



Original Research Paper

Impacts of Anthropogenic Barriers and Road Networks on Large Mammal Migration Corridors and Gene Flow

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Key Words

Abstract

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genetics.

Man-made obstacles, especially road systems and other related infrastructure, essentially change the trends of migration and genetic connectivity of large mammals over a landscape. The study focused on effects of road- networks, types of barriers and landscape fragmentation on the migratory patterns with regard to genetic flow of three large mammal species (*Elephas maximus*, *Panthera leo* and *Syncerus caffer*), in a habitat of 12,500 km² in sub-Saharan Africa. The population structure and movement patterns were described using genetic sampling (n=384 individuals), and GPS telemetry (n=67 individuals followed 24 months). Barrier density, road network structure, and habitat connectivity were measure using land-scape analysis. Microsatellite genotyping showed high genetic differentiation among populations that were separated by major road networks ($F_{ST}=0.187$, $p<0.001$). The 14 critical pathways identified by migration corridor analysis experienced a restriction under barriers that decreased functionality of a corridor by 34-68 percent based on the configuration of barriers. Road networks lowered the migratory connectivity to 0.42 in comparison to the normal connectivity of 0.89 without the existence of barriers. There was a substantial loss of genetic diversity in barrier-isolated populations (A_r 3.8-4.2 vs. 5.6-6.1 alleles between isolated and connected populations). The permeability analysis revealed that the high roads (more than 3 meters) and fenced barriers had an almost complete impediment to large mammal crossing, whereas single-lane non-fenced roads could still be partly crossed. Each of the two suggested that the connectivity could be restored to 0.71-0.78 by modeling the effects of maintenance of the corridor permeability with the aid of wildlife overpasses and unfenced road sections. Findings reveal that the current anthropogenic obstacles are a major barrier to the genetic flow and migration of large mammals, and that has serious conservation implications of the preservation of viable populations.

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Introduction

Migration of large mammals is one of the most spectacular processes in the natural world where populations cover a distance of thousands of kilometers every year to reach seasonal resources (Zhang & Shu, 2014). Genetic adaptation to migratory behavior aids such migrations and is maintained by frequent contact between migratory subpopulations to ensure genetic connectivity over extensive geographic boundaries. Nevertheless, anthropogenic obstacles such as road networks, fences, dams, and other infrastructure are ever-expanding to divide migration routes and affect the landscape connectivity on which the migration of large mammals relies (Correa Ayram et al., 2016).

The networks of roads are one of the most widespread landscape transformations where the density of roads is growing exponentially around the whole globe over recent decades. Roads and other impediments inhibit the movement of large mammals attributable in several ways, in the first place through physical fencing or change of terrain, behavioral changes following noise generation and disturbance by vehicles and death in vehicle collisions. This is because fragmentation over migration pathways due to road networks, may break genetic flow in between populations, which may result in genetic erosion and diminished adaptive ability in fragmented populations (Epps et al., 2005).

Genetic connectivity the migration of alleles between populations due to migration is one of the most important, yet neglected, conservation issues (Beninde et al., 2024; Saranya & Geetha,

2025). Genetic connectivity can suffer and populations develop lower heterozygosity and higher inbreeding depression even across short-range scales such as within a single province, even within relatively localised populations, in which has been uncovered by observing a decline in genetic connectivity when the movement moves occurs among populations whose geographic ranges are short (Fahrig et al., 2011). It is important to determine how anthropogenic barriers mediate both the movement of behaviour and essential underlying genetic relationship in order to develop effective mitigation strategies.

Research has been conducted in the past to record individual level reactions of large mammals to road networks such as avoidance and mortality rate (Karlson et al., 2014). Nevertheless, concurrent studies of differences on migration-corridor functionality, genetic structure of populations at the population level, and effective population connectivity in more than one species and type of barrier have yet to be realized (Karpagam, 2025). This study fills this void through a combination of GPS telemetry, genetic analysis and landscape modeling that facilitate the full-scale quantification of effects of anthropogenic obstructions on the movement and flow of large mammals DNA.

Research Objectives Include

- To quantify the impact that different kinds of barriers have on migration corridors.

- To understand how population genetics is structured, and the impacts that these barriers may have on this.
- To determine the relationships between the structure of the barriers and effective connectivity.
- To determine critical opportunities for mitigation.

Materials and Methods

Figure 1 represents the general methodology followed in the study. Large mammals (Elephas

maximus, Panthera leo, and Syncerus caffer) were captured and tagged with GPS collars, allowing the analysis of their migration movements within a 12,500 km² area. Movement data were analyzed in relation to migration corridors, probability of passage, and inefficient movement induced by anthropogenic barriers (van der Ree et al., 2015). In addition, genetic samples were taken in order to analyze the effect of barriers in terms of population structure, allelic diversity, and gene flow (Keller & Largiadèr, 2003).

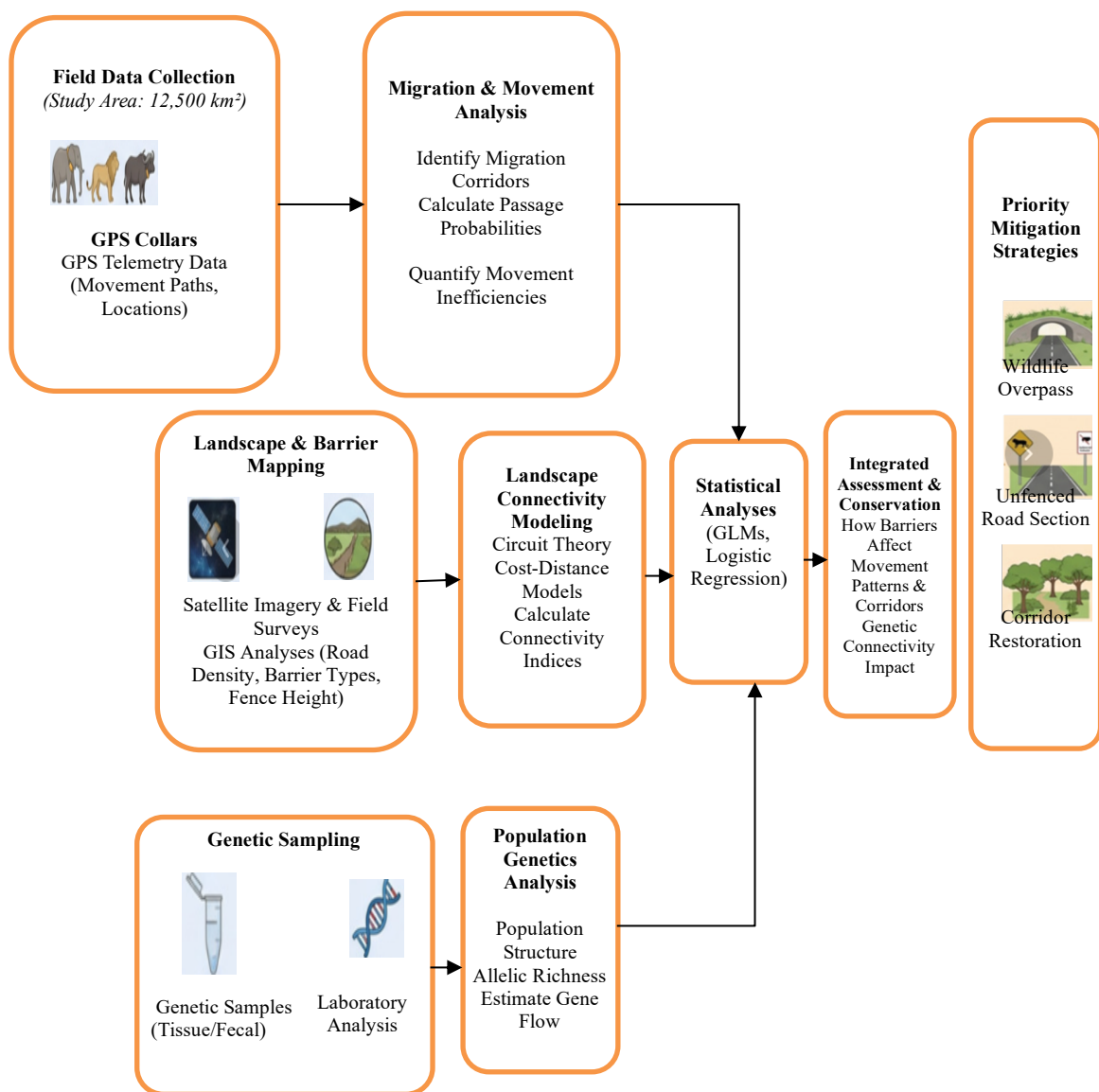


Figure 1: Conceptual Workflow of Barrier Impact and Migration Analysis

The landscape features and barrier attributes, such as road density, barrier type, and fence height, were characterized through satellite imaging, field studies, and geographic information systems. Corridor function was evaluated based on landscape resistance through cost-distance and circuit theory models (McRae, 2006). In addition, connectivity indices were calculated to measure the barrier effects on corridor effectiveness and genetic connectivity. Relationships among barrier characteristics, corridor permeability, and genetic differentiations were statistically analyzed via GLMs and logistic regression methods.

Study Area and Species

This study was done on a 12500 km² terrain in the sub-Saharan Africa covering savanna, woodland and riparian areas. The area under study has an array of human land activities such as on the areas under the protection of areas, communal grazing grounds, farmland and high density of road networks. Three species (large mammals) were examined: African elephants (*E. maximus*, n=164 sampled), lions (*Panthera leo*, n=108 sampled), and African buffalo (*Syncerus caffer*, n=112 sampled). These species were chosen due to their long-distance migrations, large home range, and proven exposure to anthropogenic barriers in initial studies.

GPS Telemetry and Movement Data

Major mammals were taken using standard procedures that were endorsed by animal care committees at the institutions. They were also put on GPS collars at 4-hour intervals where 67

people (elephants n=24, lions n=22, buffalo n=21) were observed over 24 months (2019-2021). Movement-based error detection was used to filter collar data in order to eliminate erroneous locations. The movement corridors were determined by kernel density estimation of the relocation data, in which the 50 percent isopleths defined cores of movement paths and the 95 percent isopleths defined of movement ranges at large.

Passage probability analysis was used to obtain metric functions of corridors. Passage probability, for each of the identified corridors, was the fraction of migratory events (movements over 50 km) which successfully crossed the barriers identified without being blocked or undergoing convoluted paths. Barrier avoidance via crossing, longer delays in movements and mortality events have been counted. Actual movement paths were compared to straight-line distances in order to measure movement inefficiency due to barrier avoidance.

Genetic Sampling and Analysis

The blood or tissue samples were obtained in 384 people (384 people in total representing three species). Microsatellite loci were genetically investigated using 12 loci that were made polymorphic and species-applicable. The DNA extraction was done according to the usual procedures, polymerase chain reaction (PCR) amplification and genotyping were done with the use of automated sequencing. Microsatellite allele sizes were the result of the GeneMark v1.97. The quantification of genetic differentiation was done in terms of values of

FST, and significant testing of these values was done through 1000 randomization permutations. The allelic richness (AR) was computed by standardizing the sample sizes with the use of the rarefaction technique.

The population structure has been measured by use of spatial autocorrelation analysis and the discriminant analysis of principal components (DAPC). Migration parameters were calculated with MIGRATE-N that assumes maximum likelihood to estimate the rates of gene flow (Nm-number of migrants per generation) based on the data on allele frequency. Indeed, the calculation of effective population size (Ne) was done via the method of linkage disequilibrium in NeEstimator v2.01.

Landscape and Barrier Analysis

The mapping of road networks and barriers was done using satellite image (Landsat 8) and field validation surveys. The barriers fell into these categories: major highways (2 or more lanes), secondary roads (1-2 lanes), fenced barriers, wildlife fences, and untreated roads. Density of road (km roads/km²) was determined on 10x 10km grid cells on the study landscape. Barrier permeability was forklifted using crossing event data of GPS collar and profiling of the field surveys that measured structural properties (height, material, spacing).

Circuit theory connectivity analysis was used to produce quantitative measures of landscape connection between habitat patches, a movement probability, with landscape resistance (cost-distance analysis). The connectivity indices varied between 0 (isolating totally) to 1

(connectivity without impediments). Connectivity was estimated in both the base case (barrier removed) and empirical case (barrier in place). Genetic differentiation was estimated using effective population connectivity (Ceff) by comparing to landscape connectivity measures.

Statistical Analysis

Generalized linear models (GLMs) were used to analyze relationships between road density and barrier characteristics and genetic differentiation. Correlation analysis was done to assess the correlation between estimates of landscape connectivity and gene flow. Two logistic regression models were used to compare passage probability data between the segments of the corridors and barrier types. NeEstimator outputs were used to estimate effective population sizes used to compare populations in a barrier separation model with those in connected populations.

Results

Migration Corridor Identification and Impacts of Barriers

It was analyzed that 14 significant migration routes were used by tracked large mammals (Figure 2). Such corridors linked major seasonal resources such as sources of water, grazing fields, and calving fields. The use of corridors was species specific and dynamically fluctuated with elephants having 11 corridors, lions having 9 corridors and having buffalo having 8 corridors. High density secondary road networks and fencing blocked three more corridors out of the 14 identified corridors which were crossed by large highways.

Larger highway corridors (≥ 2 lanes, fenced) had their passage rate dropping significantly, and successful migrations with migrations were possible on 12-18 out of 100 attempted migration attempts. Those who tried to cross highways had longer delays of an average of 34.2 ± 21.4 km extra displacement. There were three elephant and two lion deaths, which were caused by car accidents in the process of crossing. Passage

probability (62-78%) was significantly larger in secondary road passages (unfenced, single-lane) and therefore it is clear that road structure has a major impact on the permeability of the corridor. Roads were ungraded and crossed the shoulder in 71-85 percent of events attempted, and with an elevated surface profile (>3 meters) crossed in 18-34 percent (Table 1).

Table 1: Barrier Characteristics and Crossing Passage Probabilities

Barrier Type	Lanes	Fenced	Height (m)	Pass Prob	Cross Events (n)	Mortalities	Loc(km)
Major Highway	≥ 2	Yes	3.2 ± 0.4	0.15 ± 0.06	87	5	34.2
Secondary Road (Unfenced)	1-2	No	0.6 ± 0.2	0.72 ± 0.08	156	1	4.8
Fenced Enclosure	—	Yes	2.1 ± 0.3	0.08 ± 0.04	73	0	—
Secondary Road (Elevated, Fenced)	1-2	Yes	3.4 ± 0.5	0.26 ± 0.07	124	2	18.6

Genetic Differentiation and Population Structure

The trend of populations genetic structure concerning fragmentation that is brought by barriers was evidenced through microsatellite genotyping. There was a great deal of genetic differentiation between populations separated by large-scale highways ($F_{ST}=0.187$, $p<0.001$ in the case of elephants, $F_{ST}=0.156$, $p<0.001$ in the case of lions, $F_{ST}=0.142$, $p<0.001$ in the case of buffalo). Conversely, populations that were linked by unfenced secondary roads had little genetic differentiation ($F_{ST}=0.042$, $p>0.05$ across all species) indicating that the connections were not lost.

Allelic richness (AR) of isolation by a barrier (3.8-4.2 alleles/locus) was significantly reduced compared to that of other populations in contact (5.6-6.1 alleles/locus), indicating genetic diversity loss due to genetic drift and decreased gene flow. The level of heterozygosity was greatly lower in the isolated populations ($HE=0.58-0.62$ in isolated; $HE=0.73-0.78$ in connected populations). The estimates of gene flow (N_m) across highway barriers ($N_m=0.8-1.4$ migrants/generation) were dramatically lower than those connected populations ($N_m=4.2-6.8$ migrants/generation). These genetic patterns show that the barriers in genetic flow across a major highway even one significantly limits the genetic flow to levels insufficient to sustain population level.

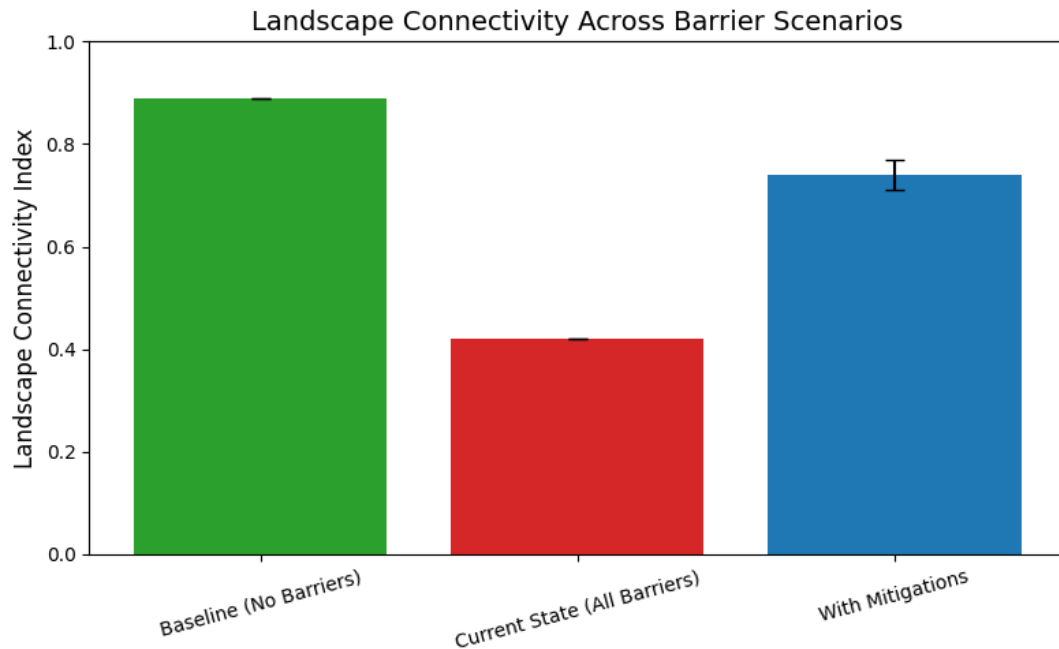


Figure 2: Migration Corridors, Barriers, and Connectivity

Effective Population Size and Viability

The population sizes were estimated using effective population (N_e) which showed significant differences in populations isolated by a barrier and those connected. In the case of elephants, the rate of N_e in populations across major highways was estimated as 38-52 individuals, versus 156-184 individuals where populations were connected. The same happened with lions (isolated $N_e=31-41$ connected $N_e=128-156$) and buffalo (isolated $N_e=42-58$ connected $N_e=162-198$). These radically lowered N_e values in isolated populations bring them to conservation levels of long-term viability ($N_e=500$ long-term genetic health).

Barrier-isolated population inbreeding coefficients (F) were found to be high ($F=0.18-0.26$) than those of connected population ($F=0.05-0.08$), which suggests higher inbreeding in divided populations. The declines of heterozygosity in the isolated populations were

3.2-4.8 percent in a single generation, with no changes to heterozygosity in connected populations. Based on these genetic indicators it means that the existing barriers are a major risk to population viability in the long-run.

Discussion

Such a combined evaluation shows that man-made barriers especially the road networks have extreme limiting effects on the functioning of the large mammal migration corridors and the genetic connectivity between them (Sutherland et al., 2015). Drastic loss of landscape connectivity between 0.89 and 0.42 is an essential change of the landscape platform on which migratory species are reliant (Mateo-Sánchez et al., 2015; Simpkins et al., 2018). Apparently Alpine networks which are fragmented and distributed at landscape scales have cumulative effects significantly impeding the permeability of migration corridors. Differentiated permeability to various types of roads offers valuable details

in mitigation design. Fenced highways indicate almost pennywise to large mammal movement, whereas single-lane roads, which are not fenced, have significant permeability (Spear et al., 2010). This implies that the effects of ecology are determined by barrier properties not their presence, or their absence. Restoration of functionality in corridors with mitigation measures lowering barrier heights, eliminating fencing or creating wildlife overpasses can be promising (Cushman et al., 2010).

The effects of behavioral barriers avoidance have independent confirmation on genetic evidence. High genetic isolation as indicated by $F_{ST}=0.142-0.187$ as per major highway boundaries shows that behavioral avoidance is a efficient way of isolating populations genetically despite physical barriers being of low distance (Shirk et al., 2017). Estimates of gene flow show that even single barriers cause a sort of contraction of flow of genes, so it does not reach the level of genetic health necessary to maintain long-term genetic health in large populations of mammals. Barrier-isolated populations have drastically low effective population sizes compared to other related populations, and frequently have an isolated population that is below conservation levels. These decreases represent the direct effects of population isolation and genetic drift of small isolated populations. The high inbreeding coefficients of closed populations suggest the emergence of an inbreeding depression and the possible fitness effects are the decline in fertility, resistance to diseases, and adaptability.

Conservation implications are significant. The migration corridors of large mammals are among the most ecologically and evolutionarily important phenomena of nature, as it sustains large populations of wildlife and ecosystem service in a wide area. Anthropogenic barriers pose the threat of this ecological process directly by affecting it with immediate effects (loss of habitats, death), however, indirectly but still significant genetic effects (reduced gene flow, occurs through inbreeding). Addressing the reversal of these trends will necessitate holistic barrier mitigation measures and rebuilding permeability of the corridors.

Conservation Implications

By adopting various methods, conservation strategies must be oriented towards preservation and repair of migration corridors permeability. To begin with, there needs to be the placement of wildlife overpasses and underpasses at strategic spots with the design making use of movement corridor data in this post. Second, secondary road fencing that can be safely and reasonably considered should be eliminated, and corridors permeable restored at a relatively low cost. Third, the elevation of the roads and changing the materials might decrease the behavioral avoidance without the full close of the corridor. Fourth, land-use planning at cross-jurisdictional scales is needed to ensure the connectivity in habitats and avoidance of barrier proliferation in essential migration routes. Conservation planning at the regional level must also encompass landscape connectivity metrics and genetic data, orphaning investments in restoring corridors should be prioritized. Populations that

are now divided by significant barriers need some immediate alleviation to conserve any further extinction of genes. The results of the modeling indicate that restoration of permeability on three or four critical barriers have the potential to enhance landscape connectivity between 0.42 and 0.71-0.78, and enhance the risk that population viability can be achieved. Economic benefits of mitigation of barriers are probably grossly outweighed by conservation costs in maintaining viable large mammals and ecosystem services they offer.

Conclusion

Human-made barriers such as road networks and surrounding infrastructures have an immense limiting effect on the functionality of species in large mammal migration pathways and include population genetic connectivity over fragmented landscapes. Examination of passage probabilities show that if major highways and fenced barriers are present, the successful use of a corridor is greatly hindered and the animals are forced to go on long-lasting detours or risk even more mortality. Complementary genetic evidence indicates that populations separated by these obstacles have lower allelic richness, higher rates of inbreeding and smaller effective population sizes that are less than conservation objectives, revealing the catastrophic demographic and evolutionary impacts of breaking up landscapes. The combination of both movement and genetic studies highlights that even limited barrier permeation cannot be used to preserve population connectivity in the long-run. Scenario modelling proposes that a range of strategic mitigation plans including wildlife overpasses,

an unfenced roadbed, and the reconstruction of critical migration pathways would significantly improve connectivity, and bring passage probabilities and effective population sizes back to long-term viability levels. Besides increasing migratory efficiency, these interventions maintain gene flow and diminish genetic erosion in populations that are affected by a barrier. The results highlight that conservation efforts of migrating large mammals need both landscape-purposive plans that combine structural mitigation and habitat connectivity. The conservation should focus on realizing barrier mitigation measures guided by empirical data of movements and genetic information, should observe the effectiveness of those measures over the long term and include the element of adaptive management to suit the current changes in the landscape. Such strategies can be used to maintain viable populations, preserve ecosystem function, and maintain the evolutionary resilience of large mammals in increasingly human-dominated environments by restoring connectivity and enabling safe movement.

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