



Review Paper

The importance of genetic variation in wildlife populations and its relationship with the structure and conservation of habitats, a critical review

T.M. Simon

School of Tourism, Hospitality and Events Management, Department of Tourism Management, Moi University, Kenya
jacksimons.mu@gmail.com

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Abstract

Other than natural causes, human actions and inactions through habitat destruction and ineffective implementation of species management and conservation plans are major causes of species extinctions. This study sought to systematically review the importance of habitats in enhancing genetic variation in preventing extinction and relate this to conservation practices. Findings confirm that intact and unfragmented habitats and genetic variation are important aspect in species conservation. Species management plans should, therefore, focus on maintaining this through preventing habitat destruction, a future ecological cost of current human practices and malpractices.

Keywords: Conservation, gene alleles, genetic diversity, genetic variation, habitat structure, species management plan, wildlife management.

Introduction

Genetic variation is both an attribute of individuals and entire populations¹. Variation within individuals of diploid species is most commonly characterized by the percentage of loci at which an individual is heterozygous². Variation within populations encompasses inter-individual variation, and is quantified by heterozygosity/gene diversity. This is by the number of distinct alleles per locus, or by the percentage of loci that are polymorphic³.

Understanding genetic diversity and its distribution in populations is crucial to conservation management efforts⁴. This is especially because the perseverance of a species is affected by the level of overall genetic diversity, and how it is partitioned among individuals through to landscapes⁵. Greater levels of heterozygosity are linked to sizeable populations⁶, which helps to neutralize the deleterious effects of inbreeding⁴. Greater levels of genetic diversity also provide cushion against stochastic events, enhance the ability for species to resist infirmity and environmental shifts^{5,7,8}.

Methodology

To address the study question, literature survey was conducted based on established guidelines⁹ - relevance to the study type and subject. A boolean search in Web of Knowledge was conducted using relevant key phrases from the title of study - Topic: genetic variation and Topic: wildlife populations or wildlife and Topic: Important* and Topic: suitable or favorable and Topic: conserve* and Topic: habitat Time span: All years. Databases: WOS, BCI, BIOSIS, DRCI, KJD, MEDLINE,

RSCI, SCIELO. Search language=Auto. Literature was selected for their inclusivity¹⁰, and on these grounds qualified as potentially addressing the question. Additional information on the study subject was sought through in-text citations of search results and from a search on Google Scholar using key phrases/words from the study topic.

The study review was addressing the question: what's the importance of genetic variation in Wildlife populations and its relationship with the structure and conservation of habitats?

Results and discussion

From the survey, a total of 35 articles were identified. 12 publications were excluded on the basis of their scope and study subject¹⁰. The remaining publications (n=23) were considered relevant to the study question and were, therefore, studied along with other literature materials derived from Google Scholar. The surveys presented important insights on the relationship between genetic variation and habitat as discussed below.

Variation is a key driver of evolution⁵. Without it, some of the basic mechanisms of evolutionary change won't operate. The variation in the DNA sequence in each of genomes of a parent in a population causes differences in the species in the population, making species unique in morphological characteristics^{4,7}. This results in valid forms (alleles) of genes which are determined by the genes inherited from the parent animal^{11,12} or at times influenced by the environmental forces around the habitat such as humans¹³. In most instances, variation ensures only the best genes are selected for and passed on. This is important in species development over time

(evolution) as it ensures adaptability of a population by passing down of favorable characteristics from one generation to the other (natural selection)¹⁴.

The diversity of alleles plays an important role in the adaptability and hence survival of a species^{1,5,15}. When a population's habitat changes, there may be need to adapt to the changing environment to ensure survival. Moreover, there is competition among individuals in a population as there is for the limited resources in the habitat^{4,16}. This means that animals with helpful variations are more likely to survive, reproduce and spread out these gene variations⁴. The lesser adapted species or individuals in a population –those with lowered variation die out.

Additionally, variation reduces a populations' susceptibility to natural shocks¹⁶. For instance, an outbreak of a deadly disease would wipe out an entire population of animals if they have no variations for resistance^{1,4,5}. Summarily, lowered variation has some negative impact on a population's fitness in its present environment, resilience to short-term threats, persistence, and the ability to adapt to changing environments^{4,15}. This has an implication that a population with low heterozygosity, heritability, and few polymorphic loci will attain lesser adaptation before reaching the limits of response to selection contrary to a more genetically diverse population^{5,17}.

Genetic diversity is pivotal to ensuring dispersal among the individual colonies in a habitat¹⁷. A study on the greater horseshoe bat *Rhinolophus ferrumequinum* highlights that fragmentation and limited dispersal has adverse effects on patterns of genetic structure and variation among populations⁴. Additionally, genetically isolated populations have lower variability resulting to stressed chances of continuity of generation⁷. It also restricts gene flow among them; an important implication for the ongoing conservation management practices on fragmented species. Demographic stability of wildlife populations is important in preserving the evolutionary potential of a species¹. Variation plays a major role in this process through ensuring genes are shuffled and distributed among the breeding members of the population¹⁸. It's also useful in maintaining balanced sex ratios, avoiding fluctuations in population size over time and extending mean generation length¹. As populations/habitats progressively become affected by human activities, many species are dependent on oversight measures to warrant their survival¹. Modern genetic conservation efforts focusing on maintaining demographic stability are thus necessary.

Genetic variation avoids inbreeding which would lead to erosion of genetic viability of populations^{4,1}. Accumulated levels of inbreeding cause "genetic dilution," limiting genetic variation due to severe bottlenecks and founding events⁵. Genetic variation, therefore, ensures continuity of generations by passage of useful genes¹. This preserves a species by way of maintaining genetically and ecologically distinctive populations.

The processes are fundamental in controlling interdependency of genetic and non-genetic processes and thus ensuring viability of populations for generational continuity⁴. Small fragmented populations for instance have decreased individual variability due to inbreeding¹⁹. Lower variation decreases populations' resistance to disease/parasites, average fitness, flexibility to environmental challenges, suppleness, and long-term adaptability⁵. Genetic drift also depletes variation and threatens viability of populations⁵. This is through suppressing natural selection as the force driving evolutionary change (natural selection through genetic variation reduces the frequency of deleterious alleles in populations that persist through bottlenecks)^{4,5}.

Variation increases the fitness of individual members in a species due to the fact that the parent animals are stronger genetically²⁰. Loss of variation can thus impact population persistence by lowering fecundity and survival of the inbred individuals^{5,17}. This ultimately depresses population growth rate, increasing the probability of extinction from stochastic fluctuations^{4,5,17}. Lower capacity for population growth also reduces ability to rebound from population declines, especially as the impacts of inbreeding on individuals are heightened in stressful environments. Heterozygosity is, however, depleted by inbreeding^{1,5,17}; perceived to cause slower growth, higher mortality, reduced mating ability, developmental unsteadiness /defects, susceptibility to disease, lowered ability to defy stress, and reduced competitive ability in a population^{5,17}.

The relationship between habitat structure/conservation and genetic variation: The nature of a habitat is a major determinant of survival chances/extinction of species⁷. For instance, the structure of a habitat is likely to affect the future of a species in that the more unfavorable/patchy a habitat is the more the likelihood for species loss through competition etc. Dominant species are, however, considered to be free of this threat because they are abundant in the undisturbed fragments that remain after destruction¹⁹. With time, the abundance of species coexisting in patchy habitats may be fleeting as continued destruction causes time-delayed but deterministic extinction of the dominant competitor^{5,17}. Further, species are predicted to become extinct, in order of competition as habitat destruction increases¹⁷.

Translocation, introduction, and reintroduction conservation efforts for a population have an inherent problem of small founding populations¹⁷. This has the implication that changes in landscape variables have a direct impact on the population morphology and asymmetry in individual populations¹⁷. The population is affected even when in introduction sites and landscapes similar to where the species previously occurred naturally¹. This may manifest phenotypically through changes in individual morphology, changing susceptibility to environmental stressors, decreased body size among others⁷; attributed to the fact that the sites differ in connectivity and amount of suitable surrounding habitat¹⁹. An example is the

summer tanager *Piranga rubra*, a genetically effected Neotropical migrant in the southwestern United States that has experienced massive declines due to extensive habitat loss of native riparian woodlands. The ability to cope with environmental/demographic fluctuations may also differ between populations with different initial propagule sizes⁷. With more naturally occurring habitats, connectivity enhances mobility of populations across the habitat and maximizes foraging opportunities thereby maintaining a larger population⁷. Better dispersal also increases the access to mates, resulting in increased genetic diversity in the population. Besides, larger habitats support better food quality and availability; providing an opportunity for populations to attain higher growth rate, reducing the effect of genetic loss²¹.

A study by Ripperger et al.¹⁶ shows that gene flow decreases with increasing geographic distance. In other words, distant/fragmented habitats may lead to species isolation which causes decreased dispersal due to reduced areas available for population foraging and mating. Additionally, decreased connectivity reduces the availability of habitat heterogeneity^{4,5}, and this affects the survival of individuals through a decreased population size and a lower chance of maintaining genetic diversity⁷. With landscapes progressively turning into heterogeneous mosaics, animal communities are simplified and the scattered survivors are partially isolated⁴. This inhibits connectivity and causes gene flow discontinuities. An example is the *Carollia castanea*, a small frugivorous bat whose loots have been affected by agriculture and settlement in north-east Costa Rica causing it to inhabit mere forest fragments.

Genetic studies by Henle et al. on populations in the context of habitat fragmentation and degradation highlight negativity due to controlled mobility²². Human encroachment especially reduces genetic connectivity among species as asserted by Keller and Largiadèr²³ and Vandergast et al.²⁴. The fluctuating environments may cause stress among individuals, result to poor connectivity within the habitat and thereby cause decreased genetic diversity and chances of survival. Additionally, Ripperger et al. posits that habitat fragmentation plays a major role in isolation especially for small populations¹⁶. This is because population's differentiation/diversity is directly correlated to habitat variables such as habitat size/connectivity¹⁶. Moreover, the effects of habitat interference through fragmentation results to gene flow discontinuities among isolated populations leading to sub-population differentiation. This increases chances of inbreeding and genetic drift²⁵.

In regards to the structure of a specific population, understanding habitat structure is important^{4,19}. This is because the nature of a habitat influences the state of a species. Patchy habitats for instance may lead to small, distant and fragmented populations¹⁹. This ultimately affects the cohesiveness of a species through genetic drift and inbreeding, leading to the loss of genetic variability and inbreeding depression²⁶.

Geographically, segregated species may show significant population differentiation as there is a discontinuous gene flow among the populations^{4,21}.

In respect to the need for shuffling of genes among populations, habitats needs to be maintained unfragmented and in their natural setting. Habitat interference causes isolation of some of the population from the larger group¹⁶. In comparison to large populations, small/isolated populations are less demographically stable and more prone to genetic erosion^{4,27}. In the absence of gene flow, the loss of genetic variation through drift is inevitable. A lack of genetic variation not only makes a population more susceptible to inbreeding depression but also less able to adapt to changing environment^{28,29}. An example is the Britain's *Rhinolophus ferrumequinum* that is confined to the milder southern areas¹⁹. It is isolated and constrained in size by climatic factors. The species has a lower genetic diversity compared with its French counterpart and this significant differentiation indicates that little or no recent gene flow has occurred³⁰ (restricted to the individual isolations where the population is smaller) and that it has probably undergone more genetic drift.

Habitat degradation, among other factors is a major driver of population extinction^{4,31}. This is because fragmented populations are susceptible to replacement by exotic competitors, and the demographic instability inherent in small numbers necessitates inbreeding^{3,32}. This is a threat to genetic processes of species and population survival, a key ingredient of genetic variation. A study on the Australian microbat specialized for foraging directly over water bodies (*Myotis macropus*) highlights that specialist species face higher extinction risks as a result of smaller, isolated populations with reduced gene flow⁴. This provides important insights into the need for considerations of the conservation of specialist species and the management of habitats.

Conclusion

In respect to gene flow and variation in a population, degradation and fragmentation of habitats particularly in rural areas where large proportions of protected areas occur is a primary force of genetic depression and is, therefore, an important consideration in conservation efforts. Moreover, habitat is the major factor influencing the genetic structure of populations. This understanding is a wake-up call for modern conservation biologists given the inherent risk of extinction faced by isolated and small populations of specialist species. Management actions should be directed towards maintenance, enhancement and linkage of habitats in view to promote the movement of uncommon species throughout landscapes (genetic variation). Conservation strategies to re-establish species should consider enhancing variability in reference to habitat and especially to improve range connectivity, and so facilitate genetic exchange among individual population colonies.

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