Review Article

Approach and prospects of landscape genetics in livestock: A review

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Abstract

The genetic constitution is unique for each population as its composition is associated with the landscape reforms. Landscape genetics helps in understanding the structural genetic difference at population and individual levels based on gene flow in different geographical and environmental constituents. Gene flow is helpful in avoiding several adverse effects such as inbreeding, loss of heterogeneity (genetic variations), depression of population fitness, demographic problems of inbreeding and to decrease extinction risk. Livestock species are following devastating trends such as the extinction rate of biodiversity, demolition of bionetwork, and vanishing genetic diversity. This resulted adversely on livestock diversity which translates into a lack of apt reaction for future generations. Over the years, intense anthropogenic selection for highly productive cosmopolitan breeds resulted in a progressive ebb in the number of native breeds. Landscape genetics analyses are therefore very helpful in the practical conservative management of species of economic importance. In situ breed conservation can be done relevant by combining relevant information from different applied fields viz. geo-referencing, eco-climatic, epidemiological, spatial diversity at a genetic level and production aspect to strategize precedence judgments. This can be of great use to realize the genetic source of animal adaptation to the varied environmental conditions and production wise co-evolution pattern of livestock structure.

Keywords conservation, gene flow, landscape genetics, livestock, seascape genetics

Introduction

Landscape genetics is a promising new discipline, first introduced by Manel et al., [1] about 20 years ago and is defined as the merger of Landscape ecology and Molecular genetics at the population level. A more refined definition was given by Storfer et al., [2] as "Research that explicitly quantifies the effects of landscape composition, configuration and matrix quality on gene flow and spatial genetic variation". The roots of landscape genetics can be traced back to the works of A. P. De Candolle and A. R. Wallace as they described the varying terrestrial distribution prototype of organisms mainly on the basis of two types of physical forces, the force that exists today and the forces which are replaced/subsided. These forces are operating at diverse time scales. Augustin-Pyramus de Candolle explained the variations in the

distribution pattern of organisms (taxa) across landscapes. During his Journey of Malay Archipelago Alfred Russel Wallace (1823-1913) [3] studied the boundaries in the fauna between the Australian Region and the Oriental Region. While considering the present scenario of climate change as mean annual temperature increases by 1.1°C to 6.4°C leads to gradual heterogeneity both in space and in time [4]. The Sixth Assessment Report (AR6, 2021) of the Intergovernmental Panel on Climate Change (IPPCC) [5] says that human endeavor is mainly responsible for global warming of approximately 1.1°C level. The reason for this change was considered as the emission of greenhouse gases since 1850-1900, and is set to continue next 20 years. The future forecast indicates that the expected 1.5°C increment in temperature leads to global warming which will deteriorate living conditions on earth. Loss of population is proportional to the intra-specific genetic diversity and loss of biodiversity due to global change and genetic variation. Such negative impact on biodiversity has other causes also such as excessive misuse, invasive alien species, contamination, changing ambiance, destruction of habitat, and fragmentation. Geo-environmental factors help in the configuration of genetic variation at both the population and individual levels, for instance, different cattle breeds adapted at different states in India *viz*. Rathi at Rajasthan and Siri at Sikkim. There are different gears/branches of landscape genetics [6] such as population genetics, evolutionary biology, micro-evolution, landscape ecology, and spatial statistics. The main intent to study landscape genetics are as
1. To restrict movement and/or to promote movement.
2. To improve our understanding about the effect of global change on the genetic pattern.

These objectives can answer queries such as for
i. How does global change affect the genetic pattern of unbiased and adaptive variation? This can be explained by the pattern of gene flow.
ii. What is the probability that species are going to be acclimatized in globally changing conditions? This can be answered by the adaptive pattern of species at different geo-climatic conditions. Landscape connectivity is dependent as the inter-patch distance resembles islands in an ocean and can be defined as the relation between the motility of organisms and the landscape reforms [7-8]. There are three patterns of landscape connectivity as Functional connectivity, Structural connectivity, and Genetic connectivity.

Functional connectivity is the key factor for population persistence provided by gene flow e.g. fragmented population. This can be defined as 'the extent that landscape helps or restrict movement among resource patches' [9]. Even a moderate global warming scenario leads to a large reduction in functional connectivity. Individuals react to landscapes by various means such as scattering, mortality, movement threat, scattering rates, and path of changed niche. Structural connectivity is the spatial combination of home scrap and the living populations to landscape structures e.g. Hedges, terrain boundaries, and pace gravels. Genetic connectivity is more complex and can be tested by a simple (partial) mantel test- Which relates a matrix of distance (individuals or population) to Euclidian distance matrices of landscapes. This can be done by three approaches
i. By causal modeling using circuit theory by simple or multiple least-cost paths.
ii. By using a mixed effect model by covariance effect of allelic frequencies.
iii. By measuring gene flow directly from raw data then use multiple regression.
The steps in studying landscape genetics are as follows:
i. Define the objectives such as to study for gene flow or selection pattern. Gene flow can be defined as the incorporation of genes from one population to the gene pool of another population by the means of dispersal or by migration. Selection is the choice of the individual to reproduce in the next generation mainly by artificial selection but can also be natural selection.
ii. Sampling for genetic markers to get genetic input data side by side spatial and temporal scaling can be done to get spatial data input.
iii. Both input data will be integrated by using some suitable statistical methods to draw meaningful conclusions.

To know how much gene flow is enough following two theories were proposed:

i. Mills and Allendorf [10] suggested 1-10 migrants per generation are considered to be appropriate.

ii. Vucetich and Waite [11] demonstrate that most populations require more than 10-20 migrants per generation.

Approaches to study gene flow are below:

1. Individual based approach

This method is applicable when the habitat has no existing population by using the least cost path [12] as species tend to travel to the new nearby populations. Genetic distances between migrant and native individuals will increase with increasing geographical distance. Cushman et al., [13] used casual modeling based on the isolation of distance and resistance landscape. They studied the movement of the black-bear (*Ursus americanus*) population by using the Geographical Information System approach (GIS). GIS are explicit systems intended to detain, hoard, control, handle, scrutinize, and symbolize geographically referenced data in digital form. GIS constitutes the merging of cartography, statistical analysis, and database technology [14]. Coulon et al., [15] used Bayesian clustering approaches to study roe-deer (*Capreolus capreolus*) movement.

2. Assignment tests

This method is applied when there is a previous reference population. It can be done by gathering first-generation migrants as "Home" and "away" genotypes. A migrant from one identified population to another known population is defined as an "away" genotype. Individuals from the reference population are genotyped. The genetic distance is subjected to the comparison between selected individuals and the known reference population.

3. Parentage analysis

Mainly used for plants. To detect the gene flow by seed dispersal in the form of pollen for maternity analysis. To identify the outliers Genome scanning and genetic sampling can be done in different types of habitats.

4. Prospect of landscape genetics

This is helpful for a wide purpose for which different examples from different temporal-spatial distributions are given below:

(a). Greater prairie chicken [16]

The species numbered 25000, 2000, and 50 individuals in 1933, 1962, and 1993 respectively. Hatching success rate was 90% and 74% in 1960 and 1990 respectively. Loss of genetic diversity was the plausible reason for a decrease in fecundity (fitness) which declined by 30% in this period. The introduction effect reversed the bird's extinction to bring in fresh genes into the population from Minnesota and Kansas and successes to achieve a 94% increase in hatching rate.

(b). Scandanavian adder [17]

Low genetic diversity and huge stillbirths were reasons behind crashing the Scandanavian adder population in 1983-1993. Inbreeding depression causes low fitness in this population. The introduction of 20 males from a bigger population for 3 years increased male recruitment with less number of stillbirths.

(c). Peromyscus maniculatus [18]

Survival rates were compared in a control population and two treatments viz., individuals were introduced in a migrant treatment group from the distant population and an inbreeding treatment with inbred population. Survival was higher in both inbreeding and migrant treatment groups with much higher survival later.

(d). Conclude history of modern breeds
Genetic diversity tends to follow a descending pattern from the center of domestication (higher) as reduced away from it. Domestication centers were traced for the major livestock species by many researchers (Table 1).

Table 1. Studies on domestication center in economically important livestock species

Species	Reference
Cattle	Ajmone- Marsan et al., [19]
Sheep	Chessa et al., [20]
Goat	Naderi et al.[21]
Chicken	Kanginakudru et al., [22]
Pig	Larson et al., [23]
Yak	Wiener et al., [24]

(e). Co-migration pattern of animal stock and humans
It can be justified as a reasonable distance and discontinuity between Italian and Turkey but cattle breeds of these two countries share haplotype patterns with each other [25].

(f). Livestock conservation
Rapid loss of genetic diversity in near future due to rapid climatic transformations, up surged market requirements and demographic invasion by human population. Landscape genomics provides an aid to the preservation of farm animal diversity in near future.

(g). In-situ breed conservation
This will become the basis of animal alteration and co-evolution patterns by Landscape Genomics with several allied disciplines such as GIS, epidemiology, population genetics, environmental science, and production information.

(h). Geological genetic variations of Sheep and Goat
This can be studied by integrating the related factors of diversity with their environment as well as to their management (Table 2). For *e.g.* Ecogene project on sheep combined the information of socio-economic condition of farmers, geo-environmental factors, and genetic factors to study the genetic diversity of a particular sheep population.

(i). Genetic proof for domestication of sheep in Indian subcontinent
M. Nagarajan [32], Assistant professor, Department of Genomic Science, CUK, compared DNA sequences of Indian sheep breeds with other breeds across the world. Haplotypes of the Indian sheep were unique and highly diverse. The high genetic diversity and statistical analysis suggest that sheep were domesticated in the country not in western Asia which was previously stated as the center of domestication for ancient sheep populations.

(j). Impact of cyclone fani on Chilika lake
Chilika Development Authority (CDA) revealed that there were two active mouths before Fani in 2019, but now found four new mouths. This could immediately impact on salinity surge and

migration of fishes [33]. This leads to bring in another branch of landscape genetics for aquatic species i.e. Seascape genetics.

Table 2. Spatio-temporal pattern of genetic diversity in small ruminants

Species	Study	Reference
Goat	Spatial pattern	Berthouly et al., [26]
Sheep and goats	Econogene project	Bertaglia et al., Peter et al., Pariset et al., [27-29]
European sheep	Association of 40 alleles with environmental parameter.	Joost et al., [30]
Goat	Adaptive variation	Pariset et al., [31]

(k). Landscape genetics and genomics

This approach link past and future with a bidirectional approach. The history of domestication and dispersion can be predicted in plants, animals, and the human population in rapid climatic variations [34]. Landscape genomics is coupled with recent developments and underdeveloped applications such as marker based and sequencing approaches [35]. Studies can be helpful to strategize conservation steps for endangered species [36]. Evolution patterns can be studied by tracing the historical background, migrations, and the dispersion of diseases in living beings by scanning candidate genes for these adaptation mechanisms. Future it is helpful in advanced studies also by identifying the dispersal patterns of the virus viz. COVID-19 with sequencing.

Conclusion

The landscape genetics' paper in 2003 enlightened that different landscapes and environments mold genetic variants. Sustainable landscapes and ecosystem harbor static climax population, compared to dynamic counterparts. While seascape genetics is a connecting link between aquatic and terrestrial platforms from large-scale sampling. Landscape genomics help us to understand the local adaptation pattern of genes to environmental heterogeneity. The study generates big data and requires integration of computer science, bioinformatics, and other allied discipline for analyzing and inferring the results. The emergence of the landscape of epigenomics with measuring and manipulating methylation is important as it has trans-generational heritable effects and also connected with the livestock disease-immunity relationship.

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