



Genetic Diversity and Evolutionary Biology of Indian Wildlife- A Review

Mainak Banerjee ^{a++*}, Jayshree Kamble ^{b++},
Saransh Kumar Gautam ^{c#}, Aneesh KS ^{d++},
Dhanraj Balbhim Bhure ^{e†}, Tejaswini Sadineni ^{f++}
and G. Sadaya Kumar ^{g‡}

^a Department of Zoology, RKDF University, Ranchi, Jharkhand, India.

^b Department of Zoology, Changu Kana Thakur Arts Commerce and Science College, New Panvel, Navi Mumbai, Maharashtra, India.

^c Department of Silviculture and Agroforestry, Rani Lakshmi Bai Central Agricultural University, Jhansi, Uttar Pradesh, India.

^d Department of Forest Resource Management, College of Forestry, KAU, Vellankkara, Thrissur, Kerala, India.

^e Department of Zoology, Yeshwant Mahavidyalaya, Nanded-431602, Maharashtra, India.

^f Department of Soil Science and Agricultural Chemistry, KL College of Agriculture, Koneru Lakshmaiah Education Foundation (KLEF), KL Deemed to be University, Vaddeswaram, Guntur, Andhra Pradesh, India.

^g Tara Government College (A), Affiliated to Osmania University, Sangareddy, Telangana, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.56557/upjoz/2024/v45i204590>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://prh.mbimph.com/review-history/4231>

Review Article

Received: 22/08/2024

Accepted: 26/10/2024

Published: 02/11/2024

⁺⁺ Assistant Professor;

[#] Ph.D. Scholar;

[†] Associate Professor;

[‡] Assistant Professor of Zoology;

*Corresponding author: Email: mainak.bio@gmail.com;

Cite as: Banerjee, Mainak, Jayshree Kamble, Saransh Kumar Gautam, Aneesh KS, Dhanraj Balbhim Bhure, Tejaswini Sadineni, and G. Sadaya Kumar. 2024. "Genetic Diversity and Evolutionary Biology of Indian Wildlife- A Review". UTTAR PRADESH JOURNAL OF ZOOLOGY 45 (20):353-68. <https://doi.org/10.56557/upjoz/2024/v45i204590>.

ABSTRACT

The genetic diversity and evolutionary biology of Indian wildlife, emphasizing the critical role of genetic variability in ensuring species adaptability and long-term survival. India is one of the world's megadiverse countries, home to a wide range of unique flora and fauna spread across its biodiversity hotspots, including the Western Ghats and the Eastern Himalayas. However, rapid habitat fragmentation, deforestation, and poaching have severely impacted the genetic health of many wildlife species, leading to reduced gene flow, population bottlenecks, and increased inbreeding. This has heightened the risk of extinction for small, isolated populations such as the Asiatic lion and the Great Indian bustard. Genetic studies using advanced genomic tools have provided key insights into the population structure, phylogenetic relationships, and adaptive potential of species like the Bengal tiger, Asian elephant, and snow leopard. Conservation strategies, including genetic rescue, habitat corridors, and the use of captive breeding programs, are recommended to preserve genetic diversity and prevent further genetic erosion. Technological advances, such as non-invasive sampling and bioinformatics, are transforming wildlife research, enabling more precise and less intrusive genetic monitoring. The integration of genetic data into conservation policies and practices is essential for developing targeted management plans that maintain the evolutionary potential of Indian wildlife.

Keywords: Genetic diversity; conservation; habitat fragmentation; speciation; phylogeography.

1. INTRODUCTION

1.1 Indian Wildlife's Richness, Biogeography, and Biodiversity

India is one of the world's megadiverse countries, harboring approximately 7-8% of all recorded species, despite covering only 2.4% of the global land area. The country's unique biogeography comprises a range of ecosystems, from tropical rainforests, arid deserts, alpine pastures, to coastal and marine habitats, which support an extraordinary variety of flora and fauna (Jamal 2020). India's biodiversity is represented across various biogeographical regions, including the Himalayas, Western Ghats, Deccan Peninsula, and Indo-Gangetic Plains. Each of these regions has distinct environmental gradients and geological histories, contributing to the high levels of endemism observed in several taxa, including reptiles, amphibians, and plants. The Western Ghats and the Eastern Himalayas are recognized as global biodiversity hotspots due to their exceptional levels of species richness and endemism, despite facing significant anthropogenic pressures. For instance, the Western Ghats alone host over 6,000 vascular plant species, of which more than 1,500 are endemic (Pullaiah 2018). The Eastern Himalayas are home to a rich assemblage of unique species, including the red panda (*Ailurus fulgens*) and the Himalayan tahr (*Hemitragus jemlahicus*). The Sundarbans, a unique mangrove ecosystem, support the iconic

Bengal tiger (*Panthera tigris tigris*), which has adapted to a semi-aquatic life. Such diversity and specialization highlight the evolutionary significance of India's landscapes in shaping the genetic diversity of its wildlife.

1.2 Importance of Genetic Diversity in Maintaining Species Resilience and Adaptability

Genetic diversity is a fundamental component of biodiversity, providing the raw material for evolution and enabling species to adapt to changing environmental conditions (Hoban et al. 2022). It is critical for the long-term survival of species as it enhances their ability to withstand environmental pressures, resist diseases, and maintain reproductive viability. In India, where habitats are highly fragmented and wildlife is under severe threat from human activities, genetic diversity becomes even more crucial for maintaining population stability and avoiding inbreeding depression. For example, genetic studies on the Bengal tiger have shown that populations in different parts of India exhibit significant genetic structuring, reflecting historical isolation and recent anthropogenic impacts (Singh 2017). Populations in Central India have experienced a reduction in genetic diversity due to habitat fragmentation and reduced connectivity, making them vulnerable to genetic erosion. Similarly, genetic assessments of the Asiatic lion (*Panthera leo persica*), currently confined to the Gir Forest, have revealed

extremely low genetic variability, raising concerns about its long-term survival and adaptability to environmental changes. The genetic health of smaller, isolated populations is particularly concerning. A study on the Indian rhinoceros (*Rhinoceros unicornis*) in Assam's Kaziranga National Park found that despite stable numbers, the genetic diversity was lower than expected due to habitat fragmentation and inbreeding (Zschokke 2016). This underscores the need for genetic management to ensure the persistence of such species. Conservation efforts that do not account for genetic factors may inadvertently lead to further erosion of genetic diversity, compromising the species' ability to adapt to future changes such as climate shifts or emerging diseases.

1.3 Objectives of the Review and Its Relevance to Evolutionary Biology and Conservation

This review aims to synthesize the current understanding of genetic diversity and evolutionary processes in Indian wildlife, with an emphasis on how these factors influence species resilience and adaptability. It will explore the distribution and structuring of genetic diversity across different species, analyze the impacts of human-induced changes on evolutionary dynamics, and highlight the role of genetic studies in informing conservation strategies. By doing so, the review seeks to bridge the gap between genetic research and practical conservation applications, providing insights that are crucial for developing effective management plans for India's wildlife (Ghildiya et al. 2023). The genetic basis of species adaptability is particularly important in a rapidly changing environment. With climate change altering habitats and resource availability, the ability of species to genetically adapt to new conditions will play a significant role in their survival. For instance, studies on the snow leopard (*Panthera uncia*) have suggested that genetic diversity within this high-altitude predator may influence its capacity to respond to the shrinking alpine habitats due to global warming (Forrest et al. 2012). Similarly, species with narrow ecological niches, such as the Nilgiritahr (*Nilgiritragus hylocrius*), may face heightened extinction risks if they lack sufficient genetic diversity to adapt to changing conditions. (Bickford et al. 2007).

2. BIODIVERSITY HOTSPOTS AND EVOLUTIONARY SIGNIFICANCE IN INDIA

2.1 Major Biodiversity Hotspots (e.g., Western Ghats, Eastern Himalayas)

India is recognized as one of the world's top biodiversity-rich countries, harboring a remarkable variety of ecosystems, many of which are categorized as global biodiversity hotspots due to their high levels of species richness and unique endemic species (Hrdina and Romportl 2017). Two of the most prominent hotspots in India are the Western Ghats and the Eastern Himalayas, which are distinguished by their unique geophysical features and evolutionary histories, making them critical regions for biodiversity conservation. The Western Ghats, stretching along the western coast of India for approximately 1,600 kilometers, is a chain of mountains that influence the monsoon climate, creating a wide variety of microhabitats. This region supports over 7,400 species of flowering plants, 330 butterfly species, 289 fish species, 157 amphibians, 227 reptiles, 508 bird species, and 120 mammal species. More than 1,500 of these plant species and around 80% of amphibian species are endemic to the Western Ghats, highlighting its role as a center of endemism (Reddy et al. 2021). The region's complex topography and climatic conditions have facilitated the formation of numerous isolated pockets, promoting allopatric speciation and contributing to its extraordinary biodiversity. The Eastern Himalayas, on the other hand, extend from the eastern part of Nepal through Bhutan and into the northern regions of India, including Arunachal Pradesh, Sikkim, and northern West Bengal. This region is known for its varied altitudinal gradients, which range from subtropical lowlands to alpine meadows, supporting a rich diversity of flora and fauna adapted to these unique ecological niches. The Eastern Himalayas are home to over 10,000 species of plants, 300 mammal species, 977 bird species, 176 reptiles, 105 amphibians, and 269 freshwater fish species (Sharma et al. 2013). Endemic species include iconic taxa such as the Himalayan Monal (*Lophophorus impejanus*), the red panda (*Ailurus fulgens*), and the recently discovered Arunachal macaque (*Macaca munzala*). The rapid uplift of the Himalayan range and the subsequent climatic changes have contributed to the high levels of diversification and endemism observed in this region.

2.2 Unique Species Richness, Endemism, and High Genetic Variability in These Regions

The Western Ghats and Eastern Himalayas are globally recognized for their unique species compositions and high rates of endemism. These regions are home to numerous taxa that are not found anywhere else in the world, reflecting both the ancient origins of these ecosystems and their complex evolutionary histories (Cox et al. 2016). The Western Ghats, for instance, exhibit a remarkable level of endemism in amphibians and freshwater fish, with more than 80% of the region's amphibian species and nearly 60% of its fish species being endemic. The amphibian genus *Nyctibatrachus*, which has radiated into over 20 distinct species within the Western Ghats, exemplifies the high levels of genetic and ecological diversification driven by the region's varied microhabitats. In the Eastern Himalayas, high genetic variability has been documented in several key taxa, such as the rhododendrons, which exhibit extensive diversification across different altitudinal zones. This high genetic diversity is also evident in faunal species like the snow trout (*Schizothorax richardsonii*), which show significant genetic structuring across different river systems due to the region's complex hydrological networks (Rodriguez-Iturbe et al. 2009). The presence of unique species such as the golden langur (*Trachypithecus geei*) and the Himalayan musk deer (*Moschus chrysogaster*) underscores the Eastern Himalayas' role as a crucible for speciation and adaptation to high-altitude environments. Genetic studies have further highlighted the evolutionary significance of these regions by revealing cryptic species diversity and deep phylogeographic breaks that often correspond to geographical barriers. For instance, molecular phylogenetic analyses of frogs from the *Indirana* genus in the Western Ghats have uncovered several lineages that are genetically distinct despite being morphologically similar, indicating ongoing speciation processes driven by habitat isolation (Vijayakumar et al. 2016).

2.3 Evolutionary History and Factors Influencing Speciation and Genetic Differentiation in These Ecosystems

The Western Ghats and Eastern Himalayas have undergone significant geological and climatic changes, which have played a critical role in shaping the evolutionary trajectories of the species inhabiting these regions. The Western

Ghats, which date back to the late Cretaceous period, were once part of the ancient Gondwanaland, and their isolation from other landmasses has contributed to the evolution of many relict lineages, such as the caecilian amphibians and the ancient plant family Dipterocarpaceae. Climatic oscillations during the Pleistocene epoch further influenced the distribution and genetic structuring of species, leading to allopatric speciation in response to shifting forest refugia (Riddle 2019). The Eastern Himalayas have experienced multiple episodes of uplift and glaciation, which have created a complex mosaic of habitats and ecological zones. These dramatic geological events have driven repeated cycles of isolation and reconnection among populations, resulting in high levels of genetic differentiation and endemism. For example, the red panda exhibits two distinct genetic lineages corresponding to separate glacial refugia, which have implications for its conservation management. In both regions, the combination of rugged topography, climatic variability, and ecological diversity has acted as a catalyst for adaptive radiation and niche specialization. The steep altitudinal gradients and isolated valleys of the Eastern Himalayas have promoted vertical stratification of biodiversity, leading to the emergence of altitudinally restricted species such as the Satyr Tragopan (*Tragopan satyra*) and the Himalayan Newt (*Tylotriton verrucosus*) (Kandel et al. 2018). The Western Ghats, with their deep riverine gorges and complex rainfall patterns, have facilitated the diversification of taxa like *Philautus* frogs and *Hemidactylus* geckos, which have evolved into multiple sympatric species with distinct ecological niches.

3. GENETIC DIVERSITY IN INDIAN WILDLIFE

3.1 Current Status of Genetic Diversity Studies on Key Indian Wildlife Species

Genetic diversity is a key determinant of species' ability to adapt to environmental changes and ensure long-term population viability. In India, genetic studies have been conducted on several iconic species, focusing on understanding genetic variation, population structure, and the effects of habitat fragmentation (Table 1). Research on the Bengal tiger (*Panthera tigris tigris*) has revealed significant genetic structuring across its range in India, with distinct genetic clusters corresponding to geographically

separated populations (Singh 2017). These findings highlight the impact of habitat fragmentation and anthropogenic pressures on population connectivity and genetic exchange. The Asiatic lion (*Panthera leo persica*), restricted to the Gir Forest in Gujarat, exhibits extremely low genetic diversity due to a severe historical bottleneck. Genetic studies using microsatellite markers have shown that the population is highly inbred, making it vulnerable to diseases and reducing its capacity to adapt to environmental changes. Efforts to establish new populations outside Gir are critical for enhancing the genetic diversity and ensuring the long-term survival of this species (Nimbkar et al. 2008). The Indian rhinoceros (*Rhinoceros unicornis*) has also been the focus of genetic studies, particularly in Assam's Kaziranga National Park, where most of the world's remaining population resides. Genetic assessments using mitochondrial DNA and microsatellites indicate low levels of genetic diversity, primarily due to the population's confinement to a few isolated habitats. This low genetic variation raises concerns about the species' ability to adapt to future environmental changes and stresses the need for habitat connectivity to promote gene flow between fragmented populations. In the case of smaller carnivores such as the leopard (*Panthera pardus*), genetic studies across India have shown varying levels of genetic diversity and structure depending on the degree of habitat fragmentation and human pressure (Bhatt et al. 2020). Populations in human-dominated landscapes exhibit reduced genetic diversity and increased isolation, which may lead to inbreeding and loss of genetic fitness over time. For other taxa, such as the Himalayan tahr (*Hemitragus jemlahicus*) and the Nilgiritahr (*Nilgiritragus hylocrius*), genetic studies have provided insights into their population structure and historical demographic changes. These studies reveal that high-altitude species often exhibit unique genetic adaptations to their harsh environments but may suffer from low genetic diversity due to naturally small population sizes and limited gene flow.

3.2 Genetic Structure and Population Dynamics in Fragmented Habitats

Habitat fragmentation is one of the primary threats to the genetic integrity of wildlife populations in India (Keyghobadi 2007). Fragmentation reduces habitat size, isolates populations, and disrupts natural gene flow, leading to genetic drift and inbreeding. For

example, studies on the Indian wolf (*Canis lupus pallipes*) have shown that populations in central and western India are highly fragmented and exhibit significant genetic differentiation, suggesting restricted gene flow between isolated groups. These fragmented populations are at high risk of inbreeding and local extinction, emphasizing the need for connectivity corridors to facilitate dispersal and gene exchange (Baguette et al. 2013). In forest-dwelling species such as the lion-tailed macaque (*Macaca silenus*), genetic analyses have revealed that small, isolated populations in the Western Ghats show significant genetic structuring and reduced genetic diversity. This is primarily due to the fragmentation of rainforest habitats, which has disrupted the macaques' social structure and breeding patterns, leading to increased genetic differentiation among populations. The Asian elephant (*Elephas maximus*) in southern India is experiencing severe habitat fragmentation, which has resulted in isolated populations with limited genetic exchange. Genetic studies using mitochondrial DNA have identified distinct maternal lineages within these fragmented populations, indicating historical separation and reduced female-mediated gene flow (Crochet et al. 2003). Such genetic isolation is a significant conservation concern because it limits the potential for genetic rescue and adaptive evolution in response to environmental changes. Genetic studies on amphibians and reptiles, which are highly sensitive to habitat changes, have also shown the detrimental effects of fragmentation. For instance, the endangered golden frog (*Indiranagundia*) of the Western Ghats has been found to have low genetic diversity and a high degree of genetic structuring, likely due to habitat fragmentation and limited dispersal capabilities. This genetic isolation can lead to inbreeding depression and reduced adaptive potential, making the species highly vulnerable to extinction.

3.3 Influence of Genetic Diversity on Species Adaptation and Survival

Genetic diversity is a critical factor influencing the adaptability and long-term survival of species, particularly in the face of environmental changes such as climate shifts, habitat loss, and emerging diseases (Pauls et al. 2013). Populations with high genetic diversity are better equipped to evolve in response to changing conditions, as they possess a wider range of alleles that may confer adaptive advantages. Populations with low genetic diversity are more likely to suffer

from reduced fitness, increased susceptibility to diseases, and an inability to adapt to new environmental pressures. In India, the importance of genetic diversity for species adaptation has been demonstrated in several studies. For example, research on the snow leopard (*Panthera uncia*) in the high-altitude regions of the Himalayas has shown that populations with higher genetic diversity are better able to cope with the harsh environmental conditions of their habitat. Genetic diversity in snow leopards has been linked to variations in physiological traits that enhance their ability to survive in cold, low-oxygen environments. Studies on the critically endangered Ganges river dolphin (*Platanista gangeticaganetica*) have highlighted the role of genetic diversity in the species' resilience to habitat degradation and

pollution (Sinha and Kannan 2014). Populations with greater genetic diversity exhibit higher levels of reproductive success and better health indicators, suggesting that maintaining genetic variability is crucial for the species' survival in the heavily polluted and fragmented riverine habitats of the Ganges and Brahmaputra. Genetic diversity also plays a significant role in the adaptation of species to climate change. In the Western Ghats, populations of endemic frogs such as the *Raorchestes* species have shown genetic adaptations to local microclimatic conditions, which are critical for their survival as the region experiences shifts in temperature and precipitation patterns. Loss of genetic diversity in these populations could reduce their ability to adapt to changing climatic conditions, leading to localized extinctions (Allentoft and O'Brien 2010).

Table 1. Current status of genetic diversity studies on key Indian wildlife species

Species	Genetic Studies Conducted	Genetic Diversity Status	Research Gaps	Conservation Implications
Bengal Tiger	Extensive genome studies and population genetics	Moderate to High in specific regions	Limited samples from Central and Eastern India	Insights for habitat connectivity and managing inbreeding
Asian Elephant	Mitochondrial DNA and microsatellite analysis	Moderate	Few studies on population structure in Northeast India	Understanding corridors and reducing human-elephant conflict
Indian Rhino	Limited genetic studies, primarily microsatellite	Low	Lack of studies on genetic diversity across habitats	Critical for managing genetic bottlenecks in fragmented areas
Asiatic Lion	Detailed genome sequencing	Extremely Low	Studies needed on disease susceptibility	Helps in planning translocation and genetic rescue initiatives
Snow Leopard	Population genetics with mitochondrial markers	Moderate to High in fragmented habitats	Limited data on cross-border populations	Guides transboundary conservation and habitat management
Nilgiri Tahr	Limited microsatellite studies	Low to Moderate	Insufficient data on genetic diversity in isolated groups	Aids in understanding isolation effects and habitat fragmentation
Ganges River Dolphin	Mitochondrial DNA and microsatellite studies	Low due to habitat fragmentation	Lack of longitudinal studies on population trends	Supports conservation of riverine corridors and pollution control
Indian Wolf	Limited genetic analysis, few mtDNA studies	Moderate	Incomplete understanding of genetic structure	Helps assess genetic distinctness and inform regional conservation
Indian Leopard	Fragmented studies across regions	Moderate to High in certain areas	Need for large-scale genetic mapping	Important for understanding adaptability in human-dominated landscapes
Red Panda	Microsatellite and mitochondrial DNA studies	Moderate to Low	Limited sampling across range	Contributes to habitat conservation and understanding of genetic drift

Source: Singh 2017, Nimbkar et al. 2008, Baguette et al. 2013

4. EVOLUTIONARY PROCESSES IN INDIAN WILDLIFE

4.1 Insights from Phylogenetic and Phylogeographic Studies in Indian Fauna

Phylogenetic and phylogeographic studies provide critical insights into the evolutionary history and biogeographic patterns of Indian wildlife. Such research has helped uncover cryptic species, identify evolutionary lineages, and understand how historical events have shaped the genetic structure of different taxa. For example, studies on the Asian elephant (*Elephas maximus*) using mitochondrial DNA markers have revealed that Indian elephants are genetically distinct from their Sri Lankan and Southeast Asian counterparts, with deep phylogeographic splits corresponding to historical population separations. This suggests that the Indian subcontinent served as a major refugium during glacial periods, contributing to the divergence of elephant populations (Vidya 2016). Phylogenetic studies on the Bengal tiger (*Panthera tigris tigris*) have shown that populations in India are genetically distinct from those in Southeast Asia, with unique haplotypes that reflect a long evolutionary history of isolation and adaptation to the diverse habitats found across the subcontinent. Recent phylogeographic analyses have identified at least three distinct genetic clusters within India, corresponding to the Shivalik Hills, Central India, and the Western Ghats, which align with major geographic and ecological barriers. These findings highlight the importance of conserving region-specific genetic diversity to maintain the evolutionary potential of tiger populations. In the case of small mammals, such as the Nilgiri marten (*Martes gwatkinsii*) and the Nicobar treeshrew (*Tupaia nicobarica*), phylogeographic studies have revealed that these species show significant genetic differentiation between populations in different regions, reflecting the impact of geographical isolation and habitat fragmentation (Joshi et al. 2018). For the Nicobar treeshrew, which is endemic to the Nicobar Islands, phylogenetic analyses indicate that the species diverged from its mainland relatives approximately 2 million years ago, likely due to rising sea levels that isolated the islands from the mainland. This phylogenetic isolation has led to the evolution of unique morphological and behavioral traits adapted to the island environment.

4.2 Mechanisms of Speciation: Geographic Isolation, Hybridization, and Adaptive Divergence

Geographic isolation, hybridization, and adaptive divergence are the primary mechanisms driving speciation in Indian wildlife. Geographic isolation is particularly prominent in species inhabiting the highly fragmented landscapes of the Western Ghats and the Eastern Himalayas. In the Western Ghats, for example, deep riverine valleys and varying altitudinal gradients create natural barriers that restrict gene flow between populations, leading to allopatric speciation (Oliveira et al. 2018). This has resulted in the formation of several distinct lineages of frogs, such as the *Raorchestes* genus, which contains multiple cryptic species adapted to specific microhabitats within the Ghats. Hybridization has also played a significant role in the evolution of Indian fauna. In the Indian subcontinent, hybrid zones have been documented in several taxa, including large mammals such as deer and wild cats. For instance, studies on the sambar deer (*Rusa unicolor*) and the Indian muntjac (*Muntiacus muntjak*) have revealed that hybridization between these species occurs in areas where their ranges overlap, leading to the emergence of hybrid individuals with unique genetic combinations (Ali et al. 2021). Similarly, hybridization between the Bengal tiger and the Indochinese tiger (*Panthera tigris corbetti*) has been suggested in regions close to India's northeastern borders, where the two subspecies historically overlapped. Hybridization can result in increased genetic diversity and novel traits, but it can also lead to genetic swamping and loss of distinct lineages if not carefully managed. Adaptive divergence, wherein populations evolve traits suited to their specific environments, is a key driver of speciation in ecologically diverse landscapes such as the Himalayas and the Western Ghats. The Himalayan Monal (*Lophophorus impejanus*), for example, exhibits marked differences in plumage color and body size across its altitudinal range, reflecting adaptations to varying climatic conditions (Gupta 2020). These adaptations may have been driven by both natural selection and sexual selection, leading to reproductive isolation between populations at different elevations. Similarly, the leaf-nosed bat (*Hipposideros speoris*) exhibits significant morphological and echolocation call divergence between populations in different parts of India, suggesting local adaptations to varying cave environments and prey availability.

4.3 Evolutionary Adaptations in Morphology and Behavior Specific to Indian Wildlife

Indian wildlife has evolved a variety of morphological and behavioral adaptations in response to the diverse and often challenging environments found across the subcontinent. In the high-altitude ecosystems of the Himalayas, several species have developed specialized adaptations to cope with extreme cold, low oxygen levels, and rugged terrain. The snow leopard (*Panthera uncia*), for instance, has a stocky build, shortened limbs, and thick fur to minimize heat loss, while its large nasal cavities help warm the frigid air before it reaches the lungs (Carwardine 2008). Behavioral adaptations such as solitary hunting and territorial marking also play crucial roles in minimizing intra-species competition in the sparse, resource-limited alpine environment. In the deserts of Rajasthan, species like the Indian desert fox (*Vulpes vulpes pusilla*) and the Great Indian bustard (*Ardeotisnigriceps*) have evolved unique adaptations to cope with extreme heat and scarce water resources. The desert fox has a pale coat color that reflects sunlight, and it is known to conserve water by producing highly concentrated urine. The Great Indian bustard, on the other hand, exhibits behavioral thermoregulation, including seeking shade and panting, to avoid overheating during the hottest parts of the day (Cabello-Vergel et al. 2021). In the rainforests of the Western Ghats, morphological adaptations such as elongated limbs and prehensile tails are common in arboreal species like the lion-tailed macaque (*Macaca silenus*) and the Malabar giant squirrel (*Ratufa indica*). These adaptations allow for efficient locomotion through the dense canopy, where competition for space and resources is intense. Behavioral adaptations, such as complex vocal communication in the lion-tailed macaque, have evolved to facilitate social interactions and coordinate group movements through the dense forest (Palombit 1992). Aquatic and semi-aquatic adaptations are also prevalent in species inhabiting the mangrove ecosystems of the Sundarbans. The Bengal tiger in this region has developed a unique tolerance for saline water and is known to swim between the mangrove islands in search of prey. This behavioral adaptation is coupled with morphological changes such as webbing between the toes, which aids in swimming.

5. IMPACT OF HUMAN ACTIVITIES ON GENETIC DIVERSITY

5.1 Effects of Habitat Fragmentation, Deforestation, and Poaching on Genetic Variability

Human activities, particularly habitat fragmentation, deforestation, and poaching, have significantly affected the genetic variability of wildlife populations across India (De et al. 2021). Habitat fragmentation is one of the most severe threats, as it reduces the size and connectivity of wildlife habitats, leading to isolated populations that are vulnerable to genetic erosion. The conversion of forests into agricultural land and urban areas, combined with infrastructure development such as roads and railways, has disrupted the natural habitats of many species, including large mammals such as tigers (*Panthera tigris*) and elephants (*Elephas maximus*). Studies have shown that fragmentation in the Western Ghats has resulted in highly structured populations of the lion-tailed macaque (*Macaca silenus*), reducing gene flow between groups and increasing the risk of inbreeding (Ram et al. 2015). Deforestation in regions such as the Northeast Himalayas and Central India has similarly fragmented habitats, leading to genetic isolation of species such as the Asiatic black bear (*Ursus thibetanus*) and the clouded leopard (*Neofelis nebulosa*). Genetic studies have confirmed that the populations of these species are now confined to small, isolated patches with limited opportunities for genetic exchange, resulting in a decline in genetic diversity. In amphibians, which are particularly sensitive to habitat changes, habitat fragmentation in the Western Ghats has led to the emergence of genetically distinct populations of frogs, such as those in the *Raorchestes* and *Micrixalus* genera, which now face a high risk of genetic bottlenecks and extinction (Abraham 2016). Poaching, which is primarily driven by the illegal wildlife trade, has exacerbated the decline in genetic variability in several Indian species. The poaching of large carnivores such as tigers and leopards for their pelts and body parts has led to a sharp reduction in their population sizes, further limiting their genetic pools. Genetic analyses of tiger populations have revealed that in areas with high poaching pressure, such as parts of the Terai Arc Landscape, genetic diversity is markedly lower compared to protected areas, indicating that poaching not only reduces population numbers but also depletes

genetic variability (Tolley et al. 2019). Similar effects have been observed in the Indian rhinoceros (*Rhinoceros unicornis*), where poaching has decimated populations in areas outside protected zones, leading to reduced genetic variability and heightened vulnerability to diseases.

5.2 Consequences of Reduced Gene Flow, Population Bottlenecks, and Inbreeding

Habitat fragmentation and poaching have severe genetic consequences, primarily by reducing gene flow between wildlife populations. Reduced gene flow increases genetic drift and inbreeding, which can result in the loss of genetic diversity and an increased risk of inbreeding depression. In small and isolated populations, inbreeding depression can manifest as reduced reproductive success, increased susceptibility to diseases, and lower adaptive potential, ultimately threatening population viability (Lacy 1997). For instance, the isolated population of the Asiatic lion (*Panthera leo persica*) in the Gir Forest shows very low genetic diversity and high levels of inbreeding, making the species susceptible to diseases such as the canine distemper virus. Genetic studies have suggested that this population is experiencing genetic erosion due to its small size and long-term isolation, with little potential for genetic recovery unless gene flow is restored through translocation or the establishment of new populations. The Indian wolf (*Canis lupus pallipes*), which inhabits fragmented grasslands in Central and Western India, is facing a severe genetic bottleneck due to habitat loss and persecution (Pandit 2007). Genetic studies have shown that these wolf populations are genetically depauperate, exhibiting very low genetic variability and high levels of inbreeding. The lack of genetic diversity limits their ability to adapt to environmental changes and may contribute to behavioral anomalies, such as increased human-wildlife conflict, further threatening their survival. Population bottlenecks, caused by sharp reductions in population size, have also been documented in several Indian wildlife species. For instance, genetic analyses of the great Indian bustard (*Ardeotis nigriceps*), which has suffered a catastrophic decline due to habitat destruction and hunting, indicate that the species has undergone a severe bottleneck, resulting in extremely low genetic diversity. Such bottlenecks not only reduce overall genetic variability but also increase the likelihood of accumulating

deleterious mutations, which can have long-term impacts on population health and adaptability (Kardos et al. 2021).

5.3 Impact of Climate Change on Genetic Diversity and Evolutionary Potential

Climate change poses an emerging threat to the genetic diversity and evolutionary potential of Indian wildlife. As climate patterns shift, many species are experiencing changes in their habitats and resource availability, which can disrupt local adaptations and lead to population declines. In India, climate change is expected to alter the distribution of critical habitats, particularly in biodiversity hotspots such as the Western Ghats and the Himalayas. Species that are highly specialized or have narrow ecological niches, such as the Nilgiritahr (*Nilgiritragus hylocrius*) and the Himalayan Monal (*Lophophorus impejanus*), may be particularly vulnerable to these changes, as they may not be able to adapt quickly enough to shifting environmental conditions (Smit and Wandel 2006). Genetic studies have shown that climate change can reduce genetic diversity by fragmenting populations and altering migration patterns. For example, the snow leopard (*Panthera uncia*) is likely to experience a decline in suitable habitat as the tree line shifts upward in response to warming temperatures, resulting in smaller and more isolated populations. This habitat loss is predicted to reduce gene flow between populations, leading to increased genetic differentiation and reduced genetic diversity. Similarly, in the Western Ghats, climate-induced shifts in rainfall patterns are expected to alter the distribution of endemic frog species, which are already facing genetic fragmentation due to habitat loss (Krishnaswamy et al.). As habitats become increasingly fragmented, the genetic isolation of these frog populations will likely increase, reducing their ability to adapt to further environmental changes. In marine and coastal species, climate change is causing shifts in sea temperature and salinity, which can impact genetic diversity by altering breeding and migration patterns. For instance, studies on the olive ridley turtle (*Lepidochelys olivacea*) along the Indian coastline have shown that rising sea levels and temperature changes are affecting nesting sites, leading to altered sex ratios and potential changes in population structure. These changes can disrupt the genetic balance of populations and reduce genetic diversity, impacting the species' long-term survival.

6. CONSERVATION STRATEGIES

6.1 Importance of Maintaining Genetic Diversity for Long-term Species Viability

Genetic diversity is a critical component of biodiversity and is essential for the long-term survival and evolutionary potential of wildlife species (DeWoody et al. 2021). High levels of genetic diversity within a population enhance its capacity to adapt to changing environmental conditions, resist diseases, and avoid the deleterious effects of inbreeding. Low genetic diversity can lead to inbreeding depression, reduced fitness, and a decreased ability to respond to environmental challenges, ultimately increasing the risk of extinction. In India, many wildlife species are experiencing significant declines in genetic diversity due to habitat fragmentation, poaching, and other anthropogenic pressures. For example, the Asiatic lion (*Panthera leo persica*) is genetically depauperate due to a severe bottleneck event in the early 20th century, making it highly vulnerable to diseases and environmental changes (Banerjee and Jhala 2012). Similarly, the endangered Great Indian bustard (*Ardeotis nigriceps*) has extremely low genetic diversity, which reduces its capacity to adapt to habitat modifications and climatic fluctuations. Thus, maintaining and enhancing genetic diversity is paramount for the viability of these and other threatened species.

6.2 Strategies for Managing Small and Isolated Populations Using Genetic Information

Conservation strategies aimed at managing small and isolated populations must prioritize genetic considerations to mitigate inbreeding depression and preserve evolutionary potential. One effective approach is genetic rescue, where individuals from genetically diverse populations are introduced into small, inbred populations to increase genetic variability and reduce inbreeding. For instance, translocation of tigers from genetically diverse populations to small, isolated reserves has been proposed as a strategy to increase genetic diversity and improve the long-term viability of these populations in Central India (Kolipakam et al. 2019). Another strategy is the establishment of habitat corridors to connect fragmented

populations and facilitate gene flow, thereby reducing genetic isolation. In India, initiatives such as the "Green Corridors" project aim to connect isolated populations of elephants and tigers by restoring habitat linkages between critical wildlife reserves. Such corridors can significantly enhance genetic exchange, reducing the risk of inbreeding and maintaining genetic diversity across the landscape (Christie and Knowles 2015).

Captive breeding and reintroduction programs are also employed for species with critically low populations, such as the Pygmy hog (*Porcula salvania*) and the Gharial (*Gavialis gangeticus*). Genetic management in captive populations involves minimizing relatedness and maintaining a representative gene pool, ensuring that reintroduced populations have the genetic variability necessary for adaptation and survival. In the case of the critically endangered vultures (*Gyps* spp.) in India, captive breeding programs incorporate genetic screening to prevent inbreeding and maximize genetic diversity (Burke 2018).

6.3 Integration of Genetic Data into Indian Wildlife Conservation Policies and Practices

The integration of genetic data into conservation policies and management practices is crucial for the effective conservation of Indian wildlife. Genetic information can be used to identify Evolutionarily Significant Units (ESUs) and Management Units (MUs), which are genetically distinct populations that require targeted management. For example, the identification of distinct genetic lineages in the Himalayan and Western Ghats populations of the Nilgiritahr (*Nilgiritragus hylocrius*) has informed region-specific conservation actions. Incorporating genetic data into species recovery plans can also aid in prioritizing populations for conservation based on their genetic health and uniqueness (Boettcher et al. 2010). The Indian government's Project Tiger has recently incorporated genetic monitoring as part of its management strategy to ensure that isolated tiger populations retain sufficient genetic diversity. Additionally, the use of genetic information to combat illegal wildlife trade, through DNA-based forensic tools, has been successfully applied in the prosecution of poachers and the prevention of wildlife trafficking.

7. TECHNOLOGICAL ADVANCES IN WILDLIFE GENETICS

7.1 Role of Genomic Tools, Non-invasive Sampling Techniques, and Bioinformatics in Wildlife Research

Recent technological advances have revolutionized wildlife genetics, enabling more precise and comprehensive analyses of genetic diversity and structure (Table 2) (DeSalle and Amato 2009). Genomic tools such as whole-genome sequencing and single nucleotide polymorphism (SNP) genotyping provide high-resolution insights into the genetic health, adaptive potential, and evolutionary history of wildlife populations. These tools have been used to assess the genomic variation in Indian species such as the Bengal tiger and the Asian elephant, revealing complex patterns of genetic differentiation and inbreeding. Non-invasive sampling techniques such as the use of feces, hair, and environmental DNA (eDNA) have greatly facilitated genetic studies in elusive and endangered species. In India, non-invasive sampling has been successfully applied in genetic monitoring of the snow leopard in the Himalayas and the Asiatic lion in the Gir Forest. These methods reduce the need for capturing or disturbing animals, making them ideal for studying rare and cryptic species. Bioinformatics tools are essential for managing and analyzing large genomic datasets, enabling researchers to identify genetic markers, assess genetic structure, and predict population trends (Moore et al. 2010). Tools such as STRUCTURE and ADMIXTURE have been used to detect genetic structuring in fragmented populations of the Indian leopard (*Panthera pardus fusca*) and the Indian wild dog (*Cuon alpinus*). The use of bioinformatics in conservation genomics allows for more accurate assessments of population viability and guides conservation strategies.

7.2 Potential of New Technologies (e.g., CRISPR) in Genetic Conservation and Management

The advent of CRISPR-Cas9 and other gene-editing technologies holds transformative potential for wildlife conservation (Menchaca et al. 2020). These technologies can be used to edit harmful mutations in small, inbred populations, thus preventing the expression of deleterious traits. In theory, CRISPR could be employed to

enhance disease resistance in genetically depauperate populations of Asiatic lions or increase the reproductive success of the Great Indian bustard by correcting genetic defects. Gene drives, which promote the inheritance of specific genetic traits, could be used to control invasive species that threaten native Indian wildlife. For example, gene drives could be used to reduce populations of the invasive common myna (*Acridotheres tristis*), which competes with native bird species in several Indian ecosystems (Garrock et al. 2014).

8. FUTURE AND RESEARCH NEEDS

8.1 Emphasis on Long-term Genetic Monitoring and the Establishment of Genetic Databases

Long-term genetic monitoring is essential for tracking changes in genetic diversity and population structure over time. Establishing national genetic databases for key species, such as the Bengal tiger, Asiatic lion, and snow leopard, would facilitate the monitoring of genetic health and support conservation decision-making. These databases can also serve as repositories for genetic information, aiding in the identification of individuals in forensic applications.

8.2 Need for Interdisciplinary Approaches Combining Genetics, Ecology, and Conservation

Effective conservation strategies require an interdisciplinary approach that integrates genetics, ecology, and social sciences (Bennett et al. 2017). Combining genetic data with ecological information such as habitat suitability and population dynamics can provide a holistic view of species' conservation needs. In India, integrating traditional ecological knowledge from local communities with genetic research has proven effective in managing species such as the snow leopard and the Indian wild dog.

8.3 Strategies for Enhancing Community Involvement and Policy Development

Engaging local communities in genetic monitoring and conservation can significantly enhance the success of conservation programs. Community-based initiatives, such as the snow leopard conservation program in Ladakh, have incorporated local herders in monitoring and

protecting wildlife, leading to improved outcomes for both people and wildlife (Jackson and Lama 2016). Strengthening community involvement and integrating genetic information into conservation policies will be crucial for the future of Indian wildlife conservation.

Table 2. Technological advances in wildlife genetics

Technology	Description	Applications in Wildlife Genetics	Advantages	Challenges
Next-Generation Sequencing (NGS)	High-throughput sequencing method allowing rapid sequencing of entire genomes	Enables whole-genome sequencing, population genomics, and evolutionary studies	High accuracy, large data output, cost-effective	Requires advanced infrastructure and bioinformatics expertise
CRISPR-Cas9 Gene Editing	A gene-editing tool that allows precise modifications in DNA sequences	Potential applications in studying gene functions, disease resistance	High precision, can target specific genes	Ethical concerns, limited application in wildlife conservation
Environmental DNA (eDNA)	DNA collected from environmental samples (soil, water, etc.)	Detects presence/absence of species in a habitat, studies on biodiversity	Non-invasive, sensitive to low-abundance species	DNA degradation, contamination issues
Microsatellite Markers	Repeated DNA sequences used to assess genetic diversity and structure	Useful for studying population structure, kinship, and inbreeding levels	Effective for fine-scale genetic studies	Limited resolution for genome-wide studies
Single Nucleotide Polymorphisms (SNPs)	DNA sequence variations at a single base pair	Population genetics, adaptive genetic studies	High resolution, informative for adaptive variation	Requires large sample sizes and data analysis resources
Mitochondrial DNA (mtDNA) Analysis	Analysis of DNA in mitochondria, often used in evolutionary studies	Traces maternal lineage, useful for phylogenetics and species identification	Highly conserved, useful for ancient DNA studies	Limited to maternal lineage, lower genetic diversity
Genome-Wide Association Studies (GWAS)	Identifies associations between genetic variants and traits	Studies genetic basis of traits like disease resistance, adaptation	Identifies adaptive traits, helps in conservation planning	Requires large sample sizes, complex statistical analysis
RAD Sequencing (Restriction site-associated DNA)	Sequencing technique that identifies genetic variants at specific locations	Population structure analysis, phylogeography, and adaptive studies	Cost-effective alternative to whole-genome sequencing	Limited to specific parts of the genome
Genotyping-by-Sequencing (GBS)	Simplifies genome-wide genotyping for multiple individuals	Enables population genetics studies in non-model species	High throughput, cost-effective	Requires careful optimization of protocols
Ancient DNA Analysis	Study of DNA extracted from old or degraded samples	Helps understand historical population dynamics, extinction events	Provides historical insights, unique evolutionary data	DNA degradation, contamination risks
RNA Sequencing (RNA-Seq)	Sequencing of RNA to study gene	Studies gene expression profiles	Identifies active genes, can study	Requires fresh or well-

Technology	Description	Applications in Wildlife Genetics	Advantages	Challenges
	expression	related to stress, adaptation, and disease	environmental impacts	preserved samples
DNA Barcoding	Uses a short genetic marker from a standard part of the genome for species ID	Species identification, biodiversity assessment	Fast, cost-effective, useful for unknown samples	Limited to species-level identification
Whole Genome Sequencing (WGS)	Complete sequencing of an organism's genome	Detailed insights into genetic diversity, adaptive evolution	Comprehensive data, useful for conservation genomics	High cost, intensive data analysis
Metabarcoding	Combines DNA barcoding and NGS to assess biodiversity from environmental samples	Community-level biodiversity assessment, diet analysis	High sensitivity, identifies multiple species in a sample	Requires high-quality reference databases
Bioinformatics and Machine Learning	Computational tools for analyzing large genetic datasets	Analyzes complex data, predicts adaptive traits, assists in species distribution modeling	Handles large-scale data, improves predictive accuracy	Requires expertise, high computational power

9. CONCLUSION

maintaining genetic diversity is crucial for the long-term survival and adaptability of Indian wildlife, especially in the face of habitat fragmentation, poaching, and climate change. Genetic diversity enables populations to withstand environmental changes, resist diseases, and avoid inbreeding depression, thus ensuring species viability. Conservation strategies such as genetic rescue, habitat corridors, and integration of genetic data into policy are essential for managing small and isolated populations. Technological advances, including genomic tools and non-invasive sampling techniques, have significantly improved our understanding of wildlife genetics, enabling more effective management. Future conservation efforts should emphasize long-term genetic monitoring, establishment of genetic databases, and interdisciplinary approaches that combine genetics with ecology and local community involvement. As anthropogenic pressures continue to threaten biodiversity, incorporating genetic perspectives into conservation planning will be vital for preserving the evolutionary potential and ecological integrity of India's unique wildlife heritage.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models

(ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Abraham, R. K. (2016). *Convergent patterns suggest parallel processes of insular anuran diversification between oceanic archipelagos of the Southwest Pacific and the sky islands of the continental Western Ghats* (Doctoral dissertation, University of Kansas).
- Ali, N. A. N. G., Abdullah, M. L., Nor, S. A. M., Pau, T. M., Kulaimi, N. A. M., & Naim, D. M. (2021). A review of the genus *Rusa* in the indo-malayan archipelago and conservation efforts. *Saudi Journal of Biological Sciences*, 28(1), 10-26.
- Allentoft, M. E., & O'Brien, J. (2010). Global amphibian declines, loss of genetic diversity and fitness: a review. *Diversity*, 2(1), 47-71.
- Baguette, M., Blanchet, S., Legrand, D., Stevens, V. M., & Turlure, C. (2013). Individual dispersal, landscape connectivity and ecological networks. *Biological reviews*, 88(2), 310-326.

- Banerjee, K., & Jhala, Y. V. (2012). Demographic parameters of endangered Asiatic lions (*Panthera leo persica*) in Gir Forests, India. *Journal of Mammalogy*, 93(6), 1420-1430.
- Bennett, N. J., Roth, R., Klain, S. C., Chan, K., Christie, P., Clark, D. A., ... & Wyborn, C. (2017). Conservation social science: Understanding and integrating human dimensions to improve conservation. *biological conservation*, 205, 93-108.
- Bhatt, S., Biswas, S., Karanth, K., Pandav, B., & Mondol, S. (2020). Genetic analyses reveal population structure and recent decline in leopards (*Panthera pardus fusca*) across the Indian subcontinent. *PeerJ*, 8, e8482.
- Bickford, D., Lohman, D. J., Sodhi, N. S., Ng, P. K., Meier, R., Winker, K., ... & Das, I. (2007). Cryptic species as a window on diversity and conservation. *Trends in ecology & evolution*, 22(3), 148-155.
- Boettcher, P. J., Tixier-Boichard, M., Toro, M. A., Simianer, H., Eding, H., Gandini, G., ... & Globaldiv Consortium. (2010). Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources. *Animal genetics*, 41, 64-77.
- Burke, M. B. (2018). *Population genetics of the bearded vulture* (Doctoral dissertation).
- Cabello-Vergel, J., Soriano-Redondo, A., Villegas, A., Maseró, J. A., Guzmán, J. M. S., & Gutiérrez, J. S. (2021). Urohidrosis as an overlooked cooling mechanism in long-legged birds. *Scientific Reports*, 11(1), 20018.
- Carwardine, M. (2008). *Animal records*. Sterling Publishing Company, Inc..
- Christie, M. R., & Knowles, L. L. (2015). Habitat corridors facilitate genetic resilience irrespective of species dispersal abilities or population sizes. *Evolutionary Applications*, 8(5), 454-463.
- Cox, C. B., Moore, P. D., & Ladle, R. J. (2016). *Biogeography: an ecological and evolutionary approach*. John Wiley & Sons.
- Crochet, P. A., Chen, J. Z., Pons, J. M., Lebreton, J. D., Hebert, P. D., & Bonhomme, F. (2003). Genetic differentiation at nuclear and mitochondrial loci among large white-headed gulls: sex-biased interspecific gene flow?. *Evolution*, 57(12), 2865-2878.
- De, R., Sharma, R., Davidar, P., Arumugam, N., Sedhupathy, A., Puyravaud, J. P., ... & Goyal, S. P. (2021). Pan-India population genetics signifies the importance of habitat connectivity for the wild Asian elephant conservation. *Global Ecology and Conservation*, 32, e01888.
- DeSalle, R., & Amato, G. (2009). The expansion of conservation genetics. *Conservation genetics in the age of genomics*, 1-24.
- DeWoody, J. A., Harder, A. M., Mathur, S., & Willoughby, J. R. (2021). The long-standing significance of genetic diversity in conservation. *Molecular ecology*, 30(17), 4147-4154.
- Forrest, J. L., Wikramanayake, E., Shrestha, R., Areendran, G., Gyeltshen, K., Maheshwari, A., ... & Thapa, K. (2012). Conservation and climate change: Assessing the vulnerability of snow leopard habitat to treeline shift in the Himalaya. *Biological Conservation*, 150(1), 129-135.
- Ghildiyal, K., Nayak, S. S., Rajawat, D., Sharma, A., Chhotaray, S., Bhushan, B., ... & Panigrahi, M. (2023). Genomic insights into the conservation of wild and domestic animal diversity: a review. *Gene*, 886, 147719.
- Grarock, K., Tidemann, C. R., Wood, J. T., & Lindenmayer, D. B. (2014). Understanding basic species population dynamics for effective control: a case study on community-led culling of the common myna (*Acridotheres tristis*). *Biological Invasions*, 16, 1427-1440.
- Gupta, G. (2020). *Data and conservation of Himalayan Galliformes* (Doctoral dissertation, Newcastle University).
- Hoban, S., Archer, F. I., Bertola, L. D., Bragg, J. G., Breed, M. F., Bruford, M. W., ... & Hunter, M. E. (2022). Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews*, 97(4), 1511-1538.
- Hrdina, A., & Romportl, D. (2017). Evaluating global biodiversity hotspots—Very rich and even more endangered. *Journal of Landscape Ecology*, 10(1), 108-115.
- Jackson, R. M., & Lama, W. B. (2016). The role of mountain communities in snow leopard conservation. In *Snow leopards* (pp. 139-149). Academic Press.
- Jamal, S. (2020). 10 Biogeographical Classification of India.
- Joshi, B. D., Matura, R., MA, P., De, R., Pandav, B., Sharma, V., ... & Goyal, S. P. (2018). Palghat gap reveals presence of two diverged populations of Nilgiri tahr

- (Nilgiritragus hylocrius) in Western Ghats, India. *Mitochondrial DNA Part B*, 3(1), 245-249.
- Kandel, P., Thapa, I., Chettri, N., Pradhan, R., & Sharma, E. (2018). Birds of the Kangchenjunga Landscape, the Eastern Himalaya: status, threats and implications for conservation. *Avian Research*, 9, 1-13.
- Kardos, M., Armstrong, E. E., Fitzpatrick, S. W., Hauser, S., Hedrick, P. W., Miller, J. M., ... & Funk, W. C. (2021). The crucial role of genome-wide genetic variation in conservation. *Proceedings of the National Academy of Sciences*, 118(48), e2104642118.
- Keyghobadi, N. (2007). The genetic implications of habitat fragmentation for animals. *Canadian Journal of Zoology*, 85(10), 1049-1064.
- Kolipakam, V., Singh, S., Pant, B., Qureshi, Q., & Jhala, Y. V. (2019). Genetic structure of tigers (*Panthera tigris tigris*) in India and its implications for conservation. *Global Ecology and Conservation*, 20, e00710.
- Krishnaswamy, J., Kelkar, N., Aravind, N. A., & Vaidyanathan, S. Climate Change and Aquatic Biodiversity.
- Lacy, R. C. (1997). Importance of genetic variation to the viability of mammalian populations. *Journal of mammalogy*, 78(2), 320-335.
- Menchaca, A., Dos Santos-Neto, P. C., Mulet, A. P., & Crispo, M. (2020). CRISPR in livestock: From editing to printing. *Theriogenology*, 150, 247-254.
- Moore, J. H., Asselbergs, F. W., & Williams, S. M. (2010). Bioinformatics challenges for genome-wide association studies. *Bioinformatics*, 26(4), 445-455.
- Nimbkar, C., Gibson, J., Okeyo, M., Boettcher, P., & Sölkner, J. (2008). Sustainable use and genetic improvement. *Animal Genetic Resources/Resources génétiques animales/Recursos genéticos animales*, 42, 49-65.
- Oliveira, E. F., Martinez, P. A., São-Pedro, V. A., Gehara, M., Burbrink, F. T., Mesquita, D. O., ... & Costa, G. C. (2018). Climatic suitability, isolation by distance and river resistance explain genetic variation in a Brazilian whiptail lizard. *Heredity*, 120(3), 251-265.
- Palombit, R. A. (1992). A preliminary study of vocal communication in wild long-tailed macaques (*Macaca fascicularis*). I. Vocal repertoire and call emission. *International Journal of Primatology*, 13, 143-182.
- Pandit, M. W. (2007). *You Deserve, We Conserve: A Biotechnological Approach to Wildlife Conservation*. IK International Pvt Ltd.
- Pauls, S. U., Nowak, C., Bálint, M., & Pfenninger, M. (2013). The impact of global climate change on genetic diversity within populations and species. *Molecular ecology*, 22(4), 925-946.
- Pullaiah, T. (2018). Biodiversity in India. In *Global Biodiversity* (pp. 109-144). Apple Academic Press.
- Ram, M. S., Marne, M., Gaur, A., Kumara, H. N., Singh, M., Kumar, A., & Umapathy, G. (2015). Pre-historic and recent vicariance events shape genetic structure and diversity in endangered lion-tailed macaque in the Western Ghats: Implications for conservation. *PLoS one*, 10(11), e0142597.
- Reddy, C. S., Joseph, A., Abraham, G. A., & Sabu, M. M. (2021). Patterns of animal and plant discoveries, distribution and endemism in India—implications on the effectiveness of the protected area network. *Environmental Monitoring and Assessment*, 193(2), 62.
- Riddle, B. R. (2019). Genetic signatures of historical and contemporary responses to climate change. In *Biodiversity and climate change: transforming the biosphere* (pp. 66-76). Yale University Press.
- Rodriguez-Iturbe, I., Muneeppeerakul, R., Bertuzzo, E., Levin, S. A., & Rinaldo, A. (2009). River networks as ecological corridors: A complex systems perspective for integrating hydrologic, geomorphologic, and ecologic dynamics. *Water Resources Research*, 45(1).
- Sharma, S. K., Rana, J. C., & Chopra, V. L. (2013). Biodiversity (plants/animals/microbes/birds): status, endemism, threatened species. *Climate change and its ecological implications for the Western Himalaya*, 180-216.
- Singh, S. K. (2017). Conservation genetics of the Bengal tiger (*Panthera tigris tigris*) in India.
- Singh, S. K. (2017). Conservation genetics of the Bengal tiger (*Panthera tigris tigris*) in India.
- Sinha, R. K., & Kannan, K. (2014). Ganges River dolphin: an overview of biology, ecology, and conservation status in India. *Ambio*, 43, 1029-1046.
- Smit, B., & Wandel, J. (2006). Adaptation, adaptive capacity and vulnerability. *Global environmental change*, 16(3), 282-292.

- Tolley, K. A., Da Silva, J. M., Jansen van Vuuren, B., Bishop, J., Dalton, D., Du Plessis, M., ... & Suleman, E. (2019). South African National Biodiversity Assessment 2019: Technical Report Volume 7: Genetic Diversity.
- Vidya, T. N. C. (2016). Evolutionary history and population genetic structure of Asian elephants in India. *Indian Journal of History of Science*, 51(2), 391-405.
- Vijayakumar, S. P., Menezes, R. C., Jayarajan, A., & Shanker, K. (2016). Glaciations, gradients, and geography: multiple drivers of diversification of bush frogs in the Western Ghats Escarpment. *Proceedings of the Royal Society B: Biological Sciences*, 283(1836), 20161011.
- Zschokke, S. (2016). Genetic structure of the Wild Populations of the Indian Rhinoceros (*Rhinoceros unicornis*). *Indian Journal of History of Science*, 51(2), 380-389.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2024): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:

<https://prh.mbimph.com/review-history/4231>