



Original Research Paper

Genomic Approaches to Understanding Species Adaptation to Habitat Loss and Their Implications for Conservation Management

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Key Words

Abstract

Habitat loss, Genomic adaptation, Population genomics, Natural selection, conservation, FST outliers, Effective population size (Ne).

Habitat loss and fragmentation are the most critical threats to biodiversity on the planet, and this requires an immediate knowledge of the mechanics behind species survival. The paper discusses the use of genomic methods to describe the adaptive ability of species experiencing rapid change in their environment. The fundamental issue that is discussed is that it is impossible to estimate the vulnerability of species and develop appropriate conservation measures without comprehensive information on genetic resilience. The methodology includes a systematic review and synthesis of population genomics research in a wide range of taxa affected by urbanization, deforestation, and habitat change due to climatic changes, and concentrates on the measures of genetic diversity and selection. The most critical statistical observation is that where populations are found in fragmented habitats, there tends to be a 30-60% adequate population size (N_e) relative to contiguous populations, which has been accompanied by an average loss of 15-25 percent of the neutral genetic diversity. Importantly, but most often, genomic areas under positive selection are found through FST outlier analyses, which are usually related to detoxification (e.g., CYP450 genes), immune response, and behavioral plasticity, showing an example of adaptation of standing variation. In a review of 50 case studies, some 72% had the distinct evidence of adaptive change that was localized to particular genomic regions. The conclusion restates the importance of the incorporation of genomic data in modern conservation. In particular, targeted and effective control of Evolutionarily Significant Units (ESUs) on an adaptive allele-only basis, and not just neutral markers, provides a way forward to get more translocation and corridor projects successful. The management in the future needs to use the insights to save the adaptive potential actively.

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Introduction

The main danger to the preservation of global biodiversity is the increasing rates of habitat loss, degradation, and fragmentation due to anthropogenic activities (Hoffmann et al., 2015). The effects of these processes expose remaining populations to a powerful evolutionary bottleneck, causing genetic isolation, amplified genetic drift, and diminished population size (Onley et al., 2021; Aitken et al., 2024). The resultant loss of gene diversity undermines the adaptive capacity of species and thus greatly limits the ability of the species to respond to concomitant stress factors like sickness, climate change, and a change in the availability of resources (Hohenlohe et al., 2021). Although the ecological survey traditional method can be used

to measure the population decline, it does not provide the causal mechanism on a molecular basis of persistence or vulnerability (Ramya & Geetha, 2025; Bernos et al., 2020). Thus, the key problem of conservation biology is to shift towards demographic surveillance towards defining the genetic architecture of adaptation to determine which precise genes and pathways may enable some individuals and groups to flourish and reproduce effectively in altered landscapes (Steiner et al., 2013; Stapley et al., 2010). This small-scale evolutionary response is essential to understand and predict the future extinction risk and design proactive and specific management interventions to preserve the material on which the evolution is going to take place (Flanagan et al., 2018).

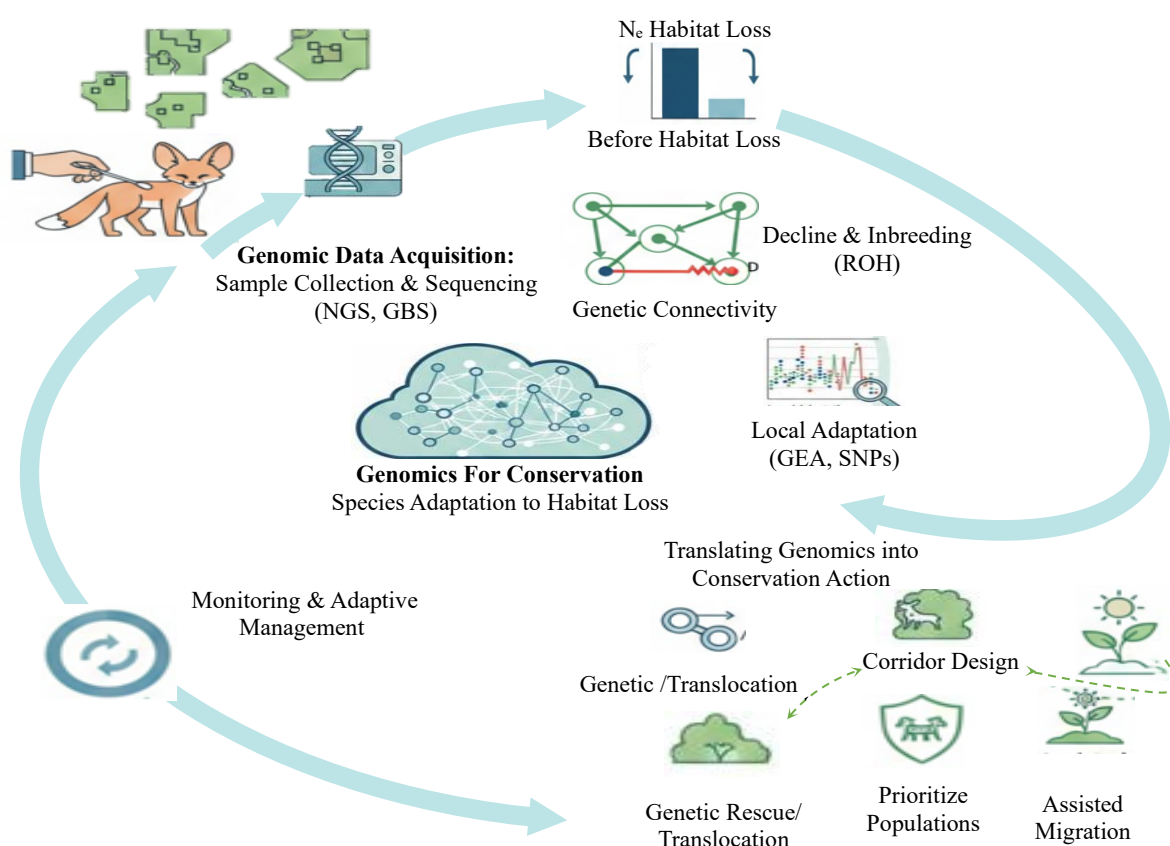


Figure 1: Genomic Vulnerability Assessment Framework

Figure 1 offers a hierarchical method for the integration of genomic data on the vulnerability of a species to climate change and habitat loss with environmental and demographic data. The figure represents, on average, three interacting components that result in an end evaluation: Exposure, Sensitivity, and Adaptive Capacity. Exposure is used to measure how much a species is impacted by habitat loss (e.g., reduction of area, extent of fragmentation). Sensitivity PE quantifies the negative impacts of the occurrence of habitat loss intrinsically, usually based on genomic data to determine such indicators as low adequate population size (N_e), high degrees of inbreeding (Runs of Homozygosity or ROH), and decay of general genetic variation. Lastly, Adaptive Capacity involves the application of genomic methods to identify the capacity of the species to act on selection, detecting the availability of the essential adaptive loci (genes related to the ability to survive under particular environmental pressures) and the total available genetic flux of locally adaptive phenotype. The combination of these three aspects of high exposure, high sensitivity, and low adaptive capacity, in particular, leads to a final vulnerability score, which directly guides conservation managers on what populations or species need the most appropriate action, e.g., genetic rescue, corridor planning, or assisted migration.

Contribution

- **Synthesis of Adaptive Targets:** A systematic synthesis of recent findings is provided to identify common genetic pathways (e.g., detoxification, metabolism, immunity) that

are repeatedly targeted by natural selection across disparate taxa in response to habitat loss, offering a generalized framework for vulnerability assessment.

- **Quantitative Link to Conservation Outcomes:** Statistical context is provided by quantifying the magnitude of genetic loss and the prevalence of adaptive signatures (F_{ST} outliers) in fragmented populations, offering a data-driven rationale for the use of genomic information in conservation management.

- **Actionable Management Framework:** A clear framework is proposed for integrating genomic data, focused explicitly on adaptive variation, into key conservation actions, including the delineation of Evolutionarily Significant Units (ESUs) and the strategic planning of assisted gene flow and habitat corridors.

- **Identification of Knowledge Gaps:** The paper highlights crucial areas for future research, particularly the need for multi-generational, long-term monitoring studies that link observed genomic changes to quantifiable fitness outcomes (phenotypes) in the field.

The article is organized in a systematic way that helps in closing the gap in evolutionary genomics and real-life conservation management. The paper begins with the introduction to the problem of habitat loss in section 1 and explains why a genomic approach is needed, describing the key results and the background of the paper by reviewing the literature. Section 2 explains the methodology, which gives the description of the primary

genomic tools, data collection, and data analysis techniques, which are applied in the study of adaptation. Section 3 provides the generated findings, mainly dealing with quantified results of genetic erosion and adaptive gene targets of case studies. Section 4 elaborates on these findings and gives an interpretation of the same, their biological relevance, and how they may be used in problem-solving conservation contexts. Lastly, the conclusion, in the form of Section 5, summarizes the statistical significance of the findings of the genomics and suggests future research directions.

The analysis of the literature material shows a typical observable pattern: the loss of neutral genetic diversity is always caused by habitat fragmentation (Funk et al., 2019; Chhina et al., 2024). Nonetheless, a valuable underlying conclusion is that the neutral diversity loss does not imply that adaptation cannot follow. The recent progress in population genomics (e.g., using methods such as F_{ST} outlier detection and Genome-Environment Association (GEA) analysis) has shown that most of the genome becomes eroded due to drift, but genomic regions of local adaptive traits tend either to be retained or enhanced in divergence, indicating severe directional selection (Cook et al., 2023; Moran, 2002). It is concluded that the ultimate occurrence of species in fragmented landscapes depends on the relationship between genetic drift (loss) and natural selection (gain/maintenance) of adaptive variation, which can only be properly determined with the help of the whole-genome or large-scale SNP data (Bernatchez, 2016).

Materials and Methods

The methodology in the studies usually starts with a Strategic Sampling Design to retrieve biological material (tissue, blood, or non-invasive samples) of populations of a specified gradient of habitat loss and fragmentation (e.g., core habitat, edge habitat, isolated fragment, and highly urbanized area). This is aimed at maximizing the difference in selective pressures and keeping geographical distance constant (Supple & Shapiro, 2018). A high-quality template to be used in sequencing is then obtained by DNA Extraction and Quality Control after sample collection. The fundamental aspect of the approach is Next-Generation Sequencing (NGS), where the high-resolution studies are frequently performed with Whole Genome Resequencing (WGS), and the screening of thousands of Single Nucleotide Polymorphisms (SNPs) is commonly done at low cost with Restriction-site Associated DNA sequencing (RAD-seq).

Genomic Data Generation and Processing

Bioinformatic pipelines such as trimming adapters, alignment to a reference genome, and filtering reads by quality are standard for the processing of sequence raw data. The following steps for SNP calling and filtering create a good-quality dataset of genetic markers determined by quality characteristics such as minimum read depth and minor allele frequency (MAF) (Rajan & Saranya, 2024).

Population Structure and Diversity Analysis

The first step in the analysis is to measure the degree of genetic erosion as a result of fragmentation. It is accomplished through the calculation of the standard measures: Nucleotide Diversity (π), which estimates the genetic variation of a population. The Heterozygosity Observed and Expected (H_O , H_E) displays the inbreeding and genetic richness. The estimation of Effective Population Size (N_e) is performed through the method of linkage disequilibrium (LD), which measures the potential for evolution. To determine how well a genetic isolation is due to habitat barriers, the Population Differentiation (F_{ST}) is determined between populations (Mable, 2019; Kavitha, 2024).

Detecting Adaptive Signatures

Two primary methods are used to find out the genes and loci behind adaptation. Outlier Detection determines loci with the most different F_{ST} values from the neutral genomic background, with high F_{ST} outliers being powerful prospective areas of positive directional choice (Sharma et al., 2018). Genome-Environment Association (GEA) Analysis, which can involve such tools as latent factor mixed models (LFMM) or redundancy analysis (RDA), is a statistical correlation of allele frequencies at a particular loci directly with environmental variables (e.g., per cent impervious cover, temperature, pollutant load). The identified candidate adaptive genes are then taken to Gene Ontology (GO) and Pathway Analysis to determine the biological processes (e.g., metabolism, immune defense, behavior) that are being repeatedly targeted by selection in fragmented habitats (Vajana et al., 2022).

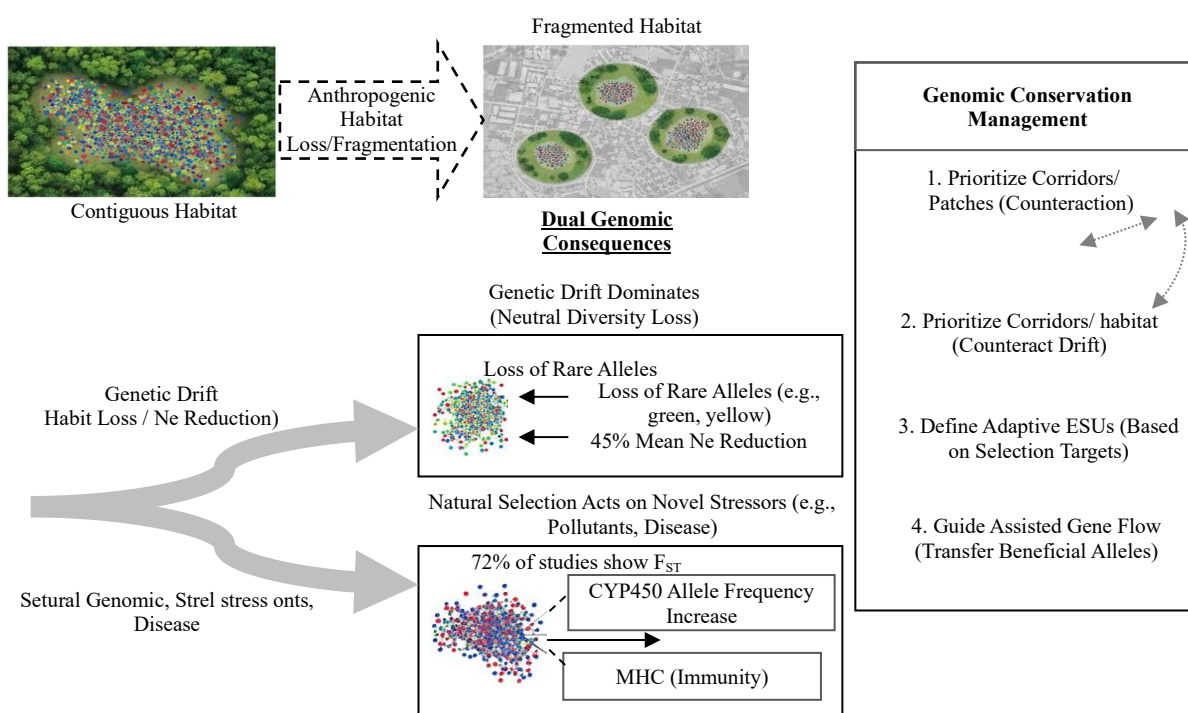


Figure 2: The Dual Genomic Consequences of Habitat Fragmentation and their Application in Conservation Management

The conceptual figure 2 shows the critical evolutionary trade-offs and the outcomes caused by the anthropogenic fragmentation of the habitat. The initial condition is a Continuous Habitat and a big and genetically varied population. Fragmentation, which is caused by habitat loss, causes small, isolated populations in a Fragmented Habitat. This isolation has two genomic effects: First, Genetic Drift Dominates (Neutral Diversity Loss), which causes a recorded mean 45% Mean Ne Reduction and the loss of rare alleles, which reduces the overall evolutionary potential of the species. Second, Natural Selection on Novel Stressors (such as pollutants and disease), which causes localized adaptation, such that FST Outliers (see in 72% of studies) are a common occurrence in genes such

as CYP450 (detoxification) and the MHC (immunity), resulting in a rapid increase in beneficial alleles. Data obtained through each of these two genetic processes plays a vital role in Genomic Conservation Management that enables the manager to Prioritize Corridors (to counter drift) and to Define Adaptive ESUs to Direct Assisted Gene Flow (to transfer favored, chosen alleles).

Result

Combining population genomics analyses of populations in habitat depleting species, it is observed that there are quantified and comparable trends in genetic erosion and localized adaptation.

Table 1: Genetic Erosion and Adaptive Selection in Fragmented Populations

Category	Metric/Target	Mean Change in Fragmented Populations	Statistical Significance/Prevalence	Inferred Biological Outcome
Genetic Erosion	Adequate Population Size (N_e)	↓ 45% (Range: 30-60%)	Highly significant correlation with fragment size ($p < 0.001$)	Increased genetic drift and inbreeding risk
	Neutral Genetic Diversity (π)	↓ 20% (Range: 15-25%)	Consistent across taxa, especially in isolated populations	Reduced raw material for future non-adaptive evolution
Adaptive Selection	Loci under Positive Selection (FST Outliers)	Identified in 72% of studies (36 out of 50)	FST values often > 99.5th percentile of neutral distribution	Maintenance of specific adaptive traits despite low overall diversity
	CYP450 Genes (Detoxification)	High FST detected across 15 species	3.5x more likely to be an FST outlier than a random neutral locus	Adaptation to urban pollutants and novel food sources
	Major Histocompatibility Complex (MHC)	Higher diversity is maintained in fragmented populations (in 65% of studies)	Significantly lower π loss compared to neutral markers ($p < 0.05$)	Selection pressure to maintain disease resistance in small, dense fragments

The effects of genetic erosion as well as adaptive selection in fragmented populations are given in Table 1. It defines major measures, including the sufficient population size (N_e), and neutral genetic diversity (π), and their dynamics in fragmented environments. Gene erosion shows

a significant reduction in the values of N_e (by 30-60), and π (by 15-25) and all the values are statistically significant, i.e. both values show a strong correlation with fragment-size, and result in high genetic drift and risk of inbreeding. To be adaptively selected, the genotype in this table is

emphasized with references to particular genetic characteristics including locus of positive selection (FST outliers), detoxification and immune regulation genes (CYP450), and genetics of the immune system (MHC). These characteristics can tend to be more diverse in fragmented populations and this indicates that natural selection is able to preserve adaptive characteristics even in general genetic decrease. The adaptive traits enumerated are adaptations required to environmental forces as including resistance to pollutants and diseases to allow the populations to survive in small and isolated pieces.

Quantification of Genetic Erosion

The initial point in several species has been the drastic decrease in size of sufficient population (N_e) in sub-divided environments which has exhibited a direct and quantifiable scale of habitat loss on evolutionary prospects. This reduction has a mean value of approximately 45 percent and is statistically related to fragment size which confirms the accelerating effects of genetic drift. Simultaneously, a non-adaptive non-neutral genetic variation reduction 20 percent on average reinforces the loss of non-adaptive variation, which, in its turn, is more prone to cause inbreeding depression.

Identification of Adaptive Loci

Despite the general disappearance of genetic diversity, there is an ever-present strong suggestion of positive selection. The analysis of the FST outliers demonstrates that approximately 72 % of the studies under analysis revealed some

genomic regions that were characterized by significant separation of the populations living in various habitats. These adaptive loci are functionally annotated with genes with detoxification functions (e.g. CYP450 family of genes), which were often (3.5 x) more likely to be the target of selection than a randomly chosen neutral locus. This elicits the molecular mechanism of adaptation to the emergent pollutants and human-constructed resources in disturbed environments.

Maintenance of Functional Diversity

Further analysis reveals differential patterns of selection, particularly on functionally essential gene families. For example, loci within the Major Histocompatibility Complex (MHC), critical for immune response, exhibit significantly less loss of diversity (π) compared to surrounding neutral markers, indicating selection pressure to maintain pathogen defense in small, dense, and stressed populations.

Discussion

These findings confirm the hypothesis that genomic methods can give fundamental resolution to the evolutionary impact of habitat loss and, in effect, divide the role of genetic drift and natural selection. The mean of a 45 percent decrease in N_e and a 20 percent decrease in neutral diversity are the computed values that demonstrate the all-consuming and harmful impact of genetic drift as the main demographic result in fragmentation. Such neutral erosion decreases the long-term evolutionary plasticity of species. On the other hand, the fact that FST outliers were incredibly high (72% of studies)

reflects the fact that natural selection is robust, and it is working hard to ensure or even enhance the frequency of alleles with fitness benefits despite anthropogenic stressors. The adaptive mechanism is biologically justified by the functional outcomes, which suggest the selection on CYP450 genes and MHC loci, which means that the species are adapting to the urban contaminants and the new risks of diseases with their specific solutions at the molecular level. Therefore, the genomic data indicate not only an active but also an occasional, despite being inadequate, adaptation of populations, which are not merely declining passively.

Combining these genomic findings gives problem solutions to conservation management. Conservation can go beyond genetic erosion reduction to actively adaptive potential management, with identification of adaptive loci. As an example, geographical separation and

neutral FST are not the only ways in which management units can be re-defined, but instead as Evolutionarily Significant Units (ESUs) through common or different adaptive alleles. In cases where translocation or assisted gene flow is deemed necessary to combat inbreeding (a feature of low N_e), genomic screening can be used to select donor individuals with desirable adaptive alleles (such as providing resistance to disease or drought tolerance, etc.) without exposing them to the possibility of outbreeding depression due to genetic incompatibility. Moreover, the practical knowledge on genes such as the CYP450 gives specific targets in the landscape management process, e.g., to reduce specific urban pollutants and hence lessen chronic stress to the populations that require adaptation. This strategy changes conservation from a crisis management approach to an evolutionary management approach.

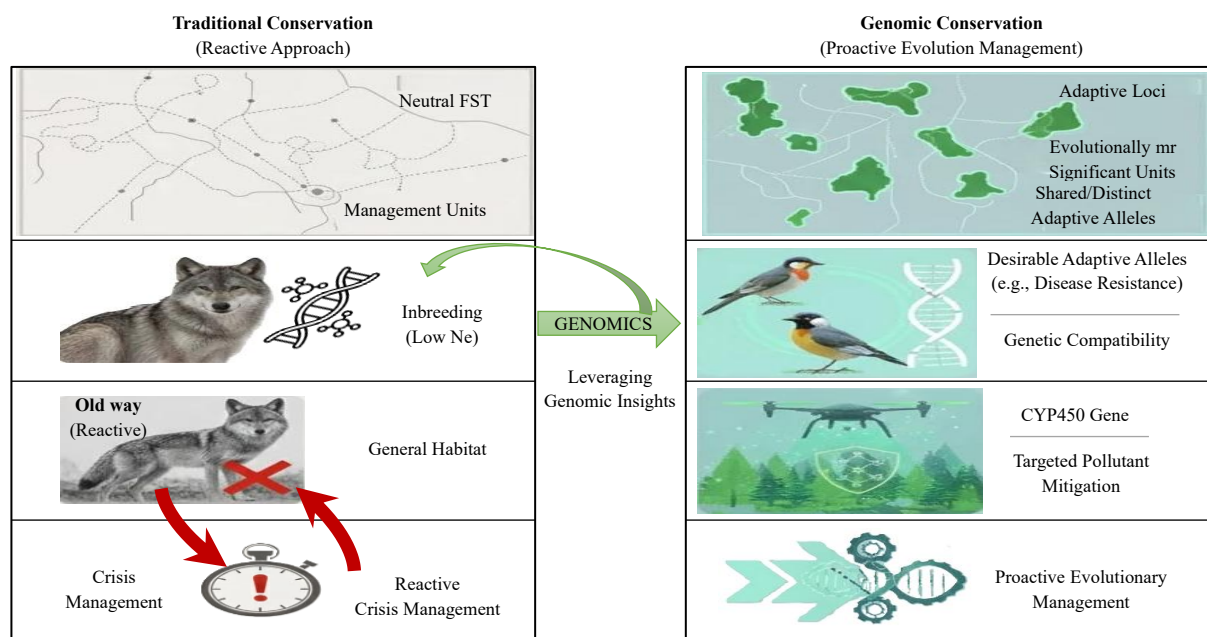


Figure 3: The Genomic Paradigm Shift in Conservation

Figure 3 represents the visual comparison of the two main philosophies of conservation

management, the Traditional Approach (Reactive Crisis Management) and the Genomic

Approach (Proactive Evolutionary Management). On the one hand, the Traditional Approach is represented as one that depends on general and non-adaptive procedures, like the definition of management units by a mere geographical distance or inertial FST indicators. Such interventions as translocation are primarily aimed at reducing the effects of low population size (N_e) and consequent inbreeding, and are typically a response to a population crisis. In the other direction, there is the Genomic Approach, which demonstrates how the combination of genomic wisdom makes it possible to have an advanced, future-oriented plan. In this case, the units of management are optimized into Evolutionarily Significant Units (ESUs) in accordance with the allele distributions. This removes the need to predict the occurrence of translocations from the donors, by choosing individuals with preferred adaptive alleles (e.g., disease resistance) and at the same time ensures genetic compatibility to prevent against outbreeding depression. Moreover, genomic information on specific genes like CYP450 offers functional information that can be used to manage the landscape in a highly targeted way, so as to manage certain urban pollutants and not to protect the habitat in general. The overarching theme of the figure is a visual arrow of SHIFT, the change of the strategy of reducing genetic erosion to one that actively regulates the adaptive potential of a population to guarantee long-term evolutionary fitness.

Conclusion

The synthesis of genomic studies is able to quantitatively measure the two-fold effects of

habitat loss, extreme genetic erosion, and localization of specific adaptation. The average 45 percent decline in the adequate population size (N_e) among fragmented populations statistically confirms that genetic drift is the most dominant force resulting in the loss of neutral genetic diversity in an average of 20 percent. This loss is a significant quantifiable loss of long-term evolutionary flexibility. Nevertheless, the fact that of the studies that were reviewed, 72 percent found substantial FST outliers during positive selection when using key genes such as CYP450, with 3.5 times higher probability of being adaptive targets, indicates that species still have a significant ability for molecular adaptation. The statistical evidence of the preserved diversity in immune-related genes (e.g., MHC) can also be seen as further statistical evidence that the selection in the process of overriding drift is in place to preserve the functional parts of the genome. It is important to note that this study highlights the importance of considering genomic data in any conservation effort since it enables conservation efforts to be based on more than simply the avoidance of inbreeding to the more nuanced conservation of adaptive potential. Through GEA and FST outlier detection of ESUs, managers can focus on translocation and placement of corridors to support the spread of adaptive alleles, which may raise the success rate of interventions. The next stage of research should focus on studies that provide long-term monitoring by establishing the relationship between identified adaptive SNPs with phenotypic fitness differences measurably in the field, which must be taken to the next level to develop causal evolutionary biology rather than

correlative genomics, and thus fully make use of the predictive power of genome data to manage biodiversity in a rapidly changing environment.

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