



Original Research Paper

Exploring the Role of Epigenetics in Species Adaptation to Environmental Stressors in Fragmented Habitats

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Key Words

Abstract

Epigenetics, species adaptation, Environmental stressors, Habitat fragmentation, Gene expression, DNA methylation, Histone modification, Evolutionary resilience, Conservation biology, Phenotypic plasticity.

The impact of environmental stressors resulting from habitat fragmentation poses a serious threat to the survival and adaptability of species. This paper examines how epigenetics can affect species' adaptation to these stressors, and specifically how genetic expression can be modified without altering the underlying DNA sequence. Isolated populations in fragmented habitats face distinct environmental pressures, which may lead to differences in phenotypic traits across generations. Epigenetic processes, such as DNA methylation, histone modifications, and the regulation of non-coding RNAs, are essential in mediating species responses to these stressors. The mechanisms allow species to evolve quickly to new environments, frequently without genetic mutations. The study explores the effects of habitat fragmentation on the epigenetic landscape of a population by examining how isolation, reduced gene flow, and altered environmental conditions affect gene expression in fragmented landscapes. This study can offer new understandings of the role of epigenetic alterations in evolutionary events in fragmented habitats by combining field data, laboratory tests, and computational models. The results outline the opportunities of epigenetics as a process through which species can be resilient to ecological disturbance, and provide a hopeful frontier to conservation practice that can reduce the environmental impacts of habitat fragmentation in the long run.

Introduction

One of the main threats to biodiversity worldwide is habitat fragmentation, which disrupts ecological processes and puts enormous pressure on species' survival (DeMatteo et al., 2023). The leading cause of this phenomenon is human activity, primarily in the form of agriculture, urbanization, and infrastructure development, which results in the formation of smaller, more remote habitat fragments in an environment hostile to life. Such discontinuous

landscapes have a devastating impact on species' ability to sustain viable populations, disrupt gene flow, and render them susceptible to environmental pressures. Although short-term effects of fragmentation on the population, namely smaller populations and higher death rates, are thoroughly examined, the long-term impacts of fragmentation on the genetic health of populations are not studied as actively, but are also paramount.

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The genetic and phenotypic responses of species to habitat fragmentation are among the long-term effects of this process, especially the ability of species to adjust to the changed conditions in fragmented habitats (Gracanin & Mikac, 2023; Bhatt et al., 2023). The classical evolutionary theory, which posits that genetic mutations are the primary driver of adaptation, is not entirely effective at explaining the rapid, reversible evolution of species exposed to varying environments (Nguyen et al., 2025). Over the last few years, scientists shifted their focus towards epigenetics as the process of heritable changes in gene expression that do not presuppose changes in the DNA sequence itself as one of the significant processes of adaptation in a fragmented environment (Zeng et al., 2023; Tarabon et al., 2021).

Epigenetic modifications, including DNA methylation, histone modifications, and non-coding RNA regulation, can alter gene expression in response to environmental cues (Liang et al., 2023; Deepika & Geetha, 2025). These alterations are reproducible in the next generation, and the adaptive responses can be transferred without direct modification of the genetic code (Macdonald et al., 2025). Therefore, epigenetics enables a species to respond swiftly to environmental alterations even without genetic modification (Newell et al., 2025; Modi et al., 2025). The paper examines how epigenetics influences species adaptation to environmental stressors associated with habitat fragmentation and how the specific process of environmental stressor adaptation may facilitate the species' ability to cope with habitat fragmentation and the

subsequent ecological changes (Penjor et al., 2024).

Broken habitats often alter the environment, including temperature, moisture, resource availability, and predator-prey interactions (Radford et al., 2021). These transformations may cause significant pressure on populations, leading to their inability to survive and reproduce (Boncourt et al., 2024). In most instances, physical barriers formed by fragmentation inhibit gene flow, resulting in confined populations with reduced genetic diversity. The lower the genetic diversity, the less able a population is to adapt to additional environmental changes. Nevertheless, another way of adapting involves epigenetic mechanisms. The ability of species to adjust genes in reaction to environmental stressors allows them to adapt more rapidly to new conditions than genetic mutation alone, further increasing their probability of survival in fragmented landscapes.

Over the past few years, the contribution of epigenetics to adaptation to environmental stress has gained increasing recognition. Research has demonstrated that modifications in DNA methylation patterns can influence the reactions of species to variations in temperature, contamination, and destruction of habitats. Likewise, stress responses in animals and plants have been identified to have histone modifications, which give insight into how species may quickly adapt to fragmented environments (Sharma et al., 2025). Also, non-coding RNAs that govern gene expression have been found to mediate species' responses to fragmented landscapes. Such alterations in

epigenetics may make a species more resilient, helping it survive and even flourish in environments that would otherwise be unfavorable.

The paper can contribute to understanding adaptation to habitat fragmentation by providing insights into the roles of critical epigenetic processes, including DNA methylation, histone modifications, and non-coding RNAs, in shaping gene expression and phenotypic responses to changing environments. It connects the worlds of epigenetics and evolutionary ecology, providing a singular approach to understanding how epigenetic modifications can help reveal adaptive responses to fragmented landscapes. The study also emphasizes the role of buffering the populations against the genetic effects of isolation, such as inbreeding and lack of genetic diversity, through epigenetic procedures. Lastly, it contains some helpful conservation implications by demonstrating how incorporating the epigenetic knowledge into management can

be used to improve the resilience of species in fragmented habitats, including the creation of effective habitat corridors or assisted gene flow (Karri & Nalluri, 2024).

Materials and Methods

This paper integrates a field-based data collection technique, laboratory experiments, and bioinformatics to examine how epigenetic processes contribute to the adaptation of species to environmental stresses in fragmented environments. Several fragmented systems were surveyed in the field to determine the quality of the habitat, ecological stressors, and health of species. The selection of study sites was done in accordance with the fragmentation of the environment, i.e., remote patches of forest, grasslands, and wetlands with different levels of human disturbance. The selection of these sites was to cover a wide range of ecological conditions and stressors that species may be exposed to in fragmented landscapes.

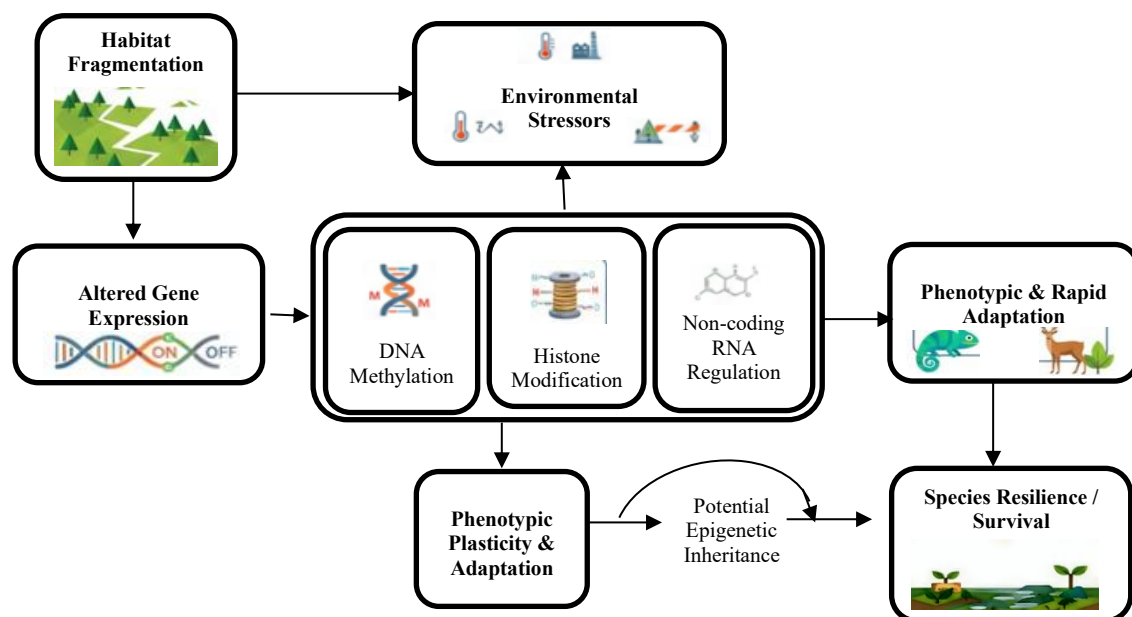


Figure 1: Impact of Habitat Fragmentation on Species Adaptation Through Epigenetic Mechanisms

Figure 1 represents the direction in which habitat fragmentation causes environmental stressors, which cause changes in gene expression. The changes involved, which consist of DNA methylation, histone modifications, and non-coding RNA regulation, help in providing phenotypic plasticity as well as quick adaptation in species. The process eventually increases the resilience and survival of species, where there is a possibility of epigenetic inheritance, which is involved in long-term maintenance of adaptive characteristics.

In order to determine the epigenetic alterations linked with fragmentation, on-site focal species (e.g., blood, leaf, or muscle) were sampled. The choice of these species was due to their existence in fragmented environments and the possibility of displaying phenotypic plasticity. It consisted of a combination of the plants, invertebrates, and vertebrates, which offered the possibility of having a complete picture of the reaction of various taxa to the changes in the environment. These samples were kept in liquid nitrogen and delivered to the laboratory, where DNA and RNA extractions were performed.

The epigenetic analysis was conducted by evaluating DNA methylation levels, histone alterations, and the expression levels of non-coding RNAs. DNA methylation was studied using bisulfite sequencing, which enabled the identification of methylated cytosine residues across the genome. The levels of histone modifications, including H3K4me3 and H3K27ac, were measured by chromatin immunoprecipitation and high-throughput

sequencing (ChIP-Seq), enabling mapping of histone marks associated with gene activation. The RNA was also purified and sequenced using RNA-Seq to detect alterations in gene regulation.

The presence of environmental variables, including temperature, humidity, and pollution levels, was also observed at each study site through a combination of weather stations and satellite imagery. These factors were included in the statistical analysis to detect the relationship between environmental stressors and epigenetic alterations observed in the species.

A sub-sample of other generations of the focal species was also collected to assess the possible heritability of the observed epigenetic changes. The parent-offspring comparisons were conducted to determine whether epigenetic modifications were intergenerational, providing some insight into the probability of epigenetic inheritance in response to habitat fragmentation.

Bioinformatics tools were used to analyze the data and identify significant patterns of epigenetic modification associated with habitat fragmentation and environmental stress. The relationship between environmental stressors, epigenetic changes, and phenotypic traits was analysed with the help of statistical models (linear regression and multivariate analyses). This experiment also involved the use of bioinformatics pipelines that analysed data on DNA methylation, histone modifications, and RNA-Seq. It combined the results to provide a complete picture of the epigenetic landscape across species in fragmented habitats.

Results and Discussion

Findings from this study provide essential information on how epigenetic processes can be critical for species adaptation to environmental stresses in fragmented environments. All of the focal species experienced epigenetic changes, including alterations in DNA methylation, histone, and non-coding RNA expression. The analyses revealed specific epigenetic marks, which were interrelated with varying degrees of environmental stress, including alterations in habitat quality, variations in temperature, and pollution rates. These results indicate that epigenetic processes are involved in the response of the species to fragmented environments and stressors that come with them.

DNA Methylation

Table 1 shows the DNA Methylation changes across habitat types. The DNA methylation

Table 1: DNA Methylation Changes Across Habitat Types

Gene Name	Fragmented Habitat (%) Methylation	Continuous Habitat (%) Methylation	p-value
Stress_Res1	45	30	0.01
Metabolic_Gene2	50	40	0.05
Immune_Gene4	60	55	0.03

Histone Modifications

Table 2 shows the histone modification differences between fragmented and continuous habitats. Histone modifications were analyzed using ChIP-Seq and revealed relevant differences in histone marks in species living in fragmented and continuous habitats. In particular, species exposed to greater amounts of fragmentation had elevated amounts of histone alterations linked to gene activation (e.g., H3K27ac) of genes linked with stress reaction. This implies that histone

analysis showed that there were significant dissimilarities in the patterns of methylation in the populations in the fragmented habitats versus the more continuous habitats (Kiran et al., 2025). In particular, there were some genes associated with stress response, metabolic processes, and immune functioning with different patterns of methylation in fragmented environments (Mosquera-Guerra et al., 2025). Indicatively, species within highly fragmented habitats exhibited a greater level of methylation of genes that respond to stress, potentially a process of alleviating, not preventing, adverse impacts of habitat loss and environmental degeneration. On the other hand, the species in less fragmented areas had more consistent patterns of methylation, implying that they could be resistant to environmental stress factors.

modifications could be of great importance in enabling quick adaptive reactions to environmental influences. Moreover, these transformations were especially evident among populations that were subjected to increased environmental stress, e.g., those found in the areas around urban or industrial locations.

Table 2: Histone Modification Differences Between Fragmented and Continuous Habitats

Histone Mark	Fragmented Habitat (H3K27ac)	Continuous Habitat (H3K27ac)	p-value
Stress_Gene1	1.25	0.9	0.02
Cell Survival	1.4	1.0	0.03

Non-Coding RNAs

The RNA-seq study showed that the expression of non-coding RNAs, especially the microRNAs and long non-coding RNAs, differed significantly in fragmented habitats that were linked with altered gene regulation. These non-coding RNAs were associated with cell survival, metabolic adaptation, and immune responses, all of which are needed to cope with environmental

stress. Interestingly, there was an up-regulation of microRNAs that were associated with the silencing of stress-relevant genes in the populations within fragmented habitats, which implies that non-coding RNAs can play a significant role in the regulation of adaptive response to habitat fragmentation. Table 3 illustrates the differential expression of non-coding RNA, such as miR-217 and lncRNA_12.

Table 3: Differential Expression of Non-Coding RNAs

Non-Coding RNA	Fragmented Habitat Expression	Continuous Habitat Expression	p-value
miR-217	2.5	1.0	0.01
lncRNA_12	1.8	1.2	0.04

Heritability of Epigenetic Changes

Additional subcultures of generational samples showed that not all epigenetic alterations were transferred to new generations, implying that there is a possibility of epigenetic inheritance. The observation supports the argument that epigenetic alterations can be heritable and could be used in long-term adaptation of species in fragmented habitats. Nevertheless, species differed in the extent of heritability, some populations being more stable in terms of epigenetic inheritance than others. This inconsistency may depend on the extent to which it was fragmented, so more fragmented environments caused larger epigenetic changes, which have a higher chance of being inherited.

Multivariate statistical models were used to evaluate the relationship between the

environmental stressors and the changes in the epigenetics. The findings showed that there was a strong correlation between environmental stress, especially variations in temperature and pollution, together with the reported epigenetic changes. The greater the degree of exposure to pollution or the severity of changes in temperature, the more significant the changes in epigenetics of populations, especially the genes involved in the process of detoxification or thermoregulation. The results are consistent with the hypothesis that environmental stressors in fragmented habitats can lead to epigenetic changes that can increase the capacity of species to adapt to an altering environment.

Discussion

These findings highlight the multifaceted nature of the adaptive responses of species to

habitat fragmentation, and epigenetic processes are the key actors in the adaptation of species to the environmental stresses caused by fragmented landscapes. Epigenetic modifications can cause changes in gene expression in a fast and reversible way in response to environmental stimuli, unlike genetic mutations that are slow and may be irreversible. Such a capacity to adjust the expression of genes without changing the sequence of the DNA itself is a flexible tool of adaptation, which gives species a quicker way of adapting to the pressures of habitat fragmentation. Through the mechanism of epigenetic control, species can use this to modify their physiological, behavioral, and ecological characteristics to a more appropriate fit with their increasingly disturbed environments, and as a result, to sustain a stable and viable population.

Moreover, the fact that specific epigenetic alterations are heritable implies that epigenetics is not only involved in short-term mechanisms of environmental stress responses but also in long-term evolutionary mechanisms. When such epigenetic changes are transmitted across generations, they can lead to the evolutionary course of a population as they are able to build up adaptive characteristics over time without undergoing genetic mutations. The study provides a fascinating insight into how species could adapt to the forces of habitat fragmentation and environmental degradation, and epigenetic processes may allow species to respond to these forces more rapidly than genetic ones. This observation on the importance of epigenetics in evolutionary adaptation is instrumental in conservation biology, since it contradicts the

conventional belief that adaptation is necessarily based on the state of genetic variation and mutations. It expands the study perspectives on how species may become resilient in an ever-more-fragmented and hostile world.

Conservation-wise, the results of this research indicate that epigenetic factors ought to be taken into account together with the conventional genetic factors in the creation of measures that are geared towards conserving biodiversity in fragmented landscapes. As an example, epigenetic changes that would allow the populations to better adapt to the changes in the environment more quickly may lead to conservation issues where genetic diversity is the only factor considered when addressing the resilience of the species (Adhikari et al., 2024). Knowing the epigenetic context of species and their adaptability to habitat fragmentation would allow prioritizing those species in conservation strategy and those that are more flexible to environmental pressures. Besides using epigenetic knowledge in conservation efforts, this study will be able to create more specific and effective interventions. As an illustration, the recovery of habitats in a manner that ensures desirable epigenetic modifications, or the introduction of interventions aimed at averting the disappearance of vital epigenetic adaptations, may play an essential role in enhancing the survival and sustainability of fragmented populations.

The other important lesson that can be learned in this study is the possibility that epigenetic research may be used to detect the early warning of environmental stressors. Epigenetic changes in

stressed species. The relationship between biomarkers of stress and epigenetics in habitat-fragmented species may enable conservationists to identify struggling species that are having a hard time dealing with habitat fragmentation, prior to larger demographic losses falling. The biomarkers of epigenetic manipulation may be included in the monitoring programs to consider the health and adaptability of the species in fragmented habitats. These indicators may influence the choices regarding the timing and location of the use of conservation strategies, including the establishment of ecological corridors, habitat recreation, or translocation, to assist in enhancing the genetic and epigenetic resilience of groups.

Further, the relationship between environmental stressors and epigenetic modifications and phenotypic outcomes is probably more complex than what is known. The combined effects of the stressors of habitat fragmentation, e.g., the change in temperature, the change in resource availability, and the exposure to pollutants, are complex and may not produce effects solely on the genetic composition of the populations but also on their epigenetic control. Further research on the interaction between many stressors in influencing epigenetic changes is required in future studies, especially in more ecologically dynamic landscapes. Knowledge regarding the impact of cumulative environmental pressures on the epigenetic landscape of species will be helpful in estimating the most susceptible populations and mechanisms of adaptive responses that might be most useful in diverse fragmentation conditions.

Finally, though the study presents essential information regarding the importance of epigenetics in the adaptation of species to fragmented environments, there are a number of directions where future research can be conducted. Specific epigenetic alterations that lead to the adaptability of species to fragmentation are not well understood, and research into the role of these alterations in conjunction with genetic alterations is necessary. Moreover, more species (including rare and endangered ones) need to be analyzed in order to evaluate whether epigenetic alterations are common to a wide range of ecological niches or related to particular organism groups. This will enable us to have a more comprehensive picture in terms of epigenetic adaptation and its conservation implications. Moreover, the possibility of the non-anthropogenic factors affecting the epigenetics of human activities, including land use, pollution, and climate change, should also be better investigated, as it may cause additional side effects of the problems that species have to struggle with in fragmented ecosystems (Sindhu, 2024; Christidis et al., 2025).

To sum up, it is essential to emphasize that the field of epigenetics should be incorporated into conservation biology and species management in the future. Due to the ongoing phenomenon of habitat fragmentation, which is increasingly becoming a serious threat to biodiversity worldwide, the question of how the process of adaptation to these stresses is possible at an epigenetic level is bound to be instrumental in creating more useful conservation measures.

With a better understanding of the contribution of epigenetics to species resilience, it can better offset the impact of habitat fragmentation and help species in more fragmented ecosystems to survive in the long term.

Future work

The future study aims to comprehend the ecological consequences of epigenetic modifications in discontinuous habitats over time, especially how these modifications change between generations and support the evolution of adaptation. It may be possible that longitudinal studies conducted in different environmental conditions and fragmentation states can provide more insight into the maintenance of epigenetic changes. Increasing the potential of the research to include a greater number of species, incorporating some rare and endangered ones, will assist in pinpointing those species that are more prone to fragmentation. Also, further research into how epigenetics is involved in the interactions of species with environmental factors such as invasive species and disease would be helpful in explaining their adaptive responses. The ability to incorporate fine-scale ecological information, including microclimate models, will enhance the prediction of the variation in epigenetic reactions to various forms of habitat fragmentation, which will help with conservation efforts. Finally, biomarkers of species health and resilience based on epigenetic signatures may be helpful in improving species conservation, enhancing restoration of epigenetic health in species at risk, and interventions that improve epigenetic health.

Conclusion

This paper brings to light the important role played by epigenetic processes in enabling species to respond to environmental stresses in discontinuous habitats. The results indicate that the controls of DNA methylation, histone alterations, and regulation of non-coding RNAs play central roles in helping species to survive the impacts of habitat fragmentation. These epigenetic modifications provide a rapid, adaptable response to environmental changes, and species can modify their gene expression to suit environmental pressures without altering their genetic code. Also, there is a possibility of epigenetic inheritance, which implies that the adaptive responses may be maintained into subsequent generations and help to build resilience in fragmented ecosystems over the long term. This study combines field data, laboratory data, and bioinformatics to examine how genetic and epigenetic factors matter in conservation biology. The genetic effects of habitat fragmentation, which include the decrease in gene flow and disappearance of genetic diversity, can be alleviated by epigenetic modification, and this has offered the species a means to survive and succeed in the fragmented environment. Epigenetics, therefore, presents viable conservation-related methods that can be used to increase the resilience of species in the context of habitat loss and environmental degradation. The results of this paper suggest the possibility of conducting further studies on the long-term effects of epigenetics on evolution and the ecosystem survival of species fragments. It is also evident that there is a need for a better

understanding of epigenetic adaptation to develop effective conservation strategies. By using epigenetic data in conservation planning, the study can create more specific conservation methods to maintain biodiversity in a fast-changing world. After all, this study points to the necessity of a more comprehensive way of looking at conservation, which is closest to the intricate interaction between the genetic and epigenetic elements of defining species adaptability to the realities of a fragmented world.

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