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Popular Article

## Understanding landscape genomics and its significance in genomic research

Ravina<sup>1</sup>, Chandana Sree Chinnareddyvari<sup>1</sup>, Pallavi Rathi<sup>1</sup>, Dharamshaw C A<sup>1</sup>, Ymberzal Koul<sup>1</sup>

Division of Animal Genetics and Breeding, ICAR-NDRI, Karnal, Haryana  
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### Introduction

Landscape genomics is a branch of genomics that utilises both environmental and genetic data for making conservation decisions by providing information and insights into how landscapes shape biodiversity. This cutting-edge field combines genomics, ecology, and geography to unravel the intricate relationship between an organism's genetic makeup and its environment. To study landscape genomics in livestock, it is essential to record the exact location of sampling and the genotyping of the required number of animals using molecular markers. Using the genetic data, ecological and geographical information (climate and topography), the effect of adaptive and non-adaptive processes on genomic variation and the effects of environmental variables on adaptive differentiation at the genomic level can be studied. Local adaptation represents a crucial evolutionary mechanism enabling plants to thrive more effectively in their native habitat as opposed to non-native environments. This phenomenon contributes to the emergence of species-wide geographic patterns characterized by adaptive genetic variations. The concept of local adaptation suggests the presence of advantageous genetic variations that provide a population in its natural environment with higher fitness compared to any other non-native population in the same environment. Methods in landscape genomics, such as genome-environment association (GEA) have gained popularity in detecting signals of local adaptation. This rise in popularity is attributed to the reduced cost of sequencing and the recent availability of detailed environmental datasets. Despite these advancements, the abundance of data necessitates the development of more efficient tools for analysis.

At the heart of landscape genomics lies the study of genomic variation – the unique



genetic codes that distinguish one organism from another. Genomic variations can be as subtle as a single nucleotide change or as extensive as large-scale structural alterations. The understanding of these genetic nuances forms the cornerstone of landscape genomics. As organisms interact with their environments, they undergo natural selection, a process that favours traits promoting survival and reproduction. Landscape genomics seeks to uncover how environmental factors sculpt the genomes of species over time. From temperature and precipitation to topography and resource availability, each element of the landscape leaves an indelible mark on the genetic makeup of living organisms.

### **I. The Tools of Landscape Genomics**

The advent of next-generation sequencing has revolutionized the field of genomics. This powerful technology enables scientists to rapidly sequence entire genomes, providing a comprehensive view of an organism's genetic landscape. In landscape genomics, this tool allows researchers to identify genetic variations associated with specific environmental conditions, paving the way for a deeper understanding of adaptation and evolution. To analyse the interaction between geographical variables and genetic variations, landscape genomics utilises a high number of molecular markers, like AFLP (amplified fragment length polymorphism), microsatellites, SNPs (single nucleotide polymorphism) and CNVs (copy number variations). Amplified Fragment Length Polymorphism (AFLP) is a molecular biology technique widely employed for the genomic fingerprinting of various organisms, including plants, animals, and microorganisms. This method utilizes a combination of polymerase chain reaction (PCR) and restriction enzyme digestion to selectively amplify specific DNA fragments from a genome. By analysing the resulting patterns of amplified fragments, researchers can gain insights into genetic diversity, population structure, and evolutionary relationships within a species. AFLP has proven valuable in ecological and evolutionary studies, offering a cost-effective and high-throughput approach to explore the intricacies of genetic variation and adaptation in diverse biological systems. Microsatellites, also known as simple sequence repeats (SSRs) or short tandem repeats (STRs), are short, repetitive DNA sequences scattered throughout an organism's genome. These genetic markers consist of repeating units of one to six base pairs, and variations in the number of repeats at a given locus contribute to genetic diversity. Microsatellites are widely employed in genetic research for their polymorphic nature, making them valuable tools for studying population genetics, gene mapping, and forensic applications. Due to their high variability and co-dominant inheritance, microsatellites provide detailed insights into the genetic structure and relationships among individuals within a population. Their versatility and wide distribution across genomes make microsatellites indispensable in various fields of biology,



including ecology, evolution, and genetics. Single Nucleotide Polymorphisms (SNPs) represent the most abundant form of genetic variation, involving the substitution of a single nucleotide at a specific genomic locus. These variations occur throughout the human genome and play a pivotal role in shaping individual differences, influencing traits. The accessibility and abundance of SNPs make them invaluable tools for characterizing genetic diversity within populations across diverse landscapes. Studying SNP-environment associations enables scientists to identify regions of the genome under selective pressure, providing insights into the adaptive evolution of species. Copy Number Variations (CNVs) are structural variations in the genome involving changes in the number of copies of specific DNA segments. Unlike single nucleotide polymorphisms (SNPs) that involve alterations at a single nucleotide level, CNVs encompass larger genomic regions and can range from kilobases to megabases in size. CNVs can have significant implications for an individual's phenotype, as they may affect the dosage of genes within the altered region. These variations can lead to differences in gene expression levels, potentially influencing traits, disease susceptibility, and adaptation to environmental changes. Geographic Information Systems (GIS) play a crucial role in landscape genomics by providing a spatial context to genetic data. By overlaying genomic information onto geographical maps, scientists can discern patterns of genetic variation across different landscapes. This integration of genetic and spatial data allows for a more nuanced exploration of the interactions between genes and environment.

Analysis methods in landscape genomics include statistical methods for estimating genetic subdivisions such as ANOVA or F-statistics. ANOVA is used to assess the variation in genetic data among different groups or populations. In landscape genomics, it helps identify whether there are significant differences in genetic characteristics among populations occupying distinct geographic or environmental regions. F-statistics, particularly  $F_{ST}$ , quantify the degree of genetic differentiation among populations.  $F_{ST}$  measures the proportion of genetic variance that exists between populations relative to the total genetic variance. Spatial autocorrelation is another useful method that is used to identify patterns of genetic clustering or dispersal. It provides insights into how landscape features influence the spatial distribution of genetic diversity within and among populations.

## II. Applications of Landscape Genomics

Landscape genomics aids in identifying populations with unique adaptive traits, guiding targeted conservation efforts to ensure the survival of diverse ecosystems. In the realm of agriculture, landscape genomics offers a promising avenue for developing crops that can thrive in specific environmental conditions. By identifying genetic markers associated with desirable



traits, such as drought resistance or disease tolerance, scientists can accelerate the breeding of crops tailored to the challenges presented by diverse landscapes. This not only enhances food security but also reduces the environmental impact of agriculture. Landscape genomics extends its reach to human health by unraveling the genetic basis of diseases. Understanding how genetic variations interact with environmental factors can provide insights into the susceptibility and prevalence of certain diseases in specific populations. This knowledge can inform personalized medicine approaches, offering tailored treatments based on an individual's unique genetic and environmental profile.

### **III. Case Studies in Landscape Genomics:**

#### **The Pika's Tale: High-Altitude Adaptation**

In the high-altitude landscapes of the Himalayas, the pika, a small mammal resembling a rabbit, has become a subject of fascination for landscape genomics researchers. By studying the genomic adaptations of pikas to low oxygen levels and extreme temperatures, scientists gain insights into the genetic mechanisms that enable survival in challenging environments. This knowledge has broader implications for understanding how other species may cope with the effects of climate change.

#### **The Tale of Two Fish: Adaptation in Divergent Environments**

In aquatic ecosystems, landscape genomics sheds light on the divergent adaptations of fish populations. By comparing the genomic profiles of fish in different habitats – from rivers to lakes – researchers unravel the genetic underpinnings of adaptations to specific water conditions. These findings have implications for fisheries management and conservation, ensuring the sustainable use of aquatic resources.

### **IV. Challenges and Ethical Considerations:**

As with any scientific endeavor, landscape genomics raises ethical considerations. The use of genetic information, especially in the context of human populations, demands careful consideration of privacy, consent, and the potential for unintended consequences. Researchers and policymakers must work collaboratively to establish ethical guidelines that balance scientific exploration with respect for individuals' rights and the potential societal impacts of genomic research.

The integration of genomic and environmental data presents a complex challenge. Combining information from disparate sources requires sophisticated analytical approaches and collaboration across disciplines. Overcoming these challenges is crucial for extracting meaningful insights from the vast amount of data generated by landscape genomics studies.



## V. Future Prospects:

As technology continues to advance, the future of landscape genomics holds exciting possibilities. Emerging tools, such as single-cell sequencing and advanced machine learning algorithms, promise to enhance our ability to decipher the complex interplay between genes and landscapes. These innovations will open new avenues for research and deepen our understanding of the evolutionary forces shaping life on Earth.

The global nature of landscapes and ecosystems necessitates collaborative efforts in the field of landscape genomics. By fostering international partnerships and sharing data across borders, scientists can build a more comprehensive picture of how genetic diversity responds to diverse environments. This collaborative approach is essential for addressing global challenges, from climate change to the preservation of biodiversity.

## Conclusion

Landscape genomics serves as a powerful lens, allowing us to peer into the genetic codes that orchestrate adaptation and evolution across diverse environments. From the heights of mountain ranges to the depths of aquatic ecosystems, this field unveils the dynamic relationship between genes and landscapes, offering profound insights with implications for conservation, agriculture, medicine, and beyond. As we stand at the threshold of a genomic era, the exploration of landscape genomics promises to unlock nature's secrets, enriching our understanding of the living world and guiding our efforts to coexist harmoniously with the planet we call home.

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