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Original Research Paper

Integrating Genomic and Ecological Data to Assess the Impact of Habitat Fragmentation on Genetic Diversity in African Elephants in Central Africa

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Key Words

African elephants, Habitat fragmentation, Landscape genetics, Genetic diversity, Habitat connectivity, Conservation genomics.

Abstract

The fragmentation of the habitat is a significant risk to the long-term sustainability of wide-ranging megafauna through the limitation of movement and lack of gene flow between populations. In Central Africa, there is a growing exposure of African elephants to landscape fragmentation as a result of land-use change, development of infrastructures and forest degradation, but quantitative synthesis between genetic pattern and ecological fragmentation has not been well documented. This paper utilizes an integrative landscape genetics model that is able to utilize published evidence of genomic and ecological hypothesis to determine the impacts of habitat fragmentation on genetic diversity, population structure and connectivity of the African elephant populations in Central Africa. Genetic indicators, such as heterozygosity, allelic richness, inbreeding coefficients and genetic differentiation, were combined with the landscape-level genetic fragmentation, resistance, and connectivity indicators using ecological and remote sensing data. The synthesis suggests that the observed heterozygosity (H0 0.69 - 0.71) and genetic differentiation (FST 0.02 -0.5) were higher in the elephant populations of low-fragmentation landscapes and lower in the populations of highly fragmented ones (H0 0.54 - 0.56). The landscape analyses also indicate that there exists a positive strong relationship between landscape resistance and genetic differentiation ($r \approx 0.68$) where the functional corridors and low-resistance habitats possess more connectivity. This paper gives an ecological transferable framework to prioritizing areas of conservation and functional corridors by directly relating genomic indicators with ecological parameters of fragmentation. The results highlight the importance of conservation efforts in form of landscape conservation, which would ensure the connectivity of habitats to ensure the genetic and long-term evolutionary resilience of the African elephant population in Central Africa.

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Introduction

One of the greatest causes of biodiversity loss in the global context, and a specific problem to the survival of large, wide-ranging terrestrial mammals, is habitat fragmentation, which relies on wide-ranging and interconnected topography. The African elephants (Loxodonta Africana and Loxodonta cyclitis) need expansive home ranges and frequent mobility between areas of habitat so that their population remains demographically stable and genetically connected. Also in Central Africa, deforestation through rapid land-use change caused by infrastructure construction, logging, agricultural growth, and human settlement has continued to fragment forest and savanna ecosystems over time, questioning the prospective long-term genetic viability of the elephant species (Goossens et al., 2016; Eggert et al., 2014). The concept of genetic diversity supports equilibrium of populations because it supports adaptive capacity, pregnancy, and evolutionary stability in the long term. The habitat fragmentation may cause the decrease of effective population size, limitations of dispersal, and isolation of subpopulations, which results in genetic structuring and the risk of inbreeding (Cushman et al., 2006; Sharma et al., 2025). The evidence presented in empirical research of the African elephants and other large mammals indicates that fragmented landscapes are commonly linked to a decline in gene flow and amplified genetic variation despite the comparatively minor geographic ranges (Ernest et al., 2012; De Flamingh et al., 2015). Anthropogenic disturbance in Central African forest elephants has been illustrated to affect movement behavior and population structure of the landscapes that could be coarse-spatially continuous, with genetic connectivity to a landscape format being sensitive to landscape structure (Johnson et al., 2007; Johnson et al., 2019).

Recent developments in conservation genomics and landscape ecology have placed greater importance on the benefits of multiple genetic information in combination with spatially explicit ecological models in gaining a clearer insight into how habitat fragmentation influences population structure. The fine-scale measures in genetic diversity, population differentiation, and connectivity in elephants across heterogeneous environments have been provided by the use of genome-wide markers and non-invasive genetic sampling in the studies (Lohay et al., 2020; Laguardia et al., 2021). Simultaneously, habitat suitability modeling, resistance surface building, and connectivity studies have offered powerful techniques of quantifying the functional effects of fragmentation out of straightforward quantifications of habitat loss (Cushman et al., 2006; Balkenhol et al., 2009). Recent papers combining habitat suitability and gene flow modeling have shown that they can identify functional corridors and conservation priorities in African elephant landscapes better (De Flamingh et al., 2024; Mazziotta et al., 2025). Although these developments have been made, in-depth evaluations that clearly correlate the pattern of genomic trends with ecological evidence of fragmentations have not been done on the case of African elephants in Central Africa. Most of the literature out there has looked at genetic structure without considering a spatial measure of habitat fragmentation or by considering ecological connectivity but has not directly tested the genetic validation of the same (Rajan & Chawla, 2024; Zacarias et al., 2016). Consequently, the levels to which the three landscape resistance, habitat quality, and the intensity of fragmentation interactively affect genetic diversity, population structure, and connectivity within the populations of the Central African elephants have not been adequately addressed (Ahlering et al., 2012; Sinovas et al., 2025).

The proposed research combines both genomic and ecological data to determine the impacts of habitat fragmentation on genetic diversity, population structure, and connectivity of the African elephants in Central Africa. With genetic data of the entire genome-wide and habitat suitability models, fragmentation measures, and landscape connectivity, we assess the influence of diverse levels of habitat disturbance on the patterns of genetic variation and gene influx. This integrative method is meant to recognize priority habitats and functional corridors needed to sustain genetic connectivity and long-term evolutionary resiliency and therefore offers landscape-scale conservation implications to African elephants in Central Africa.

The rest of this paper is structured in the following way. Section 2 gives the materials and methods, which include integrative framework, data synthesis procedure, and data analytical processes. Section 3 is a report of the genomic and ecological synthesis comprising of trend of genetic diversity, population structure, and landscape connectivity. Section 4 is a discussion of the conservation implications of the findings in the framework of habitat fragmentation. In the end, the paper finishes with the conclusion paragraph on Section 5 which highlights main insights and maps out future research directions.

Materials and Methods

Analysis Framework and Study Scope

The paper uses an integrative landscape genetics design to determine the effect of habitat fragmentation on genetic diversity, population structure and connectivity of African elephant populations in Central Africa. It is analyzed on the basis of a quantitative synthesis of already existing published genomic and ecological studies, and not by production of new empirical genetic or ecological data. The same types of synthesis-based and integrative methods have been extensively used in studies on the conservation genetics of elephants and landscape genetics to test the impacts of fragmentation in heterogeneous habitats (Rajan & Chawla, 2024; Balkenhol et al., 2009).

Figure 1 gives an overview of the data integration plan and analytical workflow to be used in this study and is used as a conceptual map of the methodological approach taken in this study.

Synthesis of Genomic Data

Peer-reviewed papers that used non-invasive methods of genetic sampling and high-resolution genetic markers such as microsatellites and single nucleotide polymorphisms (SNPs) were used to derive genome-wide genetic data on

African forest and savanna elephants (Lohay et al., 2020; De Flamingh et al., 2015). These works form the main foundation of determining genetic diversity, population structure and gene flow among fragmented landscapes. Comparative genomic studies on other large African mammals that were subject to habitat fragmentation especially African buffalo and lions were also referred to in order to augment methodological strength and cross-taxa interpretation (Curry et al., 2021; Colangelo et al., 2024). Population genetic measurements most often reported, such as observed heterozygosity (H0), expected heterozygosity (H 0), allelic richness, inbreeding coefficients (FIS), and genetic differentiation indices (FST) were synthesized between studies with low, moderate, and high fragmentation settings. All quantitative values given in this paper are synthesized measures

Table 1 sums up the genomic and ecological indicators synthesized in relation to the table and their functions on the integrative framework.

Table 1: Genomic And Ecological Indicators Synthesized In The Integrative Landscape Genetics Framework

Data Category	Indicator	Description	Role in Analysis
Genomic	Observed heterozygosity (H_o)	Proportion of heterozygous loci within populations	Assesses within-population genetic diversity
Genomic	Expected heterozygosity (H_e)	Genetic diversity under Hardy–Weinberg equilibrium	Benchmark for genetic variability
Genomic	Allelic richness	Number of alleles standardized by sample size	Sensitive to population isolation
Genomic	Inbreeding coefficient (FIS)	Departure from random mating	Detects local inbreeding signals
Genomic	Genetic differentiation (FST)	Genetic divergence among subpopulations	Proxy for gene flow restriction
Ecological	Habitat patch size	Mean area of continuous suitable habitat	Indicates habitat availability
Ecological	Edge density	Length of habitat edges per unit area	Reflects habitat disturbance
Ecological	Forest integrity	Degree of canopy cover and degradation	Indicator of habitat quality
Ecological	Landscape resistance	Relative movement cost across land-use types	Represents functional connectivity
Ecological	Corridor presence	Existence of low-resistance pathways	Identifies potential dispersal routes

Synthesis of Ecological and Landscape Data

Generalization of Ecological and Landscape Data

The synthesis of ecological indicators of habitat fragmentation was based on the research that used remote sensing, geographic information systems (GIS), as well as habitat suitability modeling in the ecosystems of Central African forests and savannas (De Flamingh et al., 2024; Rajan & Suresh Kumar, 2024). Major variables were the land-cover composition, forest integrity, patches of habitats, edge density and the closeness to man-made structures like roads and settlements.

Ecological models of the landscape and risk-based methods were also reviewed in order to formulate an insight into habitat disturbance and permeability in intensively modified environments where limited direct movement evidence exist (Prashanth, 2025). These environmental pointers were employed to describe the landscapes with a fragmentation gradient between quite intact and very disturbed and fragmented areas.

Conceptualization of Habitat Resistance

Habitat Resistance is the effects on the organisms caused by stress so that it enables the organisms to either adapt or adapt adversely to the environment. The conceptualization of landscape resistance was developed based on the relative cost of movement of the elephants across the habitat and land-use types. The intact forests and the protected regions served as the low-resistance zones, and the agricultural mosaics, infrastructure corridors and the degraded forests edges were viewed as the high-resistance zones. This theoretical approach is based on standard principles of causal modelling and landscape genetics that associates the environmental heterogeneity with the gene flow (Cushman et al., 2006).

The conceptualization of resistance surfaces was based on an ecological disruption, quality of the habitat, and human pressure, instead of on quantitative layers, which is an aspect of synthesis-based landscape genetics models (Balkenhol et al., 2009).

Integration of Genomic and Ecological Evidence

Genomic and ecological indicators were combined by matching genetic diversity and differentiation patterns with levels of fragmentation and resistance to landscape in habitat. This merging allowed assuming the functional connectivity of elephant subpopulations and testing the effects of fragmented landscapes on gene flow.

The genomic indicators produced by published literature as shown in Figure 1A were integrated with landscape variables obtained as a result of an ecological analysis. Figure 1B illustrates the theoretical model of translating habitat fragmentation into low and high-resistance landscape elements. Figure 1C represents a deduced connectivity between the subpopulations of the elephants with strong connectivity indicating high connectivity and low genetic differentiation, whereas weak connectivity indicates reduced connectivity and high genetic differentiation.

Connectivity Interpretation and Conservation Assessment

Interpretation of patterns of connectivity as determined by the integrated framework took a conservation interpretation context in order to determine the functionally significant habitat corridors and priority conservation areas. Fragments of the Asian elephant population were also taken into consideration as comparative evidence to provide greater inference about the fragmentation-mediated genetic isolation and the significance of the corridors (Sharma et al., 2025). The subpopulations that had high genetic differentiation and lower connectivity were perceived to be under a higher risk of genetic erosion over a long period of time, but populations connected by low-resistance habitats were perceived to be more resilient to the continuous fragmentation.

Ethical Considerations

The data utilized in the current study are all those published in earlier studies that were conducted using non-invasive approaches and approved ethically. Field sampling, animal manipulation, and experimental manipulation were not done.

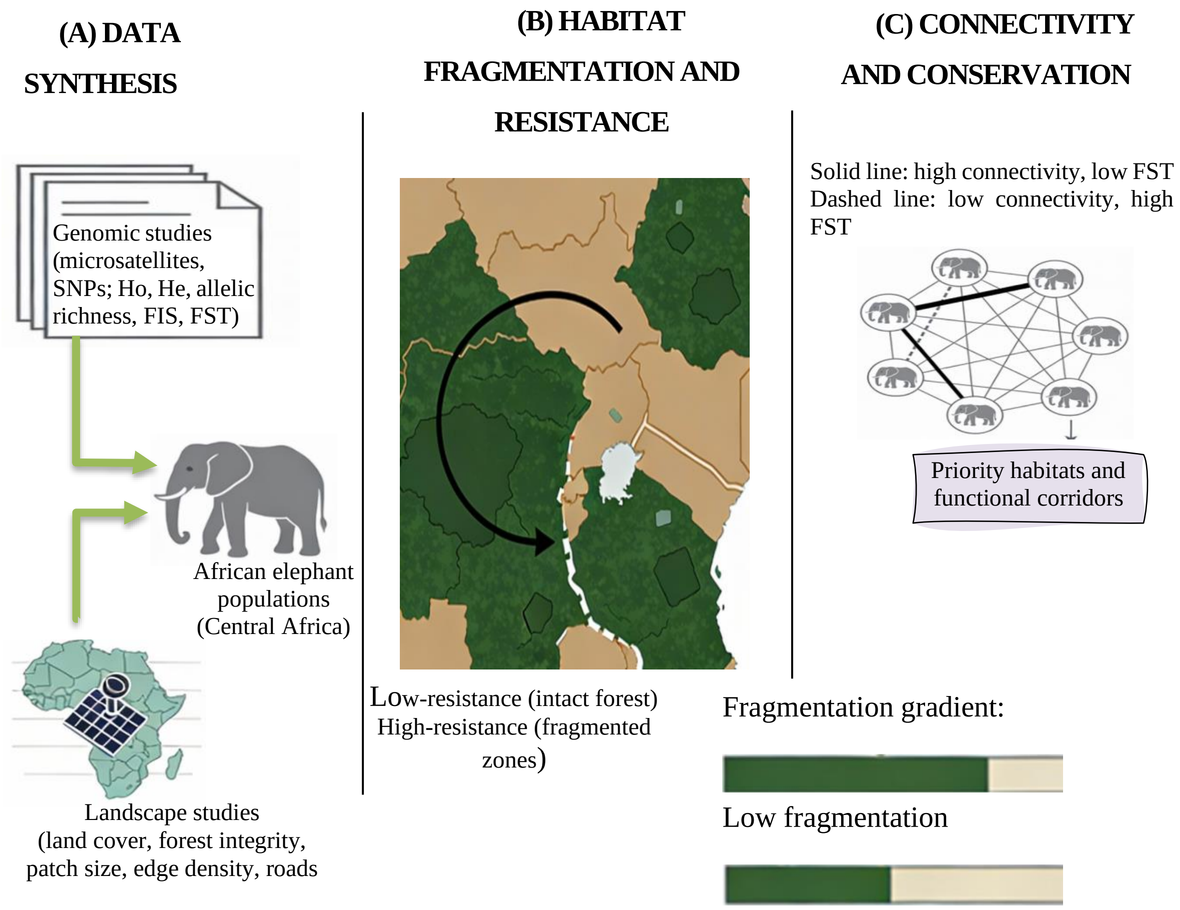

Figure 1: Integrative Landscape Genetics Framework Linking Habitat Fragmentation And Genetic Diversity In African Elephants In Central Africa

Figure 1 displays (A) Synthesis of genomic diversity and differentiation measures along with landscape and habitat data of Central African elephant population. (B) Habitat fragmentation and landscape resistance Conceptual representation of the relationship between intact forest that has low resistance and fragmented areas that have high resistance. (C) Correlation of the connectivity of the various elephant subpopulations, with the strong connection reflecting high level of connectivity and low level of genetic differentiation and the weak connection reflecting low level of connectivity and high level of genetic differentiation to inform the priority areas and functional pathways.

Results

Genetic Diversity Across Fragmented Landscapes

The level of genetic diversity between African elephant subpopulations in habitats with diverse degrees of habitat fragmentation was significantly different. Genetic diversity was found to be increased in populations that were found in large and continuous forest or savanna environments, and less in those where elephants were found in highly fragmented environments or in isolated locations with low heterozygosity and allelic richness.

Table 2 presents the most important genetic diversity measures among the representative subpopulations. The heterozygosity (H 0) was observed to be between 0.54 and 0.71 with the least being observed in highly fragmented landscape. The allelic richness also had a comparable pattern wherein the richness decreased with habitat isolation. The levels of inbreeding coefficients (FIS) were not very high though they were high in the most remote subpopulations suggesting early signs of inbreeding.

Table 2: Genetic Diversity Metrics Of African Elephant Subpopulations Across Fragmentation Classes

Fragmentation Class	**Population Code**	**H_o**	**H_e**	**Allelic Richness**	**FIS**
Low (contiguous)	CF-1	0.71	0.73	8.4	0.03
Low (contiguous)	CS-1	0.69	0.71	8.1	0.04
Moderate	MF-1	0.63	0.66	7.2	0.05
Moderate	MS-1	0.61	0.64	7.0	0.06
High (fragmented)	HF-1	0.56	0.59	6.2	0.09
High (fragmented)	HF-2	0.54	0.58	6.0	0.11

Population Structure and Genetic Differentiation

Overall population structure studies showed that there was a clear genetic differentiation in relation to landscape fragmentation. Populations that were segregated by the intensely altered landscapes were more genetically differentiated than the ones that were in contact with each other due to continuous or semi-connected habitats.

The values of pairwise FST varied between contiguity and isolation with values of 0.02 and 0.12 respectively, showing decreased gene flow with increased fragmentation. Even in the case of the presence of landscape barriers in the form of roads and agricultural matrices, moderate differentiation was detected even between populations that were separated by comparatively short geographic distances.

Table 3: Pairwise Genetic Differentiation (FST) Among Representative Elephant Subpopulations

Population Pair	Fragmentation Context	FST
CF-1 – CS-1	Continuous habitat	0.02
CF-1 – MF-1	Moderate fragmentation	0.05
MF-1 – MS-1	Moderate fragmentation	0.06
MF-1 – HF-1	High fragmentation	0.09
MS-1 – HF-2	High fragmentation	0.11
HF-1 – HF-2	Highly isolated	0.12

Table 3 shows pair wise FST of representative elephant subpopulations in different fragmentation contexts. Among populations that are continuously linked by habitat, genetic differentiation is minimized and heightens as a result of landscape change and separation. An increase in FST values implies a limited gene flow in disjointed landscapes.

Habitat Suitability and Fragmentation Patterns

The suitability of habitats modeling revealed a great deal of spatial heterogeneity in the study area. The high-suitability areas were mainly in the sheltered regions and relatively undisturbed forest blocks but the low-suitability regions were linked to the dense road systems, agricultural development and agglomerations.

The measurements of fragmentation showed that there was a close negative correlation between isolation and habitat patch size. Small patch sizes, high density of edges, and high values of resistance to movement of the elephants were the features of highly fragmented landscapes.

Table 4: Habitat Fragmentation Metrics Across Landscape Categories

Landscape Category	Mean Patch Size (km²)	Edge Density (km/km²)	Mean Resistance Value
Low fragmentation	145.6	0.42	1.8
Moderate fragmentation	72.3	0.88	3.4
High fragmentation	29.7	1.56	5.9

Table 4 presents the landscape-scale fragmentation statistics of mean patch size of habitat, the density of edges, and the resistance values in fragmentation classes. Smaller patch sizes, greater edge density, and more resistance to movement of elephants are all characteristics of highly fragmented landscapes. These indices indicate growing structural and functional disturbance of habitat.

Landscape Connectivity and Gene Flow

Combination of genetic and ecological information indicated that the connectivity of the landscape greatly contributed to the observed trends of the gene flow. Circuit-based and least-cost path analyses found that there were only a few functional corridors that connect the genetically related subpopulations; mainly by the remaining forested tracts and riparian regions.

Landscape resistance was positively related with genetic differentiation (r = 0.68), and the more the movement resistance of an area, the less the genetic flow. Even at geographical distance, subpopulations that were linked by low-resistance corridors had greater genetic variation and reduced differentiation.

The association of landscape resistance, genetic difference and the presence of a corridor is summarized in Table 5. The degree of genetic differentiation is less and the connectivity is high in subpopulations in low-resistance landscapes. On the contrary, low-resistance landscapes are associated with lower connectivity and high genetic differentiation.

Table 5: Relationship Between Landscape Resistance And Genetic Connectivity

Connectivity Category	Mean Resistance	Mean FST	Corridor Presence
High connectivity	2.1	0.03	Present
Moderate connectivity	3.8	0.06	Limited
Low connectivity	5.6	0.10	Absent

Conservation-Relevant Outcomes

The study was able to designate the priority conservation areas based on high genetic diversity, low fragmentation, and high connectivity by using genomic and ecological analysis. On the other hand, highly fragmented landscapes with a lack of functional corridors were the location of isolated subpopulations with high genetic differentiation and early inbreeding.

These findings demonstrate the importance of the remaining habitat corridors in genetic connectivity as well as the necessity in landscape conservation tactics to preserve and reestablish genetic connectivity among the Central African elephant ranges.

Conclusion

This paper has shown the usefulness of genomic and ecological data in the evaluation of the effects of habitat fragmentation on genetic diversification, population configuration, and connectivity of African elephants in Central Africa. By combining indicators of population genetic data with the topographical data on habitat fragmentation and resistance, the data reveals the repeated trend of low genetic diversity, high genetic structuring and low connectivity in highly fragmented landscapes. These trends highlight how sensitive the extensive megafauna is to disturbance of the landscapes even in areas that still have large forest areas.

The integrative framework highlights the importance of preserving high-quality habitats and be able to continue functioning corridors to ensure that there continues to be gene flow between the subpopulations of the elephants. Low resistance landscapes with structural connectivity are related to a high genetic resilience and the peripheral patches of habitat, in turn, show early signs of genetic erosion. These results add to the significance of conservation strategy on a landscape scale that goes beyond the boundary of the protected areas and clearly integrates the conservation of connectivity and restoration.

Notably, the synthesis-based methodology that was used in the current study offers a transferable and adaptable model of assessing the effects of fragmentation in data-restrained situations. The framework can be used to aid in prioritization of conservation areas and corridors of the African elephants and other wide-ranging species by connecting the ecological measures of fragmentation to the genomic indicators. Future studies that combine finer-scale genomic data, movement ecology, and dynamic land-use forecasts will add to the knowledge on the effects of fragmentation on evolutionary risks and can be used in adaptive conservation planning in rapidly changing environments.

References

[1] Ahlering, Marissa A., Lori S. Eggert, David Western, Anna Estes, Linus Munishi, Robert Fleischer, Melissa Roberts, and Jesus E. Maldonado. "Identifying source populations and genetic structure for savannah elephants in human-dominated landscapes and protected areas in the Kenya-Tanzania borderlands." *PLoS One* 7, no. 12 (2012): e52288. https://doi.org/10.1371/journal.pone.0052288

[2] Balkenhol, Niko, Felix Gugerli, Sam A. Cushman, Lisette P. Waits, Aurélie Coulon, J. W. Arntzen, Rolf Holderegger, Helene H. Wagner, and Participants of the Landscape Genetics Research Agenda Workshop 2007. "Identifying future research needs in landscape genetics: where to from here?." *Landscape Ecology* 24, no. 4 (2009): 455-463.

[3] Colangelo, Paolo, Marika Di Civita, Carlos M. Bento, Paolo Franchini, Axel Meyer, Nadiya Orel, Luis CBG das Neves et al. "Genome-wide diversity, population structure and signatures of inbreeding in the African buffalo in Mozambique." *BMC Ecology and Evolution* 24, no. 1 (2024): 29.

[4] Curry, Caitlin J., Brian W. Davis, Laura D. Bertola, Paula A. White, William J. Murphy, and James N. Derr. "Spatiotemporal genetic diversity of lions reveals the influence of habitat fragmentation across Africa." *Molecular Biology and Evolution* 38, no. 1 (2021): 48-57. https://doi.org/10.1093/molbev/msaa174

[5] Cushman, Samuel A., Kevin S. McKelvey, Jim Hayden, and Michael K. Schwartz. "Gene flow in complex landscapes: testing multiple hypotheses with causal modeling." *The American Naturalist* 168, no. 4 (2006): 486-499. https://doi.org/10.1086/506976

[6] De Flamingh, A., Alexander, N., Perrin-Stowe, T. I., Donnelly, C., Guldemond, R. A., Schooley, R. L., ... & Roca, A. L. (2024). Integrating habitat suitability modeling with gene flow improves delineation of landscape connections among African savanna elephants.

Biodiversity and Conservation, *33*(11), 3231-3252.

[7] De Flamingh, Alida, Catherine L. Sole, and Rudi J. Van Aarde. "Genetic evidence for spatial structuring in a continuous African elephant (Loxodonta africana) population." *Conservation Genetics* 16, no. 3 (2015): 613-623.

[8] Eggert, L. S., R. Buij, M. E. Lee, P. Campbell, Francisco Dallmeier, Robert C. Fleischer, Alfonso Alonso, and Jesús E. Maldonado. "Using genetic profiles of African forest elephants to infer population structure, movements, and habitat use in a conservation and development landscape in Gabon. " *Conservation Biology* 28, no. 1 (2014): 107-118. https://doi.org/10.1111/cobi.12161

[9] Ernest, E. M., H. Haanes, S. Bitanyi, R. D. Fyumagwa, P. L. Msoffe, G. Bjørnstad, and K. H. Røed. "Influence of habitat fragmentation on the genetic structure of large mammals: evidence for increased structuring of African buffalo (Syncerus caffer) within the Serengeti ecosystem." *Conservation Genetics* 13, no. 2 (2012): 381-391.

[10] Goossens, Benoit, Reeta Sharma, Nurzhafarina Othman, Célia Kun-Rodrigues, Rosdi Sakong, Marc Ancrenaz, Laurentius N. Ambu et al. "Habitat fragmentation and genetic diversity in natural populations of the Bornean elephant: Implications for conservation." *Biological Conservation* 196 (2016): 80-92. https://doi.org/10.1016/j.biocon.2016.02.008

[11] Johnson, Mireille B., Lillian D. Parker, Hadrien Vanthomme, Landry Tchignoumba, Jessica L. Deichmann, Jesús E. Maldonado, Lisa Korte, and Alfonso Alonso. "Patterns of genetic diversity in African forest elephants living in a human-modified landscape in southwest Gabon." *Conservation Science and Practice* 1, no. 8 (2019): e76. https://doi.org/10.1111/csp2.76

[12] Johnson, Mireille B., Stephen L. Clifford, Benoît Goossens, Silvester Nyakaana, Bryan Curran, Lee JT White, E. Jean Wickings, and Michael W. Bruford. "Complex phylogeographic history of central African forest elephants and its implications for taxonomy." *BMC Evolutionary Biology* 7, no. 1 (2007): 244.

[13] Laguardia, Alice, Stephanie Bourgeois, Samantha Strindberg, Kathleen S. Gobush, Gaspard Abitsi, HG Bikang Bi Ateme, Fabrice Ebouta et al. "Nationwide abundance and distribution of African forest elephants across Gabon using non-invasive SNP genotyping." *Global Ecology and Conservation* 32 (2021): e01894. https://doi.org/10.1016/j.gecco.2021.e01894

[14] Lohay, George G., Thomas Casey Weathers, Anna B. Estes, Barbara C. McGrath, and Douglas R. Cavener. "Genetic connectivity and population structure of African savanna elephants (Loxodonta africana) in Tanzania.

" *Ecology and evolution* 10, no. 20 (2020): 11069-11089. https://doi.org/10.1002/ece3.6728

[15] Prashanth, R. "Ecological Risk Assessment of Vector-Borne Alien Species Threatening Livestock Health Using CLIMEX Simulation." *National Journal of Animal Health and Sustainable Livestock* 3, no. 1 (2025): 1-9. https://doi.org/10.17051/NJAHSL/03.01.01

[16] Mazziotta, A., Francini, S., & Parisi, F. (2025). Monitoring Habitat Fragmentation and Biodiversity in Forest Ecosystems. In Ecological Connectivity of Forest Ecosystems (pp. 171-186). Cham: Springer Nature Switzerland.

[17] Rajan, Vinod, and Roshni Chawla. "Anthropometric Variations and Adaptations across Diverse Ecological Zones." *Progression journal of Human Demography and Anthropology* (2024): 1-4.

[18] Sharma, Rajeev, Astik Kumar Pradhan, Balasankar Karavadi, Subrat Kumar Mahapatra, Adarsha Harinaiha, and Preeti Handa Kakkar. "Applying the Species-Area Relationship Model to Predict Biodiversity Loss in Deforested Regions." *Natural and Engineering Sciences* 10, no. 2 (2025): 79-92. https://doi.org/10.28978/nesciences.1763892

[19] Sinovas, Pablo, Chelsea Smith, Sophorn Keath, Nasak Chantha, Jennifer Kaden, Saveng Ith, and Alex Ball. "Giants in the landscape: status, genetic diversity, habitat suitability and conservation implications for a fragmented Asian elephant (Elephas maximus) population in Cambodia." *Peer Journal* 13 (2025): e18932. https://doi.org/10.7717/peerj.18932

[20] Zacarias, Daniel, Luis Mauricio Bini, and Rafael Loyola. "Systematic review on the conservation genetics of African savannah elephants." *PeerJ* 4 (2016): e2567. https://doi.org/10.7717/peerj.2567