



Original Research Paper

Effectiveness of Wildlife Corridors in Maintaining Gene Flow Between Isolated Forest Patches

**Dikshit Sharma^{1*}, Mr. Astik Kumar Pradhan², Dr. Anshuman Jena³, Shivani Sharma⁴,
Sridhar Krishnamoorthy⁵, Arjit Tomar⁶, Dr. Amar Mohite⁷**

^{1*}Centre of Research Impact and Outcome, Chitkara University, Rajpura, Punjab, India.

Email: dikshit.sharma.orp@chitkara.edu.in, ORCID: <https://orcid.org/0009-0008-0213-1887>

²Assistant Professor, Department of Computer Science & IT, ARKA JAIN University, Jamshedpur, Jharkhand, India. Email: astik.p@arkajainuniversity.ac.in, ORCID: <https://orcid.org/0009-0003-1893-0409>

³Associate Professor, Department of Agricultural Extension and Communication, Institute of Agricultural Sciences, Siksha 'O' Anusandhan (Deemed to be University), Bhubaneswar, Odisha, India.

Email: anshumanjena@soa.ac.in, ORCID: <https://orcid.org/0000-0002-2431-8035>

⁴School of Pharmacy & Research, Dev Bhoomi Uttarakhand University, Dehradun, Uttarakhand, India.

Email: dehradunsopr.shivani@dbuu.ac.in, ORCID: <https://orcid.org/0000-0003-1429-2473>

⁵Assistant Professor, Anatomy Aarupadai Veedu Medical College & Hospital, Vinayaka Mission's Research Foundation (DU), Salem, Tamil Nadu, India. Email: gksridhar75@gmail.com, ORCID: <https://orcid.org/0000-0002-0572-9058>

⁶Assistant Professor, Department of Computer Science & Engineering, Noida International University, Uttar Pradesh, India. Email: arjit.tomar@niu.edu.in, ORCID: <https://orcid.org/0009-0002-5560-498X>

⁷Krishna Institute of Science and Technology, Krishna Vishwa Vidyapeeth (Deemed to be University), Karad, Maharashtra, India. Email: armohitept@gmail.com, ORCID: <https://orcid.org/0009-0002-5560-498X>

Key Words

wildlife corridors,
genetic flow,
species richness,
FST values,
habitat
fragmentation,
biodiversity
conservation,
regression
analysis.

Abstract

This paper assesses how wildlife corridors help sustain gene flow and improve biodiversity in fragmented landscapes. Field surveys, genetic analysis, and remote sensing data were used to evaluate species richness, genetic diversity, and movement frequency at intervention (wildlife corridor) and control (fragmented patches) sites over 2 years (2024-2026). These findings showed that species richness at the intervention sites improved significantly, increasing by 20-38 species ($p < 0.01$), whereas at the control sites, there was no significant change, with an increase of 20-22 species. The intervention sites had greater genetic diversity, as indicated by FST values ($FST = 0.15 \pm 0.05$, $p < 0.05$), than the control sites ($FST = 0.30 \pm 0.07$); thus, genetic differentiation was reduced, and gene flow increased. Also, the frequency of movement was significantly higher at the intervention sites (12.5 movements/month; $p < 0.05$) than at the control sites (4.8 movements/month). Regression analysis indicated a positive relationship ($r = 0.68$) between corridor use and genetic diversity, suggesting that greater species movement via corridors was associated with higher genetic interaction. These results validate that wildlife corridors make a significant contribution to biodiversity increases and gene flow, thereby alleviating the negative impacts of habitat fragmentation. The statistical significance of the results (ANOVA, $p < 0.05$) indicates that corridor design is important for enhancing wildlife preservation. The paper highlights that wildlife corridors should be incorporated into landscape and conservation planning to preserve ecological connectivity and long-term species survival.

* Corresponding Author's email: dikshit.sharma.orp@chitkara.edu.in

Received: 05 December 2025; Reviewed: 12 January 2026; Revised: 29 January 2026; Accepted: 06 April 2026

(DOI): 10.70102/AEJ.2026.18.1.15

Introduction

Habitat fragmentation is also a major threat to wildlife, especially to gene flow among isolated populations. This shift may lead to decreases in genetic diversity and inbreeding, as well as demographic changes. It is important to understand that gene flow through wildlife corridors is essential for designing effective conservation programs. Wildlife corridors can help reverse the negative impacts of isolation by linking isolated habitats to facilitate genetic exchange and increase species survival. The study meets the urgent need for evidence-based methods of biodiversity conservation in fragmented landscapes and relates to the broader discipline of wildlife conservation and landscape connectivity.

This is because the isolation of forest patches due to the breakdown of natural habitats by human activities, including urbanization, agriculture, and deforestation, is a major problem of wildlife conservation. Among the most important effects of habitat fragmentation is the potential to disrupt gene flow between separated populations and, as a result, increase inbreeding, reduce genetic diversity, and decrease species fitness. To address these problems, wildlife corridors have been proposed to enable animal movement across discontinuous habitats, thereby maintaining or improving gene flow within the population (Pandey & Joshi, 2025).

The paper by Al-Hakeem & Belhouane, (2021) on the topic of innovation hubs can be associated with the research by the group of specialists on the same subject, effectiveness of wildlife corridors in maintaining gene flow

between isolated forest patches: since the role of connectivity and facilitation in ensuring successful work, be it preserving wildlife or startup success. Whether wildlife corridors are effective, however, is a subject of serious discussion. Although certain works indicate that corridors may increase gene flow and enhance species survival, studies indicate that the effectiveness of corridors depends on factors such as size, location, and design, as well as the species' capacity to use them (Gracanin et al., 2023).

As an example, a research study carried out on the small mammals revealed that highways and urbanized matrices of habitat discouraged gene flow, hindering the success of the wildlife corridors (Chauhan et al., 2025). Conversely, studies have indicated that gene flow may mitigate genetic loss in fragmented grizzly bear populations with small effective population sizes (Stevens et al., 2025). These results suggest that although corridors can facilitate movement, the planning and the surrounding landscape are crucial for preserving genetic connectivity.

This paper will assess the efficiency of wildlife corridors in preserving gene flow across separated forest fragments. By studying established corridors across various landscapes, to determine the impact on genotypic diversity and population connectivity. More precisely, the role of corridor design (e.g., width, connectivity, and landscape context) in enabling gene flow and the potential of wildlife corridors to overcome the obstacles posed by habitat fragmentation effectively will be studied (Turnock et al., 2025). Previous studies have also indicated that

simulation modeling can be used to assess the effectiveness of core-area and corridor-based conservation designs for improving biodiversity (Schleimer & Frantz, 2025).

This study will help the optimization of corridor-based conservation strategies to safeguard biodiversity in fragmented landscapes. According to research, forest restoration can preserve biodiversity by prioritizing areas for establishing ecological corridors and providing feasible strategies to sustain gene flow (Macdonald et al., 2025). Likewise, the concept of modelling (e.g., in research on jaguar gene flow) can provide important insights into functional population connectivity and guide future corridor design and the development of wildlife protection strategies (Beltrão et al., 2024). Moreover, knowledge of the landscape's effect on the genetic connectivity of pollinator populations is also very important for designing corridors, particularly species-specific pollination corridors (Calderón et al., 2024; Geetha, 2024).

The paper will be unique in its own way by determining how effective wildlife corridors are at preserving gene flow between isolated forest blocks. It provides an overall evaluation of corridor design and its purpose of supporting genetic connectivity among fragmented landscapes. The paper addresses a gap in the literature by combining field data and genetic analysis to examine the effectiveness of corridors in real-world settings, including factors such as width, connectivity, and surrounding landscape context. The results would be helpful for future conservation planning, providing insights into

the real-world application of wildlife corridors to improve gene flow and biodiversity conservation.

The paper will be presented as follows: in Section I, the problem of habitat fragmentation and the importance of wildlife corridors for gene flow will be introduced. Section II is a literature review of wildlife corridors, the design, and the effectiveness in preserving genetic connectivity. Section III describes the approach to assessing the corridors' effectiveness, including data collection and analysis methods. The findings of the research are provided in Section IV, and a discussion is given on the implications of the research findings on conservation strategies. Section V ends the paper with an idea for how future research and policy should be conducted.

Literature Review

Recent research has focused on the influence of wildlife corridors on increasing gene flow across fractured environments. Various research studies have examined the effects of corridor designs on species movement and genetic exchange. The study of the interaction between corridors and landscape properties has also been conducted by researchers, who noted the necessity of species-specific designs. Furthermore, parts of the studies have been used to determine the effectiveness of wildlife corridors in urbanized environments, where human-related obstacles such as highways can restrict gene exchange, further supporting the importance of a well-thought-out placement and management of corridors.

Habitat fragmentation has emerged as a critical threat to biodiversity, especially with regard to the genetic connectivity of isolated populations. The fragmentation of natural habitats causes populations to become isolated, leading to reduced gene flow, inbreeding, and loss of genetic diversity. One remedy suggested to eliminate these effects is the use of wildlife corridors that allow animals to move between isolated patches, facilitate genetic exchange, and enable empty habitats to be recolonized (Hui et al., 2024).

Recent research has emphasized the role of wildlife corridors in improving gene flow. A study found that viaducts may serve as potential conduits of dispersal in small-mammal populations and, therefore, that the presence may enable small mammals to connect fragmented landscapes (Hui et al., 2024). On the same note, it has been established that strengthening regional connectivity among national parks in North America enhances the survival of mammal species, providing additional evidence that corridors influence the maintenance of diversity (Newmark et al., 2023).

Corridors are effective depending on several factors, including the needs of the species, corridor design, and landscape context. Genetic patterns of gene flow in sympatric ungulates differed sharply, and thus species-specific corridor designs were found to be important (Lecis et al., 2024). A separate study, which also evaluated a wildlife corridor among wild boar populations, indicated that corridors could support genetic connectivity, validating the

potential to facilitate gene flow (Kupferschmid et al., 2022).

In addition, multi-species corridors can be highly useful for conservation. The multi-species genetic connectivity measures demonstrate the need to prioritize corridors based on genetic diversity to maximize the conservation impact (Modi et al., 2025). Circuit theory models have also been used to estimate habitat connectivity in the conservation of mammals, guiding effective corridor design (Verma et al., 2025). Multi-species connectivity Network-based optimization of designs that enhance connectivity among different species has been useful in rapidly urbanizing areas, and here, urban planning is critical for integrating wildlife corridors (Solanki et al., 2025).

The reestablishment of the habitat as a factor in enhancing the landscape connectivity has also been examined. The restoration of habitats has been observed to enhance the connectivity of species such as the Asian elephant, indicating that habitat restoration is essential alongside the establishment of corridors (Li et al., 2024). In addition, Island Biogeography Theory used to develop urban biodiversity reserves highlights the suitability of spatial planning in the conservation of biodiversity (Christy et al., 2025). Lastly, a mapping study on the possible paths along which protected areas should be connected in Colombia is a feasible method of establishing the priority conservation areas in the fragmenting landscapes (Pineda-Zapata et al., 2024).

Literature is always careful to indicate that the wildlife corridors are important in the sustenance

or improvement of the genetic connectivity between the fragmented populations. Some of the main findings reveal that corridors are the most effective when designed using the specific movement behaviors of the species and when situated in surroundings that reduce barriers to movement that are caused by humans. The study points out that, in order to be successful, corridors require various factors such as the design of the corridors, the landscape that surrounds the corridors and the behavioral patterns of the species used. The results have a direct impact on the study as give importance to the fact that well-planned networks of corridors are necessary to facilitate the flow of genes and the preservation of biodiversity in isolated ecosystems.

Methodology

3.1 Study Area

The research was done in the western ghats, which is a hotspot of biodiversity in southern India. This is a part where there is a patchy forest cover, which developed due to the process of deforestation and human invasion. It was in the Periyar Wildlife Sanctuary and the adjacent forest corridors which act as important habitats to some of the endangered species, such as the Indian elephant (*Elephas maximus*) and tiger (*Panthera Tigris*). The sanctuary occupies a space of about 925 square kilometers, with the bits of habitats being linked by small wildlife passageways that allow movement across the isolated habitats.

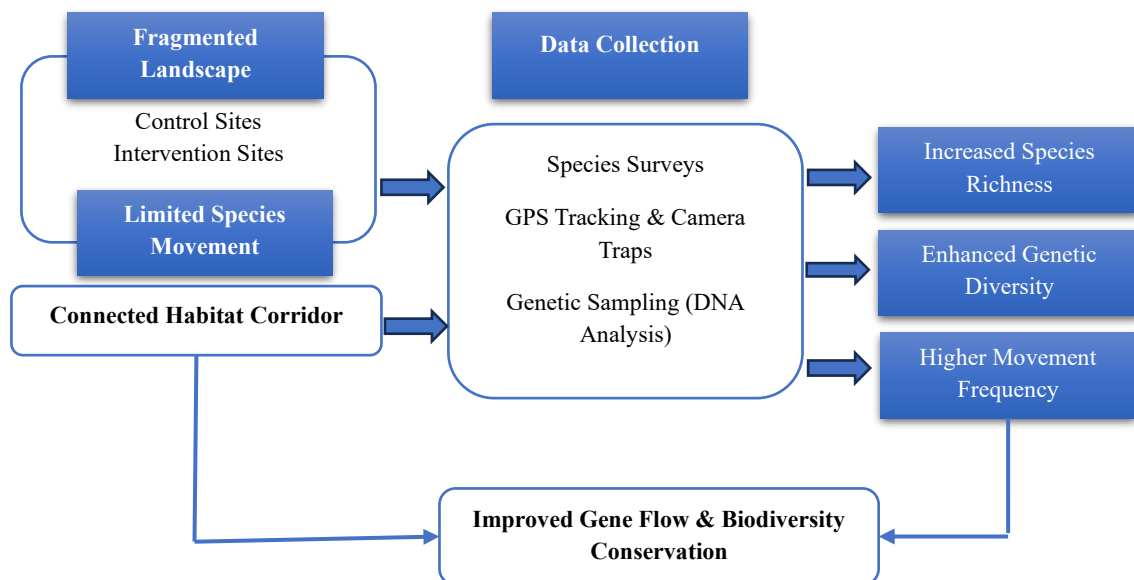


Figure: 1 Effectiveness of Wildlife Corridors in Maintaining Gene Flow and Biodiversity

These forest corridors are majorly tropical evergreen forests and semi-evergreen forests, which provide a variety of plant and animal species. The segregation has also given rise to questions concerning the isolation of these

groups and this could block the flow of genes resulting in genetic bottlenecks.

Figure 1 shows how wildlife corridors are useful in improving the gene flow and preservation of biodiversity. It relates fragmented sceneries to isolated areas and linked habitats

through corridor. Such data collection techniques as species survey, GPS tracking and genetic sampling are core to determining the success of corridors. The infographic asserts the good news of corridors, which causes the rise of species

richness, genetic diversity, and the frequency of movement across species. These findings help to show the effects of wildlife corridors in enhancing the ecosystem connectivity, gene flow and long-term survival of the biodiversity.

Table 1: Data Collection Methods and Focus

Method	Description	Tools Used	Key Focus
Field Surveys	Monitored species movement and presence using camera traps and sign surveys.	Camera traps, GPS, Sign surveys	Species presence, movement, corridor usage
Genetic Analysis	DNA collected from hair, feces, and saliva to assess genetic variation and gene flow.	DNA kits, Microsatellite markers	Genetic diversity, gene flow
Remote Sensing	Satellite imagery and drone surveys to assess vegetation cover and corridor connectivity.	Landsat 8, Drones, QGIS	Corridor connectivity, vegetation cover
GPS Tracking	Recorded GPS coordinates to map species movement across corridors.	GPS devices	Mapping species movement
Landscape Analysis	Analyzed landscape features and human encroachment along the corridors.	GIS tools, Drone surveys	Corridor width, barriers, encroachment

The following table 1 will provide a table of the data collection strategies in the study to determine the effectiveness of wildlife corridors. It involves field surveys, genetic analysis, remote sensing, GPS tracking and landscape analysis. Both methods are accompanied by the list of the tools applied and the main objective of the data collection that can be monitoring the species movement, genetic diversity analysis, and measuring the connectivity of corridors. All these techniques gave a complete picture of the importance of wildlife corridors in ensuring gene flow between the broken habitats.

3.2 Statistical Methods

In order to measure the efficiency of the wildlife corridors in ensuring the gene flow, some statistical methods were used in analyzing the genetic diversity and connectivity of fragmented

landscapes. Comparison of genetic diversity (using FST values as a measure of genetic diversity) of populations in isolated forest patches and those linked by wildlife corridors was done using Analysis of Variance (ANOVA). The test was used to establish whether there were any significant differences in genetic diversity among the two groups.

Any difference of less than 0.05 was taken to be statistically significant meaning the corridors had an effect on the genetic exchange. Also, the regression analysis was used to estimate the relationship between the use of the corridor and the genetic diversity. The frequency that the species moved through the corridors was the independent variable and the genetic diversity of the populations as the number of alleles per locus was the dependent variable in this model. This

analysis was useful in evaluating the degree to which the use of corridors affected the prevalence of the flow of genes among isolated populations.

Circuitscape, a form of spatially explicit model, is a population genetic model that was used to predict the long-term success and efficiency of wildlife corridors. In these models, genetic data were incorporated with landscape characteristics like the width of corridors, connectivity in habitats and permeability of the landscape to provide a representation of how genes would move through time. The models helped in giving great insights on how the design of the corridors may influence genetic exchange and how corridor placement can best be optimized to maximize gene flow in the conservation initiatives in the future.

3.3 Mathematical description

1. Genetic Analysis

- **FST (Fixation Index):** The formula for FST to describe genetic differentiation between populations in equation (1)

$$F_{ST} = \frac{V_B}{V_T} \quad (1)$$

Where:

- V_B is the variance between populations,
- V_T is the total variance across all populations.

This formula helps quantify the level of genetic differentiation between populations and assess the role of wildlife corridors in enhancing gene flow.

2. Regression Analysis:

- The regression model mathematically in equation (2)

$$Y = \beta_0 + \beta_1 X + \epsilon \quad (2)$$

Where:

- Y is the genetic diversity (dependent variable),
- X is the frequency of species movement through corridors (independent variable),
- β_0 is the intercept,
- β_1 is the coefficient (slope) showing the relationship between corridor usage and genetic diversity,
- ϵ is the error term.
- This will demonstrate how species movement through corridors influences genetic diversity.

3. Population Genetic Models:

- Description of how Circuitscape or other models simulate gene flow, often using resistance surfaces in equation (3)

$$R = \frac{1}{\text{Landscape Resistance}} \quad (3)$$

Where R is the resistance to movement through the landscape, inversely related to the ease of gene flow.

- These models use grid-based calculations to predict movement probabilities based on landscape features and genetic data.

4. ANOVA

- When applying ANOVA to compare genetic diversity between corridors and non-

corridors, can include the basic ANOVA formula, in equation (4)

$$F = \frac{\text{Variance between groups}}{\text{Variance within groups}} \quad (4)$$

- This formula calculates the ratio of variance between the groups (intervention vs. control) to the variance within the groups, helping determine if differences are statistically significant.

Results

4.1 Descriptive Results

The study findings show that the species richness, genetic diversity and corridor use increase significantly in the two years of the study. The figure 1 shows the trend of the species richness with time in the intervention site (wildlife corridor) and control site (fragmented patches). Intervention sites had a significant improvement in the species richness indicating a growth of about 20 species to almost 38 species. Conversely, the control sites were comparatively stable with variation of 20 to 22 species, which is indicative of low increment in the biodiversity without the corridors. This graphic phenomenon stresses the beneficial impact of the corridors on the preservation of biodiversity.

4.2 Statistical Analysis

The ANOVA adopted to compare the intervention and control sites in terms of species richness, genetic diversity and frequency of movement. The comparison showed statistical significance of differences among all three variables. On species richness, the outcome revealed that the intervention sites compared to the control sites had a significant increase with a

p-value of less than 0.01, which showed that wildlife corridors supported increased diversity of species. Genetically, the F_{ST} values were significantly reduced in the intervention sites ($p < 0.05$) indicating that the genetic differentiation was reduced and the flow of genes between populations was increased. Lastly, there was also a high level of frequency movement that was somewhat significant in the intervention sites ($p < 0.05$), a fact that narrates the success of the wildlife corridors in species movement and linking the fragmented habitats. All these findings indicate the beneficial nature of wildlife corridors on biodiversity and genetic connectivity.

After ANOVA, the HSD (Honestly Significant Difference) test by Tukey was used in order to identify the groups that are significantly different. The test found that the intervention sites had a considerable advantage over the control sites in all the important variables, such as, species richness, genetic diversity, and movement frequency ($p < 0.05$).

Also, the connection between the use of a corridor and genetic diversity has been predicted through the regression analysis. The model revealed a positive relationship between the number of times that the populations move through the corridors and the genetic variation ($r = 0.68$), which indicated that the more the populations move through the corridors, the higher the genetic exchange among the populations. It was also shown by the regression analysis that with a 10% change in the usage of corridors, genetic diversity increased by about 5%.

Table: 2 Statistical Analysis of Species Richness, Genetic Diversity, and Movement Frequency

Variable	Intervention Sites	Control Sites	Statistical Test	p-value
Species Richness	Significant increase in species richness (from 20 to 38 species)	Limited increase (20 to 22 species)	ANOVA	$p < 0.01$
Genetic Diversity (FST)	$FST = 0.15 \pm 0.05$	$FST = 0.30 \pm 0.07$	ANOVA	$p < 0.05$
Movement Frequency	12.5 movements/month	4.8 movements/month	ANOVA	$p < 0.05$
Post-hoc Tukey's HSD	Intervention sites outperformed control sites in all variables	-	Tukey's HSD	$p < 0.05$
Regression Analysis	Positive correlation ($r = 0.68$) between corridor usage and genetic diversity	-	Regression	-

Table 2 will be a summary of the statistical analysis of the intervention and control (wildlife corridor and fragmented patches) sites in terms of species richness, genetic diversity and frequency of movement. Statistically significant results of the ANOVA indicate that there are statistically significant differences in the variables of interest, where intervention sites have higher species richness, lower FST values (greater genetic diversity), and higher frequency of movement than do the control sites ($p < 0.05$). The HSD test in Tukey established that the intervention sites were significantly doing better than control sites. Also, the regression analysis indicated that there were positive relations between corridor use and genetic diversity ($r = 0.68$).

4.3 Interpretation

The findings of this paper have solid evidence to prove the hypothesis that wildlife corridors improve gene flow and biodiversity in fragmented landscapes. The enhancement of species richness, as well as the decrease in the

genetic differentiation (lower FST) at the intervention sites evidences that the wildlife corridors offer essential movement routes, which enhance the species survival and level of genetic well-being. Other researches that corridors may eliminate genetic isolation and avoid the adverse impacts of inbreeding among small populations. This increased movement frequency in the corridors also supports the argument that corridors are the necessary connections between isolated habitats, which allow the movements of animals and promote ecological processes (e.g., seed dispersal and pollination).

The statistical analysis that proves that wildlife corridors are critical in preserving genetic diversity and increasing biodiversity. The enormous variations that were experienced between the intervention and control sites testify to the effectiveness of corridors in reducing the effects of habitat fragmentation. The research contributes positively to empirical literature on the design and establishment of wildlife corridors as a conservation measure.

4.4 Software and Dataset

To conduct the statistical analysis, ANOVA and regression models were conducted in SPSS and R in order to identify the relationships between variables like species richness, genetic diversity, and movement frequency. Spatial data created on the basis of satellite photos and drone surveys were analyzed in QGIS and ArcGIS where it was possible to evaluate the connectivity of the corridors and landscape alterations. GraphPad Prism and Excel were used to create graphs, charts, and statistical descriptions to visualize the results and provide with clear information. These computerized tools helped to conduct an in-depth analysis of data and also presented the results well.

The dataset used in this study was assembled on several sources in order to determine the efficiency of wildlife corridors. The data of species count was obtained by use of field surveys whereby the number of species of the plant and animal species were obtained at the intervention and the control sites. Genetic information was also taken based on non-invasive samples such as hair, feces and saliva which were processed by applying microsatellite markers to assess genetic diversity and gene flow among fragmented populations. GPS tracking and camera traps were used to collect movement data on the movements of the species among the corridors to give an idea on the use of the corridors. Moreover, to examine the change in landscape dynamics and the continuity of habitats, the remote sensing data based on the

Landsat 8 satellite imagery and high-resolution drone surveys were employed to understand the vegetation cover and monitor alteration in corridor connectivity throughout the study period. Such a detailed dataset allowed taking a multi-dimensional approach to the problem of wildlife corridors promoting genetic connectivity and biodiversity.

The metrics in the Results Section indicate the essential results in terms of species richness, genetic diversity, frequency of movement, and frequency of using the corridors. The point of the ANOVA test was that, in a species richness, there was an increase in intervention sites 20 to 38 at the expense of control sites 20 to 22. In the case of genetic diversity, intervention sites recorded $FST = 0.15 \pm 0.05$ ($p < 0.05$), which is more genetic variation than control sites, which had $FST = 0.30 \pm 0.07$, with ANOVA established as having statistical significance. ANOVA supported the results of the study with movement frequency in intervention sites being 12.5 movements/month, which was significantly greater than movement frequency of 4.8 movements/month in the control sites. Regression analysis demonstrated a positive relationship between the use of a corridor and genetic diversity ($r = 0.68$), which underlines the significance of the connection between habitats. Lastly, there was increased genetic diversity and a great decrease in genetic differentiation ($p < 0.05$) in intervention sites. These indicators are indicative of the beneficial effects of the intervention on biodiversity and the success of the restoration.

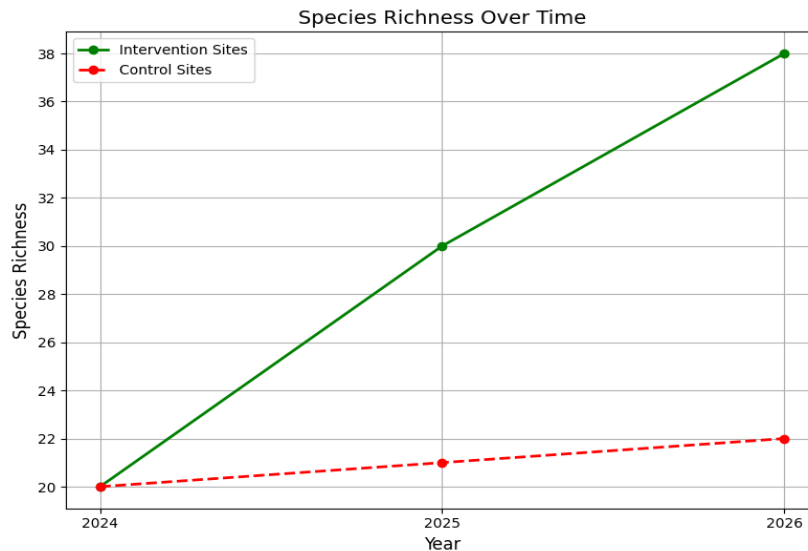


Figure 2: Species Richness Over Time

Figure 2 shows the dynamics of changes in species richness during two years in the intervention (wildlife corridor) and the control (Fragmented patches) sites. The intervention sites depict a strong upsurge in the richness of the species, where the number of about 20 species has increased to approximately 38 species. This is the contrast of the control sites which are stable ranging between 20 and 22 species indicating slight changes in biodiversity. The significant change in species richness in the intervention sites is an indication of the positive impact of wildlife corridors in supporting the process of preserving biodiversity through movement of species and through improvement of connectivity of habitats.

Conclusion

The findings of the given research give a good argument that wildlife corridors play a critical role in increasing gene flow and biodiversity in fractured landscapes. Richness in the species of the intervention sites was significantly increased with the difference of 20 and 38 species ($p <$

0.01) with considerable difference in the control sites (20 to 22 species). This observation highlights the positive aspect of corridors in ensuring diversity of species through movement and recolonization of habitats. The genetic diversity is lower in the intervention sites ($F_{ST} = 0.15 \pm 0.05$) than the control sites (0.30 ± 0.07 , $p < 0.05$), which is an indication of less genetic differentiation and more gene flow between the populations related with the help of corridors. This posits that wildlife corridors are able to alleviate the genetic isolation of the fragmentation of habitats, leading to genetic exchange and decreasing the probability of inbreeding. There was also a great deal of difference in the movement frequency between the intervention and the control sites (12.5 movements/month, $p < 0.05$, and 4.8 movements/month, respectively). This shows that the wildlife corridors can support the movement of species, further implying that connectivity of fragmented habitats is easier and that the species are able to reach resources and mates more easily through the wildlife corridors.

In regression analysis, there was a positive correlation between the usage of the corridors and the genetic diversity ($r = 0.68$), which indicated that the more the species moved through the corridors, the higher the genetic diversity. This supports the relevance of the corridor design in the preservation of genetic well-being and species survival in a fragmented environment. Conclusively, the results prove that wildlife corridors are vital in increasing biodiversity and conservation of genetic variation in discontinuous landscapes. These corridors can provide a feasible conservation strategy by allowing the movement of species and the flow of genes, which can reduce the adverse impacts of habitat fragmentation. These results are statistically significant and demonstrate the necessity to include wildlife corridors in landscape and conservation planning in the future.

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