individuals for physiological studies, controlled breeding, gamete collection, and application of advanced reproductive technologies, which are prerequisites for nearly all genetic interventions. However, captivity introduces significant genetic challenges, including relaxed selection, adaptation to captive conditions, and reduced fitness [178]. This generates a well-documented "demography–genetics trade-off" [179]: longer periods in captivity allow greater demographic growth and more individuals for release, but also increase the accumulation of genetic load and reduce post-release fitness. TGI provides a compelling solution by targeting and preserving—or even enhancing—wild-type adaptive traits, potentially breaking the link between time in captivity and fitness decline.

Gene editing approaches such as CRISPR–Cas9 [180] can introduce advantageous variants directly into genomes to accelerate adaptation [175,181], enabling "synthetically assisted conservation translocations" [182]. Genetic modification has long been used in crops to circumvent reproductive barriers in plant breeding [183]. Although the application of such technologies to wildlife has progressed more slowly [184], several promising examples are emerging. Synthetic methods are being explored to enhance thermal tolerance in branching corals [185] and combat chytridiomycosis in amphibians [186]. The American Chestnut Research and Restoration Project has used transgenesis to insert a wheat gene conferring blight tolerance into the American chestnut genome [187]. The resulting strain, "Darling-54," is currently under review for wider planting by the USDA, FDA, and EPA, though The American Chestnut Foundation withdrew support in 2023 [188].

6.1. Facilitating the Spread of Adaptive Traits with TGI

TGI can be used to intentionally spread advantageous genetic variants that already exist in some populations but are absent in others that would benefit from them [181]. This approach avoids transgenesis and the introduction of 'foreign' DNA into species and may not be strictly regulated as genetic modification [189]. Implementation begins with a comprehensive genomic survey—ideally using low-coverage whole-genome sequencing [190]. Once genomic variation is characterized at scale, candidate adaptive loci can be identified through genotype–environment association analyses [34,171], followed by functional validation using genome annotation and gene ontology [34], and, when possible, expression or physiological evidence linking loci to traits of interest. Experimental validation can then confirm that manipulating these genes yields meaningful phenotypic improvements, such as enhanced tolerance to warming or disease [191].

After identifying and validating target variants, CRISPR-based editing [180] can be integrated into ex situ conservation breeding programs to introduce these alleles into fertilized embryos from populations that lack them. Before release, edited individuals must be evaluated in contained ex situ environments to assess performance, fitness, and potential unintended effects. Initial applications should focus on species that are already highly fragmented and at high risk of extinction.

TGI offers several advantages over conventional translocation-based genetic rescue. It reduces demographic pressure on source populations, avoids introducing linked deleterious alleles that may contribute to outbreeding depression, and preserves unique variation in recipient populations. It also eliminates the risk of pathogen transfer associated with moving whole individuals. Most importantly, for species that are genetically depauperate, inbred, and facing increasingly limited conventional conservation options, TGI may represent the only viable path to restoring adaptive potential and preventing population collapse.

6.2. Challenges and Promises for TGI

Despite its theoretical appeal, TGI is not without criticism [176,192]. Kardos and Shafer [176] caution that such approaches may be ineffective at best and counterproductive at worst. A central challenge is that most fitness-related traits of conservation interest, such as thermal tolerance, disease resistance, growth, and reproduction, are highly polygenic, influenced by hundreds or thousands of loci of small effect [176,193,194]. Identifying a small number of “target genes” that meaningfully shift such traits may be unlikely, and even the best-supported candidates typically explain only a small fraction of the underlying genetic variance [193].

Focusing on a narrow set of beneficial alleles also risks eroding genome-wide genetic diversity, which remains the primary buffer against unpredictable future environments [176]. By promoting specific alleles and narrowing the breeding pool, TGI may reduce effective population size and accelerate genetic drift, potentially worsening long-term outcomes. In addition, strong selection on individual loci can have unintended effects through pleiotropy or linkage, enabling deleterious alleles to “hitchhike” to high frequency [195].

Even if these biological and technical hurdles are addressed, bringing TGI into practice will require more than scientific feasibility. It demands a governance model that is ethically grounded, publicly legitimate, and internationally coherent [196]. Because TGI involves heritable changes to wild populations—shared public goods rather than private entities—its implementation must be guided by robust ethical frameworks, ongoing and inclusive stakeholder engagement, and regulatory systems capable of assessing ecological risks over landscape and generational scales [197]. The recent IUCN policy [198] on synthetic biology offers an initial foundation, emphasizing precaution, transparency, and the requirement of Free, Prior, and Informed Consent from affected communities. Yet regulatory pathways remain underdeveloped, public trust cannot be assumed, and governance must be proactively designed rather than adapted from agricultural or biomedical precedents [196]. Ultimately, even if TGI is technically feasible, its viability will depend on whether society is willing to accept and carefully steward its use.

7. Conclusions

Across fragmented landscapes, conservation efforts increasingly require a coordinated strategy that integrates habitat restoration, population management, and genetic insight [127]. A central message emerging from this perspective is that genetic work does not detract from traditional conservation approaches; rather, it strengthens them. The cost of generating genetic data is modest compared to the immense financial and logistical investments required for large-scale restoration, and these data can dramatically increase the efficiency and impact of those investments [128].

Genetic information provides a powerful basis for prioritizing restoration sites by identifying populations most at risk and landscapes where connectivity can deliver the greatest ecological and evolutionary benefits [127]. Restoration alone, however, rarely "fixes" genetically depauperate populations. Without renewed connectivity to genetically diverse sources—or direct genetic intervention—recovery of diversity can take many generations. Critically, the genetic outcomes of restoration cannot be inferred without baseline data and follow-up monitoring, underscoring the need to incorporate genetic assessments as standard practice [11], and to broaden population genomics to the community-level [27].

Practitioners should incorporate genomic data into their monitoring toolkit. Several reasonable data types for manager use exist depending on the scope of the project, ranging from microsatelittes and single nucleotide polymorphisms (SNPs) to low-coverage and whole-genome sequencing, allowing for a variety of survey tools of sampled individuals' genomes to assess success of the project [199]. Sampled individuals should be from a range of age classes, to ensure multiple generations (pre- and post-intervention) are included. This data can be used in post-intervention monitoring, which will, at minimum, require two timepoints: baseline (collected before or at the time of intervention) and short-term (collected after 1–2 generations). This schedule will help determine if gene flow is occurring between connected or introduced populations, with the potential for annual and long-term (collected several generations after intervention) monitoring. However, specific monitoring timelines will rely heavily on the species of interest, considering generation time, dispersal, reproductive system, and intervention type [200,201].

Translocation offers a more direct mechanism for restoring genetic diversity: moving individuals is ultimately moving genes, assuming subsequent breeding. When implemented carefully, assisted gene flow and genetic rescue can counteract drift, replenish adaptive variation, and bolster long-term persistence [164]. Yet translocation also carries demographic, ecological, and logistical constraints that limit its utility for many species.

Connectivity between patches, achieved through habitat restoration or facilitated by translocation, does come with associated risks to the persistence of the intended conservation species. Re-establishing connectivity can provide pathways for invasive species spread and the introduction of novel pathogens or even increase the abundance of predators/competitors, whereas translocations are more commonly associated with disease spread and intraspecific competition pressure [159,160,202]. While increasing connectivity may introduce or increase risks to ecosystem health and stability, the demographic and genetic benefits gained may outweigh these costs and are likely not achieved using other means.

Looking ahead, the future of genetic rescue may lie in Targeted Genetic Intervention (TGI). TGI seeks to accelerate the spread of advantageous genetic variants already present within a species, effectively mimicking—and in some cases surpassing—the goals of traditional translocation while reducing pressure on donor populations and minimizing unintended consequences [174]. Although TGI remains in early development and faces scientific, ethical, and governance challenges, its potential to restore adaptive capacity in severely fragmented or rapidly declining species is substantial.

Collectively, restoration, translocation, and emerging genetic interventions should not be viewed as competing pathways but as complementary tools within a unified management framework. Integrating genomic data throughout these efforts will be essential for ensuring that conservation actions not only rebuild habitat and populations but also restore the evolutionary potential required for species to persist in an increasingly dynamic world.

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