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LEAD ARTICLE

Lessons Across Scales: Molecular Ecology and Wildlife Conservation

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Abstract | We humans have single-handedly (as a species) changed the ecology of the planet; we are also learning why this, in the long term, is a terrible idea. As we grapple with the fallouts of increasing urbanization, deforestation, loss of wildlife, and human–wildlife conflict, we are beginning to realize that conservation must use every tool available to protect what is left of our natural world. Since molecular ecology—a hybrid field of molecular biology and ecology—is an invaluable tool in understanding how genetics affect animal populations, it has often been used to inform conservation efforts. Wildlife conservation has and will continue to depend heavily on molecular ecology to make predictions on species survival, decisions regarding conservation practices, and monitoring of conservation efforts. The influences of molecular biology-based techniques and tools on various aspects of conservation, namely, population genetics and health, taxonomy, wildlife disease management, climate change, and changing landscapes, will be broadly examined in this article.

1 Introduction

The two fields—molecular ecology and wildlife conservation—are scales apart in scope.

Molecular ecology uses biological molecules such as DNA and proteins to find and explain patterns in the natural world. Ecological data from field observations on wild and captive animals are combined with molecular information to understand ecological and evolutionary processes in this hybrid field.

Wildlife conservation is also a hybrid. However, unlike molecular ecology, it does not include just two major fields of science. Wildlife conservation encompasses biological science, medicine, anthropology, economics, sociology, public policy, agriculture, and a host of other subjects in a practical effort to protect nature.

Yet many successes in wildlife conservation, especially those in the last half a decade, have been driven by advances in molecular ecology. Despite being scales apart, these two fields work well together.

2 The Conception of Conservation

Conservation as a conscious human effort perhaps began in the mid-1660s, when John Evelyn, a British author and landscape architect wrote ‘Sylva, or a Discourse of Forest-Trees and the Propagation of Timber’[1]. The paper, which was later published as a book, was a warning and plea to English landowners to begin reforestation or face the consequences of timber scarcity. However, the *lassaiz-faire* economics practised during that time and political will heavily in favour of private landowners considerably set back conservation efforts; ultimately, conservation was only erratically and sporadically practised by isolated groups in Europe.

A resurgence in practical conservation occurred in the mid-1800s, when scientific principles of conservation were applied to forest management in India and Burma by the British Empire. Around the same time, the American conservation movement began in the early 1900s, with the United States of America creating its

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first national parks and nature reserves. However, it was only in the 1960s and 70s that real efforts to protect endangered species from extinction began. During this time, the field of wildlife conservation began in-depth explorations into issues with human–wildlife conflict, captive breeding programmes, and species' population health.

3 The Marvels of Molecular Ecology

Meanwhile, in the early 1900s, explorations in molecular biology showed that one could use proteins as genetic markers and established that many proteins occurred in different forms or variants in different individuals. In 1966, Lewontin and Hubby published two back-to-back studies on the genetic diversity of the fruit fly, *Drosophila pseudoobscura*, by looking at genetic variations in 18 proteins[2,3]. Their work provided one of the first pictures of how much genetic diversity there could be within a population. This soon opened the floodgates to a tidal wave of information on genetic variation patterns in hundreds of organisms over the next 10 years. Not long after, molecular ecology came into being as more and more studies in molecular genetics began to analyse genetic patterns in the context of ecological factors.

However, within the wildlife conservation community, interest in molecular genetics was kindled only after a study on the highly endangered northern elephant seals. These seals, which were hunted nearly to extinction in the eighteenth century, were monomorphic (that is, showed no genetic variation) in 21 of the 24 protein markers surveyed; this sparked fears amongst conservationists that the species would experience a population collapse due to inbreeding[4].

Although wildlife conservation has evolved to use tools from reproductive physiology and clinical medicine, molecular ecology has overtaken these disciplines in shaping conservation efforts over the last 50 years. As the field matured, molecular ecologists began to rely on DNA instead of proteins to identify genetic differences.

Molecular ecology has become a driving force in conservation with its involvement in breeding programs, controlling disease outbreaks, taxonomy, and the demographics of managing wild animal populations.

Techniques that involve using mitochondrial DNA (mtDNA) sequences, DNA fingerprinting, single nucleotide polymorphisms (SNPs), microsatellite markers, amplified fragment length polymorphisms (AFLPs), and DNA barcoding have revolutionized conservation practices[5,6]. For example, studies using molecular markers first identified how African cheetahs had very low genetic variation (up to 100 times lower than other animals), which explained why breeding programs for these endangered cats failed so often[7,8].

Today, with all the improvements in molecular biology and sequencing technology that the last two decades have seen, molecular ecology is a literal Swiss army knife for wildlife conservation.

3.1 Complications in Conservation: Genetics and Population Management

Before the advent of molecular ecology, conservation was likely regarded as a game of numbers. The simplistic notion that if enough members of a species could be saved and allowed to reproduce, it could survive extinction, was dispelled in the late 1970s and early 1980s. Conservationists were finding that captive and wild populations of animals—cheetahs, lions, Père David's deer, pygmy hippopotamus, Dik-diks, and muntjacs to name a few—were dwindling due to low fertility, high infant mortality rates, and rapidly spreading diseases[7–9]; in other words, many populations of these animals were simply unviable. The African cheetah has become an iconic example of a species fighting to survive despite extensive efforts to conserve it.

From their inception in the 1950s, cheetah breeding programs struggled with low reproductive success. Physiological studies indicated that the sperm of captive cheetahs in both South Africa and USA not only had fewer sperm (10 times lower than those in domestic cats), but that a high percentage of the sperm cells (~ 70%) were abnormal. In addition, cheetah populations also showed high infant mortality rates of 30% (in captive populations) to 70% (in some wild populations). Investigations using 200 molecular markers revealed that that the genetic variation in this species was 10–100 times lower than that of most other animals[8.] Further molecular studies also revealed that cheetahs were monomorphic for the MHC (major histocompatibility complex), a gene set responsible for fighting off infections. This was thought to be the reason for the unusually high impact of feline infectious peritonitis—a viral disease that usually only kills < 1% of domestic cats—which decimated the cheetah population in a breeding facility at Oregon, USA[8].

The cost of inbreeding in cheetahs spurred conservation programs to assess and mitigate inbreeding in captive and protected populations of other endangered species. Accordingly, 'genetic rescues' by introducing new individuals and genes into inbred populations to increase genetic diversity have been attempted in Mexican red wolves, Puerto Rican crested toads, and African lions[10–12].

On the other end of the spectrum, species such as the Atlantic salmon and Arabian oryx exhibit 'outbreeding depression'[13,14]. In such species, some populations exist in relatively isolated conditions and have very limited gene flow with other populations. Under such situations, specific genetic variants sometimes allow individuals to survive local conditions better, leading to the phenomenon of 'local adaptation'. When breeding programs in these cases attempt genetic rescue by establishing gene flow between two separate populations to reverse inbreeding and recover genetic diversity, things can go wrong. The offspring of individuals from different populations may end up with genetic combinations that leave them unable to survive in either of the two local conditions. Overall, molecular ecology studies to assess inbreeding/outbreeding in endemic and endangered amphibians, elephants, and tigers have been invaluable in defining geographic ranges, which in turn have helped in delineating protected areas and informed conservation policies[15–19].

Based on the lessons learned from both inbreeding and outbreeding depression, conservationists have begun to reconsider wildlife population management in the light of molecular ecology contexts such as genetic variation and viable population sizes. Breeding programs and conservation efforts must now obtain data on the natural genetic structures of wild populations, assess the genetic structures of captive populations, define breeding management groups to avoid both inbreeding and outbreeding depression, and reassess the genetic structures of isolated populations at regular intervals[20].

3.2 Tales of Taxonomy: Molecular Systematics and Conservation

Although avoiding inbreeding/outbreeding depression and maintenance of genetic diversity are core drivers of decisions on conservation measures, there is another field of biology that is indispensable to conservation policy—taxonomy.

At first thought, academic tussles over ambiguities in taxonomy may not seem important in conservation efforts. However, nothing could be further from the truth. Taxonomic distinctions are the basis for the recognition, and therefore, legal protection that endangered species receive; consequently, ambiguities in classifications can have very real and significant impacts on the survival of species.

The traditional methodology of taxonomy—which identifies, describes, and names species on the basis of morphological descriptions of a few collected specimens—is no longer adequately reliable for conservation purposes. Molecular systematics, which relies on information from organisms' DNA sequences to resolve taxonomic disagreements and correct misclassifications, has, therefore, been very useful in identifying units of conservation.

Taxonomic imprecision has led to the mismanagement of several endangered species, of which four examples stand out: the colonial pocket gopher, dusky seaside sparrow, tuataras, and African ungulates.

The colonial pocket gopher was first described as a distinct species (*Geomys colonus*) in 1898 with a range consisting of a single county within the State of Georgia, USA. When the species was 'rediscovered' in the 1960s, it was found to have less than 100 individuals and was consequently managed as an 'endangered species'. Subsequently, a molecular genetic analysis of these gophers revealed that they were genetically no different from the common gophers, *G. pinetis*[21–23].

The dusky seaside sparrow story begins in 1872, when a melanistic (darker) form of the seaside sparrow (*Ammodramus maritimus*) was discovered and identified as a separate species (*A. maritimus nigrescens*). Due to their low numbers and restricted range, these sparrows were listed as endangered and an unsuccessful captive breeding program to preserve them was launched in 1980, with the last dusky seaside sparrow dying in 1987. Two years later, a molecular genetic analysis revealed that the dusky seaside sparrow was genetically indistinct from other sparrow populations in the United States Atlantic coast[24].

In both the cases described above, conservation efforts based on morphological features ended up being wasted on populations that had been misclassified as distinct species[22,23].

On a different note, in African ungulates and the tuatara, distinct species that had been 'clubbed' together and managed as a single species have faced major problems. In the African ungulates, such misclassifications have caused neglect of endangered species, maladaptation in some populations due to unsound translocations, and failed captive breeding programs[25]. In the case of the tuataras, of which there are currently two species, conservation measures have entirely ignored one species. This has led to the belief that the tuatara was 'relatively widespread' and that the loss of 10 populations out of 40 in the last century was a minor issue[26,27].

Molecular taxonomy has also been particularly useful in forensic DNA analysis of poached and illegally traded wildlife products. Molecular markers such as microsatellites (varying lengths of repetitive DNA sequences) and mitochondrial DNA have been used to not only identify species, but the country and even specific populations from which the illegal wildlife samples originated[28–30]. Such information can be instrumental in planning wildlife protection law-enforcement actions and development of anti-poaching strategies especially in India, Nepal, and Africa[29–31].

3.3 Molecular Ecology and Wildlife Disease Management

Another area in which molecular ecology has impacted conservation, is in disease management. Advances in PCR (polymerase chain reaction) techniques now allow accurate and rapid detection of even low intensities of viral, bacterial, and parasitic infections[32]. Most notably, molecular tools have been leveraged to develop diagnostic tests for avian malaria and West Nile virus in birds, as well as white nose syndrome in bats, all of which are directly responsible for species endangerment[33–35].

Studying the molecular genetics and phylogeny of the parasites themselves can help in understanding how diseases spread, including routes of transmission and identifying reservoir hosts. For example, fine-scale genetic data has been used to understand the spatio-temporal patterns of how wild animals pick up ticks[36], and landscape genetics has been used to identify factors affecting the spread of rabies (in grey foxes, raccoons, and skunks)[37,38] and chronic wasting disease (in deer)[39]. Insights into parasites' genetic structures and transmission patterns could also be used to model the spread of recessive drug-resistance genes, which could have critical implications for epidemiology[40].

Molecular details of host–pathogen interactions can also help conservationists understand why and how some individuals/species are more resistant, tolerant, or susceptible to certain infections. Studies on the genetics of MHCs have helped in identifying genetic variants in wild great tits that are resistant to avian malaria[41]. Similarly, much molecular research has focused on how amphibians fight off chytridiomycosis, a fungal infection that affects their skin. The fungal infection, which has affected about 30% of all amphibians since the 1990s, has been implicated in massive die-offs and extinctions[13]. Studies on the evolution of immune-related resistance to this infection indicate that breeding more resistant individuals is a possible solution, though it will likely extract a genetic cost in the form of inbreeding[42].

3.4 Conservation in a Changing World: Using Molecular Ecology to Craft Conservation Strategies

Besides parasites and diseases, wildlife conservationists must now also account for the effects of climate change when crafting conservation policies for endangered species. To do this, they need to understand how climate change can affect the future survival, reproduction, and habitat range of a species. For example, comparative genomic studies in the frogs *Rana kukunoris* and *R. chensinensis* from the Tibetan plateau have revealed 14 genes that may be responsible for adaptation to high elevations. This data could help in predicting how populations of frogs could survive climate change by moving to higher elevations[13,43].

Similarly, several studies have used molecular genetics to understand how past and present climate change have affected migration patterns, dispersal, breeding behaviour, population structures, and abundances of Arctic marine mammals[44]. These data can be used to identify genes that directly affect fitness in these animals, which in turn, can be used to model the consequences of various climate change projections on different species and populations[44].

In addition to climate change, as more and more land is converted into agricultural or urban landscapes, natural habitats have become fragmented and degraded. The most well-known effects of these changes is on the population genetics of wildlife. However, land-use changes have also impacted the prevalence of diseases such as West Nile virus, avian malaria, toxoplasmosis, trypanosomiasis and others in wildlife[45,46] and resulted in 'spillover events' evident from the recent series of zoonotic diseases that have emerged in the last 10–20 years[47]. Molecular ecology and conservation have played key roles in assessing and mitigating the effects of these changes[48].

3.5 Molecular Ecology and Wildlife Conservation in India

In India, molecular ecology is slowly but surely being integrated into wildlife conservation measures. Recent studies on the population genetics of blackbuck and managed gharial populations show that molecular ecology data is crucial for designing conservation strategies for endangered species[49,50]. Work on how human activities affect the population genetics of predators in fragmented landscapes in central India highlights how important such empirical data could be for landscape-level conservation planning[51]. Furthermore, molecular taxonomic studies are demonstrating that the species richness of drier landscapes in India, such as the northern areas of the Western Ghats, have been underestimated[52]; it is increasingly apparent that such landscapes must also be protected alongside the lusher tropical regions that are currently the foci of conservation measures.

4 Conclusion

We humans, with our world-changing ideas, are conducting the largest selection experiment ever undertaken by any single species on the Earth[53]. Global warming has brought about planet-wide climate change that has affected nearly every organism in our world. It is, therefore, our duty to not only improve our species' quality of life, but also to protect the natural world. In this respect, it is natural that the tools and techniques in molecular biology, which have been developed to better human lives should also be used to aid wildlife conservation. Therefore, it is abundantly clear that the future of conservation has and will continue to rely heavily on molecular ecology.

Publisher's Note

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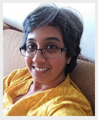

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