ZIBELINE INTERNATIONAL™
PUBLISHING
ISSN: 2521-0858 (Print)
ISSN: 2521-0866 (Online)
CODEN: SHJCAS

Science Heritage Journal (GWS)

DOI: http://doi.org/10.26480/gws.02.2025.62.72

REVIEW ARTICLE

DISRUPTED GENE FLOW AND GENOMIC EROSION: MOLECULAR AND LANDSCAPE PERSPECTIVES ON POLLINATOR ADAPTIVE POTENTIAL IN FRAGMENTED ECOSYSTEMS

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ARTICLE DETAILS

Article History:

Received 23 July 2025
Revised 28 August 2025
Accepted 24 September 2025
Available online 16 October 2025

ABSTRACT

Rapid industrialization, agricultural intensification, and climate extremes are fragmenting ecosystems at unprecedented scales, isolating pollinator populations critical to global food security. Such fragmentation reduces effective population size, disrupts gene flow, and accelerates genetic drift, driving genomic erosion, loss of allelic richness, and heightened vulnerability to environmental change. Our synthesis integrates landscape ecology with cutting-edge molecular and genomic approaches to elucidate the mechanistic interplay between structural and functional connectivity and pollinator adaptive capacity in fragmented habitats. We demonstrate that strategically designed ecological corridors and stepping-stone networks can attenuate extinction vortices by restoring metapopulation gene flow, buffering against stochastic demographic collapse, and safeguarding long-term evolutionary potential. Advancing pollinator conservation necessitates an urgent paradigm shift toward integrative strategies that unite habitat restoration, molecular diagnostics, and evolutionary-informed management, leveraging high-resolution genomic surveillance and landscape-level connectivity modelling to pre-empt biodiversity collapse and fortify ecosystem resilience in the Anthropocene.

KEYWORDS

Habitat fragmentation, genomic erosion, effective population size, pollinator conservation, landscape connectivity

1. INTRODUCTION

1.1 The use of The Importance of Pollinators and The Global Challenge of Habitat Fragmentation

Pollinators provide essential ecosystem services that are inseparably connected to human well-being. Flower-visiting pollinators influence approximately 75% of globally imported crop types, enhance yield and quality, and secure reliable and diverse food production (Gudowska et al., 2024). Pollination is a vital process for plant communities and food production, and pollinators should be studied in greater depth to find realistic patterns in these highly modified environments (Graffigna et al., 2024). Insect pollinators are significantly responsible for the food supply. Research suggests that 35% of global agricultural production is animal-pollinated (primarily by insects), providing higher nutrient ratios than wind-pollinated crops (Mallinger et al., 2021). Increasing pollinator diversity can enhance pollination services, and encouraging a wider range of pollinators may increase stability and provisioning of pollination services. Currently, wild and unmanaged pollinators may be more efficient than honey bees, as bumble bees in gold kiwifruit (Buston et al., 2022).

Habitat fragmentation triggers profound changes in terrestrial ecosystems, leads to isolation and edge effects, and causes global loss of biodiversity. In this situation, the shifting of pollinator guilds and alteration of foraging occur, and greatly affects pollinator behavior. Although specialists are more affected and often may be extirpated by an influx of generalist species (Surina et al., 2024).

Agricultural systems are the main drivers of habitat fragmentation (Feigs et al., 2022), causing loss and spatial isolation, and fragmentation eventually negatively affect biodiversity and many ecosystem functions and services. Fragmentation can increase the supply of ecosystem services by maximizing crop pollination through optimizing interspersion with crop land, as spatial coexistence creates an opportunity for a spillover effect that extends ecological interactions across habitat boundaries and propagates into ecological functions. This effect can be more complex in fragmented landscapes and may limit our capacity to manage biodiversity-based ecosystem service provision, affecting food security (Montoya et al., 2021).

Habitat loss and fragmentation are the predominant processes that can cause population declines by disrupting the processes of survival, dispersal, and gene flow. Different biomes 75% biodiversity reduced because of the rapid increase in habitat fragmentation. It occurs in 2 processes: loss of habitat and fragmentation of existing habitat, which has been the center of research focus for ecologists and conservationists over the past two decades (Tan et al., 2023).

1.2 The Role of Landscape Connectivity in Maintaining Pollinator Diversity

The majority flowering plants depend on pollination for reproduction. Diversity determines the quality, magnitude, and resilience of pollination services (Figure 4). The most significant drivers of pollinator declines are off-label pesticide use, extreme changing climatic conditions, invasive or alien species, pests and pathogens, and landscape alteration. Changes in

Quick Response Code	Access this article online	
	Website: www.jscienceheritage.com	**DOI:** 10.26480/gws.02.2025.62.72

Cite The Article: Anika Yesmin Sorna, Farhana Yeasmin and Md. Mamunur Rahman (2025). Disrupted Gene Flow And Genomic Erosion: Molecular And Landscape Perspectives On Pollinator Adaptive Potential In Fragmented Ecosystems. *Science Heritage Journal (GWS)*, 9(2): 62-72.

landscape pattern affect ecological sustainability, maintenance, and biodiversity. Landscape connectivity, an aspect of landscape configuration, is important for maintaining biodiversity because different disturbances that aggravate landscape fragmentation ultimately compound habitat and biodiversity loss (Vasiliev and Greenwood, 2023).

In recent decades, the literature has described the decline in pollinators globally, which is a consequence of changes in land-use that lead to homogenization of landscapes. As resource diversity varies at a spatial scale in different landscapes, heterogeneity may support more diversity because more habitats imply more ecological niches. The availability of feeding resources is highly dependent on flower diversity variation, which has a significant impact on the composition of pollinator communities (Gómez-Martínez et al., 2022).

1.3 The Genetic and Ecological Consequences of Fragmentation for Pollinators

Population genetics theory predicts the loss of genetic variation and a highly structured population in small and highly fragmented landscapes due to genetic drift. Gene flow can regain the genetic diversity but increasing fragmentation effect can disrupt pollen and seed dispersal vectors, risking plant species to extinction, resulting in genetic erosion, inbreeding depression, and/or loss of mating types shown in figure 3 (Delnevo et al., 2021; Cristóbal-Pérez et al., 2021). Fragmentation negatively affects mutualistic plant interactions, changing pollinator behavior may reduce fruit-set, both the quantity and quality of seeds (Cristóbal-Pérez et al., 2021). The habitat fragmentation directly influences associated plant populations. Moreover, reduced allelic richness and genetic differentiation are found among spatially isolated populations of insects having low mobility and pollen-mediated gene flow restricted (Feigs et al., 2022).

This paper synthesizes existing literature on the impacts of habitat fragmentation on the perspective of population genetics and molecular ecology of pollinators, mainly animal pollinators, identifying and categorizing the key factors of genetic and molecular consequences of landscape fragmentation, habitat loss, homozygosity, fitness potential, drift debt, and the bottleneck effect, allee effect, founder effect, ultimately extinction vortex that greatly risks biodiversity. Additionally, described the possible long-term strategies for biodiversity rescue combining the knowledge of population genetics, molecular ecology, evolutionary processes, and conservation systematics for habitat restoration, connectivity enhancement, and biodiversity conservation.

2. Key Population Genetic Principles Relevant To Fragmentation

2.1 Genetic Drift, Gene Flow, Increased Inbreeding, and Effective Population Size in A Fragmented Ecosystem

Habitat loss and population fragmentation directly affect biodiversity, interrupt natural dispersal and breeding, which decreases effective population size (Figure 1). Geographically isolated populations rapidly lose genetic diversity because of genetic drift and reduced fitness for higher inbreeding, which makes populations vulnerable to changing climatic conditions and elevating extinction risks (Figure 3) (Turnock et al., 2025). Widespread habitat destruction and the ongoing onslaught of invasive species result in highly fragmented distributions of many native animals and plants. Thus, the remnant population becomes vulnerable to the negative effects of genetic drift and inbreeding, which leads to the expression of deleterious alleles and a reduction of population fitness (Figure 2).

Moreover, these situations elevate risks of maladaptation and erosion of standing genetic diversity. Gene flow is not even adequate to overcome risks in 26%, 29%, and 55% in invertebrate, vertebrate, and plant species, respectively, in fragmented landscapes. But when gene flow is not present population will be dependent on standing genetic variation within them and the generation of de novo mutations, and both of these will be greatly affected by a smaller population size in fragmented landscapes. In addition, climate change decreases the adaptiveness and further compromises the genetic integrity (Hoffmann et al., 2021).

2.2 Impact of Habitat Fragmentation on Conservation Genetics

In conservation genetics climate change influence in the genetic diversity of populations is a very significant concern, as the demographic history is directly related to the genetic composition of populations. Intensive land use, causing habitat loss and fragmentation, jeopardizes the sizes and connectivity of the population. Fragmentation decreases genetic diversity, threatening the adaptive potential and persistence of populations. Additionally, the reduction of effective population size enhances genetic drift and stochastic loss of genetic variants, giving a barrier to the gene flow expressing more genetic load (inbreeding depression) (Figure 3) when the population is geographically isolated (Ho et al., 2025). Small populations exhibiting genetic drift and inbreeding depression reflect the actual extinction risk (Pruett et al., 2025). Genetic diversity is vital for ecological consequences and substantial effect on productivity and population recovery paramount in conservation genetics (White et al., 2025). Inbreeding depression in a small population result in the expression of deleterious alleles (Figure 2). Moreover, a lack of immigration from other populations creates chaotic changes in genetic variation. Thus, maintaining a large connected population is the ideal way to conserve biodiversity, approaching genetic rescue (Figure 5) (Kardos, 2021).

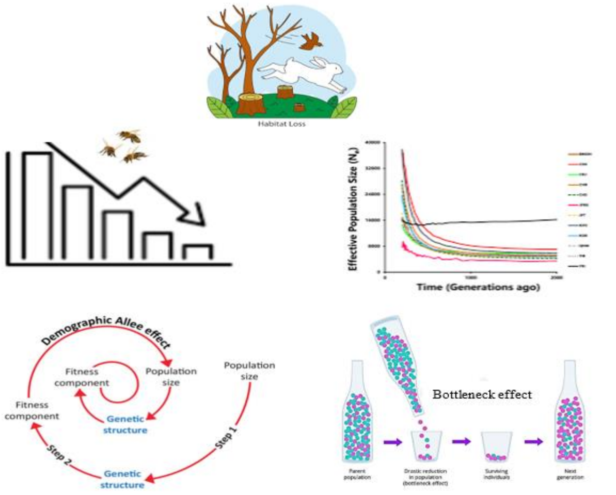
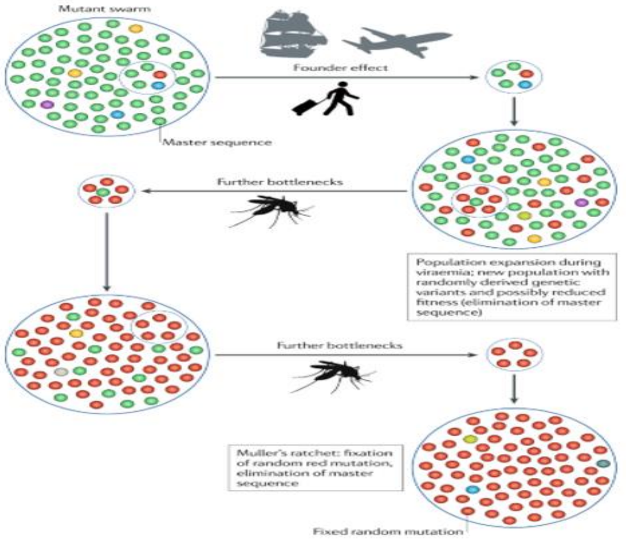


Figure 1: This figure shows how fragmentation and habitat loss reduce the number of effective population size, causing demographic stochasticity, enhancing the Allee effect, where survival fitness decreases at lower population densities, endangering species conservation and when population drastically decreases in size can be exacerbated by habitat fragmentation because fragmentation reduces gene flow between isolated populations, leading to reduced genetic diversity and potentially increased inbreeding within the smaller, fragmented groups.



Founder effect in small effective population

Loss of biodiversity

Figure 2: The above pictures depict the founder effect, one kind of genetic drift in the context of habitat fragmentation, when a small, isolated group of an insect population establishes in a previously unoccupied landscape and the new population carries only a fraction of the genetic diversity of the original, larger population, potentially leading to unique genetic characteristics and reduced overall genetic variation after repeated bottleneck effects in small effective population. Some rare alleles even the deleterious allele present in the original population may be more common or even dominant in the new, founder population not because they are better just by luck/chance due to random sampling, which can arise the extinction potential of that population. That will result in biodiversity loss.

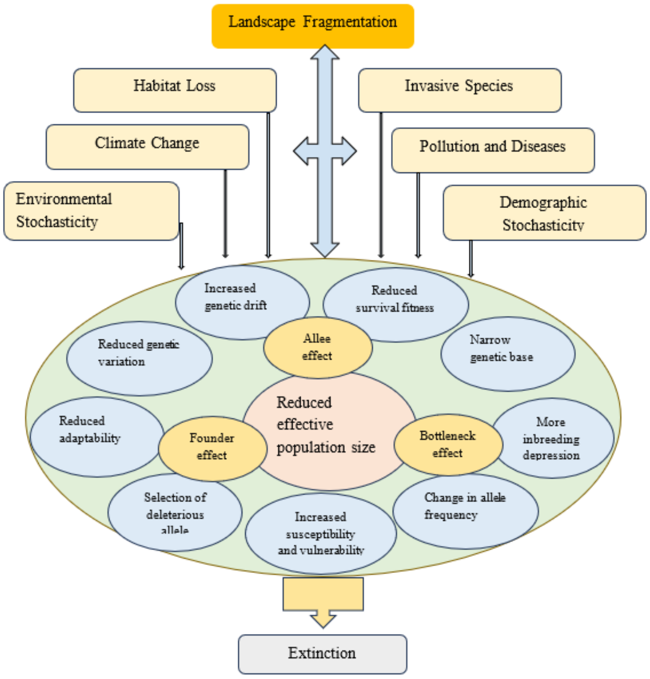


Figure 3: This figure shows how the fragmentation of landscapes, along with other very related factors (habitat loss, climate change, invasive species, pollution and diseases, demographic and environmental stochasticity), are responsible for the reduction of effective population size, which plays a crucial role in risking biodiversity conservation and increasing extinction potential.

3. LANDSCAPE ECOLOGY AND MOLECULAR ECOLOGICAL TOOLS

3.1 Landscape Ecology (E.G., Matrix Effects, Corridors, Patch Size/Isolation)

Landscape ecology is an interdisciplinary science of landscape structure, function, and dynamics of landscape elements (i.e., patches, corridors, and matrix) for analysis of spatial heterogeneity, landscape services, and landscape sustainability (Wang et al., 2025). Human society's expansion puts large pressure on natural ecosystems and affects the structure and function of landscapes. Resource landscape patches should be connected through a landscape ecological network for the protection of landscape integrity and biodiversity (Xu et al., 2021). Human land use effects initially ignored the matrix, but the matrix can have as strong as or even stronger the spatial attributes of habitat patches as the surrounding matrix explains more variation than the patch area and isolation across the plane. Furthermore, it is more influential than habitat loss and can alter the evolutionary process, restrict gene flow, and alter population differentiation (Fletcher et al., 2024).

3.2 Integration of Molecular Ecological Tools

Molecular data provide information on evolutionary processes for biodiversity conservation, but are rarely used for spatial conservation. In this era of biodiversity crises, resilience, species persistence, and adaptive potential approaches for biodiversity conservation are necessary. Molecular ecology provides suitable data for systematic conservation planning from the concept of extinction probabilities and landscape connectivity, as spatiotemporal genetic variation offers multiple evolutionary metrics focusing on connectivity (describes gene flow between populations), diversity, adaptive potential, differentiation, and demography (Nielsen et al., 2023). The integration addresses complex biological questions from the genetic to the ecosystem level, emphasizing conservation management and evolutionary processes. Genomics, proteomics, and bioinformatics enable analysis of genetic information with resolution, revealing the genetic mechanisms that drive ecological interactions and adaptations. These techniques identify genetic variation that correlates with environmental gradients, offering explanations for adaptation and speciation, elucidating migration patterns, breeding systems, food web dynamics, enriching ecological knowledge, and biodiversity assessments (Shikha et al., 2024). The genetic and demographic impacts of fragmentation are supported by advanced molecular marker technologies (Abate et al., 2025). The use of microsatellites-simple sequence repeats (SSRs) renders grasps into genotypic distribution and population dynamics encompassing the effective population size, sex ratio, and degree of stochastic mating, enhancing understanding of genetic diversity as these are markers of genetic differences (Pan et al., 2024).

4. IMPACTS OF FRAGMENTATION ON POLLINATOR GENETIC DIVERSITY

When a habitat is divided into two or more fragments reduces the total amount of area and brings changes in the habitat's spatial configuration, limiting dispersal and food and mates is termed as habitat fragmentation (Berger and Saltz, 2019). A population persisting in a fragmented area may experience genetic erosion with limited gene flow and reduced diversity within the population. Fragmentation strongly affects dispersal as resource availability is limited and landscape connectivity is disrupted. Habitat fragmentation has a weighty effect on bee pollinators for their haplodiploid genetic system, resulting effective population size of not more than 75% (Hernandez and Suni, 2024).

4.1 Reduced Genetic Diversity (E.G., Heterozygosity, Allelic Richness) in Fragmented Ecosystems Populations

Habitat fragmentation undermines the number of effective alleles and outcrossing rates, eventually affecting genetic diversity, restricting pollen flow, and disrupting mating and pollination systems and other reproductive strategies determining genetic susceptibility. Thus, obligate outcrossing species will undergo comparatively major losses of alleles and polymorphic loci. In this case, genetic erosion can only be curtailed by asexual reproduction, apomixis, or clonal growth (Chiapero et al., 2025). Fragmentation reduces the effective population size, increasing inbreeding depression, resulting in sterile diploid males endangering the genetic diversity of pollinators and evolutionary potential (de Matos Barbosa et al., 2022). Number of individuals increases but distance between population reduced, keeping low relatedness for conservation and restoration along with maladapted genotypes with lower reproductive fitness greatly affects heterozygosity and allelic richness (Finger et al., 2023).

4.2 Factors Influencing Genetic Diversity in Fragmented Ecosystems (E.G., Pollinator Mobility, Life History Traits, Habitat Type, Landscape Configuration)

Organisms that are not adapted to small populations restricted to isolated habitats and exhibit traits that limit a species' ability to colonize new habitats with increasing prone to extinction (Naff et al., 2021). Environment and spatial filters affect trait diversity in patches and landscapes. Functional richness (multidimensional space of traits), functional dispersion (average distance of individual species), and functional divergence (distance of the species to the gravity center of the functional space) altogether define functional diversity (Coutinho et al., 2021). Fragmentation may change abundance and foraging behavior of pollinators, and reduced pollen competition or reduced female choice expresses low-fitness phenotypes from high genetic load. Species with less mobile pollinators are more sensitive to fitness with increasing probability of selfing (Breed et al., 2015). A landscape that is more subject to rapid historical changes may have species communities more susceptible to extinction due to habitat fragmentation and habitat loss. Moreover, habitat fragmentation has negative effects on habitat, species richness, and biodiversity (Aguirre-Gutiérrez et al., 2015)

Table 1: Studies of Pollinators in Fragmented Landscapes

Pollinator species (Common name, scientific name)	Taxonomic group	Geographic Region of study	Type of Fragmentation	Genetic Marker type	Key Findings Related to Fragmentation	Landscape genetic models	References (APA)
Beetles, butterflies, flies, wasps, and wild bees, hoverflies and bee flies	Hymenoptera	*Olea europea* communities across Mallorca (39°37′ N, 2°59′ E), the main island of the Balearic Archipelago (Spain) in the Western Mediterranean Basin	Agricultural landscape	R package *iNEXT* v. 2.0.20	Pollinators are able to adapt their diet to resource changes at local and landscape scales	Used *metaComputeModules, 000 null models using the vaznull function*	Gómez-Martínez at al.,2022
Ashy mining bee (*Andrena cineraria), greater bee fly (Bombylius major)*	Hymenoptera	Luxembourg	Human altered landscape (Natura 2000 areas, industrial zones, settlement areas, meadows, forests and arable land form a landscape mosaic	Used 25 microsatellite loci, mitochondrial marker of the cytochrome *c*-oxidase subunit I (COI) gene	Genetic homogeneity was most likely the result of high levels of gene flow that compensate for the effects of genetic drift	A principal component analysis (PCA),	Schleimer et al.,2024
Bee species 7, genus *Euglossa*	Hymenoptera	Southern Costa Rica, the Las Alturas Biological Research Station, Las Cruces Biological Research Station, the La Gamba Biological Research Station, the Saladero Ecolodge, the Bromelias Ecolodge, the northern part of the Osa Peninsula	Forest fragments, pastureland, palm oil plantations, and small towns	SNP	Genetic structure was higher for species with greater resource specialization, positively associated with parameters reflecting gene flow and genetic diversity	Maximum Likelihood of Population Effects (MLPE) mixed models, generalized least squares (GLS) models, Euclidian geographic distance	Hernandez and Suni, 2024
Stingless bees (*Tetragonisca angustula)*	Hymenoptera	The Southeastern Atlantic Forest, in the Cantareira-Mantiqueira corridor region of São Paulo State, Brazil	Forested, agricultural and urban landscapes, pasture, crops,	Single-nucleotide polymorphisms (SNPs)	Forest cover negatively influenced the heterozygosity at a 500-m scale. Gene flow was explained mainly by geographic distance	The *model.sel* function of the *MuMIn* package, Akaike information criterion (AICc), principal component analysis (PCA),	Barbosa et al.,2022
Bees from 125 species (families Apidae, Halictidae, Andrenidae, and Megachilidae)	Hymenoptera	Mucugê-Ibicoara agricultural development region, Chapada Diamantina, Bahia, Brazil	Agroecosystem (mass effect)	Not defined	Landscape and local scale management can promote functional diversity in pollinator communities may be an effective mechanism for supporting increased pollination services	Akaike information criterion, Shannon landscape diversity index (SDI), Spatial autocorrelation	Coutinho et al.,2021
Pollinator groups (bees, hoverflies and butterflies)	Hymenoptera, Diptera, Lepidoptera	Netherlands	Grassland, moors/peat, deciduous/mixed forest, and sandy soils as suitable habitats, and agriculture, coniferous forest, urban, water		The limited value of a one-size-fits-all biodiversity conservation measure highlights the importance of considering landscape history when planning biodiversity conservation actions	Spatial autocorrelation, (lowest BIC)	Aguirre-Gutiérrez et al.,2015

5. Population Genetics, Gene Flow, And Connectivity In Fragmented Landscapes

Insect pollinators have varied levels of dispersal success across human-altered landscapes, and some species maintain high genetic connectivity across agricultural and non-agricultural landscapes, the crystal skipper Atrytonopsis quinteri, the red-tailed bumble bee Bombus lapidaries, the Eastern carpenter bee Xylocopa virginica, etc. Although some pollinators' activity and gene flow are hampered by anthropogenic landscapes. Population genetics data play a significant role in long-term consequences on population connectivity as it tests the effect of heterogeneous landscapes (Schleimer et al., 2024).

5.1 Gene Flow Using Molecular Markers

Microsatellites have been widely used intensively in the analysis of genetic diversity to investigate genetic variation and population differentiation. To detect the genetic consequences of habitat fragmentation, genetic diversity at both the population and species levels should be compared by nuclear microsatellite genotypic data. Historical and current gene flow comparison is required to identify the effect of habitat fragmentation (Jiang et al., 2022). Use of advanced genetic markers, EST-SSRs, and cpSSRs will insight genetic health and demographic trends with long-term conservation strategies (Moosavi, 2025). Along with microsatellites spatial component to the genetic structure and genetic diversity can be analysed through STRUCTURE (LOCPRIOR), isolation by distance tests, and spatial autocorrelation analysis (Melosik et al., 2024).

5.2 The Role of Different Landscape Features (E.G., Deforestation, Altitude, Urban Areas, Agricultural Fields, Natural Barriers) As Barriers to Gene Flow

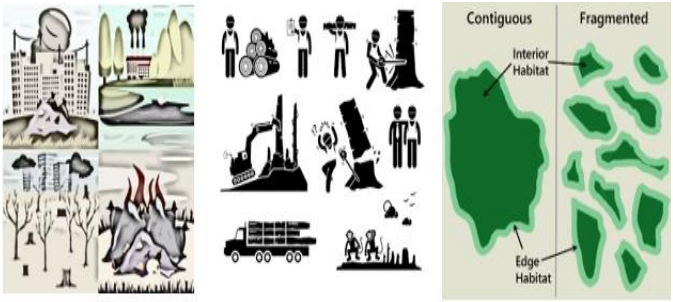
Landscape with diverse topography and environmental conditions in large heterogeneous landscapes (mountain valleys), gene flow performed well for landscape connectivity but was restricted in homogeneous topography. Deforestation disrupts connectivity and causes habitat fragmentation (Figure 4). Cold mountain environments' species are more vulnerable to habitat fragmentation than species of lower altitude for physiological constraints in harsher climates (Klinga et al., 2019). As fragmentation disrupts connectivity, structural connectivity (physical configuration, size, shape, location, and barriers of movement) and functional connectivity (dispersal, landscape structure, and element-movement patterns) are greatly hampered. Physical Transformations as deforestation, agriculture, urbanization, and roads, are barriers to gene flow in fragmented landscapes. Fragmentation results in interspecific dispersal dependency with reduced genetic diversity and increased allee effect sensitivity (Figure 1) and extinction (Figure 3) (Barger-Tal and Saltz, 2019). Ecological corridors enhance movements and gene flow, mitigating human-created linear barriers as roads and canals. Linear infrastructures are the primary impediments to species movement and also increase the mortality of many species. The road network provides a good proxy for fragmentation altering quality and connectivity (Figure 4) (Lapin et al., 2024).

Agricultural processes cause deforestation, intensive practices, harsh tools, and technological application on land following mechanization to cope with increasing population are causing fragmentation and biodiversity loss. Moreover, vehicle wildlife collisions, impact of energy sectors, mortality and toxicity of petroleum oil, extraction and transportation, catastrophic failure, chronic environmental contamination, coal mining, wind turbines, high voltage electronics transmission lines, and gold mining are all the result of industrialization, which is the foremost reason for habitat and biodiversity loss. Urbanization is the primary cause of habitat loss and fragmentation, having a negative impact on hydrological systems, causing air and water pollution, affecting local and regional climate, and increasing predation by mesopredators, pets, and pest rodents. The construction of roads requires the destruction of wetlands, leading to biodiversity loss (Scanes, 2018).

5.3 The Effectiveness of Ecological Corridors or Stepping Stones

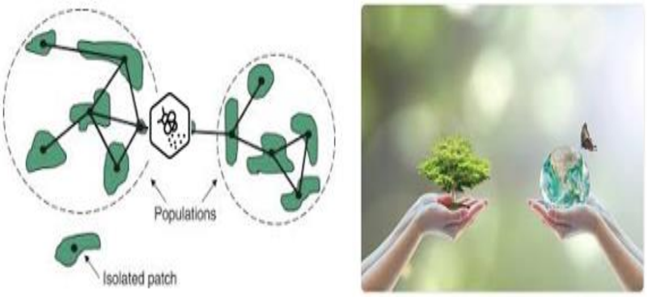
The connectivity enhancement of stepping stone approaches is more effective than barrier restoration. Conservation planning is crucial for restoring degraded habitats, bringing sustainability and biodiversity protection. Management actions can increase connectivity and facilitate species movement, including the establishment of corridors on biodiversity hotspots and stepping stone reserves encompassing the spatial distribution and successive species movement, focusing on linear structure (habitat corridors) and small patches (stepping stones), which will act as a decision-making tool for conservation planning (Lapin et al., 2024). Management of streams, rivers, and riparian areas, management of urban, suburban, and industrial land uses in or near corridors, and management of agricultural land is necessary to reduce the negative effects of fragmentation (Gregory et al., 2021).

Ecological security pattern employed to achieve maximum ecological connectivity with minimal ecological investment from a spatial perspective, where ecological sources are interconnected through ecological corridors, facilitating ecosystem integrity and ecological processes, focusing restoration between fragmented landscapes to safeguard biodiversity, ecosystem services, and regional ecological security. Those connect ecological sources for materials, energy, and information flow as well as landscape connectivity, conservation effectiveness, and ecosystem resilience. Stepping stones are resting places for long-distance migratory species, mainly in natural lands (Xu et al., 2024). In the era of modernization and industrialization, many advanced approaches are reason to habitat fragmentation, and for habitat restoration and biodiversity conservation, ecological corridors and stepping stones both together play a vital role and incorporating barrier restoration with stepping stones will enhance landscape connectivity.



Anthropogenic activities cause landscape fragmentation and barriers to gene flow

Effective ecological corridors for fragmented habitat connectivity



Landscape connectivity enhances gene flow and biodiversity conservation

Figure 4: Figure showing anthropogenic activities, primarily urbanization, industrialization, deforestation, and road network, along with different inevitable climatic catastrophes causing landscape fragmentation and barriers to gene flow. In fragmented landscapes, species become geographically isolated, and their genetic variation reduces with reduced pollination activity. As a consequence, they create a barrier to gene flow. Effective ecological corridors and stepping stones can connect the isolated patches, helping gene flow and maintenance of effective population size that will be naturally fittest for survival with genetic variation, broader genetic base and environmental adaptability, ultimately ensuring conservation of biodiversity.

5.4 Isolation-By-Distance Vs. Isolation-By-Resistance Patterns

Isolation by distance (IBD) patterns in which geographical isolation restricts dispersal among populations, for increasing genetic differentiation with geographical distance (Berger-Tal and Saltz, 2019). Landscape genetics assesses and quantifies features that influence gene flow and genetic connectivity. Isolation by resistance (IBR) is central to landscape genetic studies, the concept of isolation by resistance where different landscape element reduces movement and gene flow to varying degrees. The IBR hypothesis postulates relative resistance for different features and compares them with each other and also to the hypothesis of IBD. Isolation by distance (IBD) describes spatial genetic pattern among populations under restricted or limited movement, as in fragmented landscapes but IBR describes how a broad range of landscapes influences gene flow and movement (The functional connectivity), predicting ecological and evolutionary consequences of landscape change, and how landscape can alter gene migration and genetic connectivity where IBD (geographical isolation)explains alteration of gene flow and genetic connectivity (Asadi Aghbolaghi et al., 2023). Landscape genetics explicates landscape influences on microevolutionary processes with a detailed understanding of connectivity in population genetics and genomics fundamental for ecology, evolution, and conservation (Fletcher Jr et al., 2022; Moreno-Contreras et al., 2023).

6. MOLECULAR TOOLS AND METHODOLOGICAL ADVANCES

Population genetics and population genomics describe spatial patterns of genetic variation, and landscape genomics identifies the landscape factors and evolutionary processes understanding force genetic drift, gene flow, and selection, which generate genetic variation, population connectivity, adaptation, and conservation or restoration management. Hence, assimilating landscape data with genetic analysis was impossible until the development of genetic markers (microsatellites and single-nucleotide polymorphisms) with the integration of high-resolution spatio-environmental data through a geographic information system and climate model. Genomics even delivered cost-effective approaches facilitating and identifying loci involved in local adaptation (Aitken et al., 2024).

6.1 The Evolution and Application of Different Molecular Markers (E.G., Microsatellites, Snps, Genomic Approaches Like Ddradseq, Whole-Genome Sequencing)

The genetic markers in biological research result in the ability to analyze more efficiently in the context of population genetics. Microsatellites-simple sequence repeats (SSRs) or short tandem repeats (STRs) are widely distributed throughout the nuclear genomes of eukaryotes because they are highly polymorphic, used for purposes that include fingerprinting, parentage identification, genetic mapping, conservation, and population studies (genetics). Identification of the mechanism of mutation through a stepwise mutation model describing evolution varies among loci and the behavior of a given locus (Putman and Carbone, 2014). Next-generation sequencing holds great promise but has not been tested in highly mobile species. In case of population fragmentation and conservation of species genetic survey is an essential part of the management of threatened species, enhancing population connectivity.

Populations within fragmented landscapes are homogenized by recurrent gene flow and reduced genetic diversity. Additionally, the population genetic analysis should depend on the number of loci used, and microsatellite combines the mutation rates that generate incalculable alleles to gauge gene flow and diversity among divergent populations. Moreover, restriction-site associated DNA sequencing (RAD-seq; double-digest ddRAD-seq) became a popular method to genotype 100-1000 single nucleotide polymorphisms (SNPs) across populations multiple applications, such as high resolution phylogeography and genetic studies of weak species describing biogeographic history, social organization, philopatry, regional dispersal, and long-distance migration shaping genetic structure (Dufresnes et al., 2023). Environmental DNA (eDNA) is also used to detect species (analysis of haplotypes in short regions of the mitochondrial genome) through the analysis of genetic material present in environmental samples (with environmental data- climate, soil, topography). Metabarcoding of eDNA allows for rapid, cost-effective assessments of species richness, approaches in short- and long-term biomonitoring programs, biodiversity assessments, and conservation (Andres et al., 2023).

6.2 Analytical Approaches (E.G., Bayesian Clustering, Spatial Autocorrelation, Landscape Genetic Models)

6.2.1 Bayesian Spatiotemporal Models

Bayesian spatiotemporal model combines spatial and temporal dependencies, uncertainties, and intricate interactions concerning mapping, prediction, and regression analysis (Wang et al., 2024).

6.2.2 Bayesian cluster analysis

For datasets with low-frequency minor alleles, STRUCTURE software can be used to estimate population structure in continuously distributed species, which is for low genetic divergence, allelic richness, and molecular variance (Hopken et al., 2025).

6.2.3 Spatial autocorrelation

Spatial autocorrelation depicts the relationship between observations that are distributed across geographical landscapes and covers research of spatial econometrics, ecology, and biology; it conducts spatiotemporal analysis discussing transmission and influencing factors (Luo et al., 2022). Can detect boundaries and transition zones between clusters to identify geographic clines and geographic extent (Hopken et al., 2025).

6.2.4 Landscape genetic models

6.2.4.1 IBD model

Simplest model, positive correlation between genetic distance and geographical distance, and explicit influence of landscape features describing molecular phylogeography and population genetics (Wiens and Colella, 2025).

6.2.4.2 Resistance-Based Connectivity Model

To construct corridors for landscape connectivity, habitat restoration, and biodiversity conservation (Zhang et al., 2021).

6.2.4.3 Beyond Least Cost Paths: Circuit theory

Least-cost path (LCP) analysis calculates the cheapest path, represents hypothesized corridors for gene flow and circuit theory borrows concept from electrical circuit theory views landscapes as conductive surface where genetic flow is analogous to electrical current allows for the modeling of dispersal pathways and connectivity across entire landscapes (potential mobility) (McLean and Rubio-Campillo,2022).

6.2.4.4 Emerging technologies and analytical method

Table 2: Performance of Landscape Genetic Models

Model Type	Landscape Variable(s) Tested	Statistical Method	Goodness-of-Fit Matric	P-value or Significance Level	Key Interpretation	References (APA)
Species distribution modelling IBD, structural and functional connectivity analyses, and Moran's eigenvector maps	Landscape genetic patterns	Multivariate regression approaches	The highest significant correlation with H_0 at a distance of 10 km, integral index of connectivity, *dIIC*, reached its highest significant correlation with H_0 and H_E at a distance of 10 to 20 km	Distance thresholds ranging from 5 to 20 km ($P < 0.05$) compared to distances of 5 to 15 km ($P < 0.01$)	Merged multifaceted andscape habitat modelling with genetics to detect and design biological corridors to test corridor efficacy for gene flow in a fragmented landscape	Klinga et al.,2019

Table 2 (Cont): Performance of Landscape Genetic Models

Model Type	Landscape Variable(s) Tested	Statistical Method	Goodness-of-Fit Matric	P-value or Significance Level	Key Interpretation	References (APA)
IBD and IBR, ndividual-based approaches, and esistance surface modeling	Landscape genetic tests, gene flow, and genetic structure	R package ResistanceGA (MLPE)	Heterozygosity (H_E) per locus was 0.489, genetic diversity (H_O: 0.417, H_E: 0.489)	The mean inbreeding coefficient (F_{IS}) was 0.149 ($p < .01$)	Mixed models with maximum likelihood using the R package nlme and using a correlation structure specified by corMLPE	Asadi Aghbolaghi et al.,2023
Isolation by Resistance, the spatial absorbing Markov chain, population genetic models, stepping stone model	Landscape genetics, nigration, mortality, and resistance to migration	Circuit theory and least-cost analysis	This model explained 2.4× the variation (Rm2=0.75;) as circuit theory (Rm2=0.31) and 1.7× the variation as least-cost distances (Rm2=0.44;)		Different types of potential directional migration: directional flow across a partial arrier, migratory routes, source–sink dynamics and a dendritic network	Fletcher Jr et al.,2022
Isolation by barrier (IBB; isolation by nvironment, IBE; isolation by resistance, IBR)	Genetic istances/differentiation and patterns of gene low in allopatric species	Single nucleotide polymorphisms (SNPs) from the NextRAD data set using 'VCFtools' v.0.1.17, principal component nalysis (PCA), R-package 'pcadapt' v.4.3.3	The first 10 axes (*Euclidean*$_{PCA\text{-}10\ axes}$) for 56.97% of the variation	$p < .05$, $n = 39$	Examined population genomic structure using different assignment methods and genomic differentiation and diversity	Moreno-Contreras et al.,2023
Clustering analyses,	Range-wide lifferentiation, little sex-biased dispersal, and strong isolation by listance that associated with significant genetic structure	Clustering analyses by he *snmf* algorithm	Observed heterozygosity H_O of 0.537 (0.383–0.671), a mean expected heterozygosity H_S of 0.557 (0.395–0.694) and an overall heterozygosity H_T of 0.588 (0.418–0.734).	$r = 0.49$, $P < 0.001$	Compared nicrosatellite and RAD-sequencing (RAD-seq) analyses to investigate population structure, investigated the relation between llele frequencies and observed heterozygosity for both marker sets	Dufresnes et al.,2023

7. Genetic Implications For Pollinator Fitness And Adaptation

Landscape fragmentation continuously occurs due to changes in landscape configuration and habitat loss for changing landscape composition. For pollinators, fragmentation often results in habitat isolation. Connectivity between habitat patches is crucial for maintaining pollinator biodiversity as it can enhance community composition, functional diversity, species evenness, presence of extinction debt, and genetic diversity (Vasiliev and Greenwood, 2023). Even in fragmented small area habitat loss is profound along with reduction in dispersal (required for organisms to migrate successfully to more suitable climate as climate change is severe) between population, effected by cumulative effects of genetic drift and deduced gene flow resulting fitness loss and erosion of genetic diversity leaving them less resilient to environment and demographic stochasticity more likely to extinct (Auffret et al., 2017). Biodiversity is at great risk from strong environmental changes, along with intensified land use abruptly altering different trophic groups. Pollinators (plants with butterflies) have strong associations between both functional and phylogenetic diversity in heterogeneous landscapes, but landscape fragmentation creates homogeneous populations for continuous selfing, amplifying inbreeding depression with loss of fitness (Rotchés-Ribalta et al., 2018). As homogeneous populations' genetic constitution resembles their relatives, they have a very narrow genetic base, making them highly susceptible and vulnerable to extreme climatic change (less adaptive).

7.1 How Genetic Factors Might Influence Inbreeding Depression or Reduced Adaptive Potential in Fragmented Pollinator Populations and Resilience to Environmental Change

Loss and degradation of habitat cause reduction in population size and gene flow in isolated subpopulations, increases inbreeding depression and genetic drift with vulnerable genomic erosion, damage inflicted to species genome or gene pool due to loss of genetic variation, genetic load, and maladaptation and deleterious variation, which can cause genetic disorders, infertility, mortality with inbreeding expression. In essence, they cause a long-term threat to declining populations and result in debt drift (the time-lag of evolutionary genetic change) (Pinto et al., 2024).

Inbreeding depression in fragmented landscapes with risk of extinction and the primary reason is recessive deleterious mutations become homogeneous due to inbreeding. Initiating genetic rescue by increasingly translocating individuals from a large population to mitigate biodiversity loss and extinction risk. A study was done in a small population using a novel genetic simulation framework, investigating the role of genetic diversity, deleterious variation, and demographic history in mediating extinction risk due to inbreeding depression. They found a high risk of extinction for strongly deleterious mutations, and a genetic rescue strategy can be used for long-term targeting moderate-sized source of populations where there will be no recessive strongly deleterious mutations (Kyriazis et al., 2021).

8. CONSERVATION APPLICATIONS AND MANAGEMENT IMPLICATIONS

Integration of molecular ecology and systematic conservation planning to evolutionary features crucial for biodiversity conservation in a world with extreme climatic conditions (Figure 5). Molecular data provide insights by identifying revolutionary significant units (ESUs) that measure gene flow, adaptability, diversity, differentiation, and decision support tools for conservation planning to generate prioritizations measuring demographic, structural, and genetic connectivity (Nielsen et al., 2023).

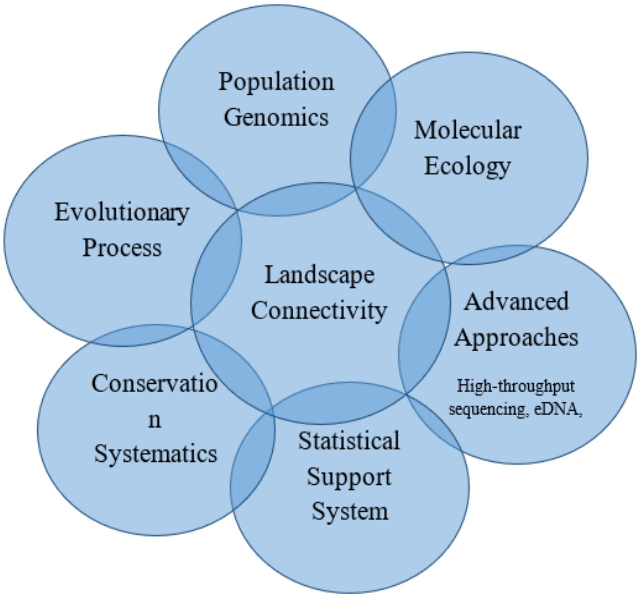


Figure 5: This figure showing combination of management approaches to ensure landscape connectivity for fragmented habitat restoration.

8.1 Gaps, Challenges, and Future Directions

The integration provides unique and timely opportunities for biodiversity conservation, but the molecular data potential needs to fulfill all the objectives of conservation planning. Molecular data are not generally available for all species for conservation planning, and are often limited by molecular marker types. Even high-throughput sequencing is invaluable for identifying the adaptive potential of natural populations. Recently, the innovation of environmental DNA (eDNA) metabarcoding, effective for community monitoring and able to give near real-time data on species diversity, and in fact, within-species diversity for conservation planning. Detects the endangered organisms through spatial and temporal high-resolution data and provides essential insights into connectivity and adaptive capacity (Nielsen et al., 2023; Oettel et al., 2025).

9. CONCLUSION

Habitat fragmentation is a vital point at issue of biodiversity loss, triggering profound changes in terrestrial ecosystems, leading to isolation and edge effect within pollinators' habitats. Flower-visiting pollinators influence approximately 75% of globally imported crop types, enhance yield and quality, and secure reliable and diverse food production. Fragmentation of landscapes shifts pollinator guilds, altering foraging behavior and limiting functional connectivity and ecological niches, reducing allelic richness and genetic differentiation. In fragmented landscapes, effective population size declines, increases genetic drift, inbreeding depression, reduces genetic diversity, reduces fitness, and reduces environmental adaptiveness. A small effective population size is the primary reason for allee effect, the bottleneck effect, and the founder effect; all these together have consequences that risk the biodiversity conservation rapidly in addition to extreme climatic conditions. Landscapes are subjected to rapid historical changes, making species susceptible to extinction, narrowing their genetic base and survival fitness as the fragmentation acts as barriers to gene flow. The effectiveness of analytical approaches, ecological corridors, and stepping stones for habitat connectivity establishment can ensure gene flow among the fragmented ecosystems. The knowledge of population genomics, molecular ecology, evolutionary processes, and conservation systematics with advanced tools and strategies of management ensuring fragmented habitat restoration through isolated landscapes connectivity enhancement, to ensure survival of the fittest, not the lucky individuals. The effective connection between isolated patches will have the potential to prevent the inbreeding depression, abrupt allelic frequency, and selection and survival of deleterious mutations. The broad genetic variation with wider environmental adaptability can impede genetic erosion of populations, perpetuating genetic variation of pollinators and sustaining biodiversity conservation.

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