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Conservation Genetics for Managing Biodiversity

Nurul Izza Ab Ghani, Wardah Arifin and Ahmad Ismail

Abstract

Conservation genetics is a field derived from a combination of evolution, ecology, behaviour, and genetics. It is an applied discipline of crisis-oriented science of biodiversity resource management that is highlighted when the world realizes the increasing anthropogenic impact and natural populations are declining towards species extinction. It helps to understand and explain the importance of evolutionary factors — mutations, non-random mating, gene flow, genetic drift, and natural selection — for the survival of populations/species that justify the need for prudent biodiversity management. The four justifications for maintaining prudent biodiversity are the economic value of bioresources, ecosystem services, esthetics, and rights of living organisms to exist ensure functioning community and ecosystem services. Hence, conservation genetics must be an essential part of policies and programs in wildlife and biodiversity management.

Keywords: biodiversity, conservation, evolutionary factors, genetic management, genetic variability

1. Introduction

The need to preserve wildlife arises because the earth's biological diversity is rapidly depleted as a direct or indirect result of human action. To date, a number of unknown but many species have become extinct, meanwhile many other species have reduced population sizes and putting them at risk of extinction. IUCN [1] reported that more than 38,500 species are threatened with extinction — highlighting 26% of mammals, 14% of birds, 41% of amphibians, 37% of sharks and rays, 28% of selected crustaceans, 34% of conifers, and 33% of reef corals. Hence, many species are now required human intervention to ensure their survival through effective management and conservation of biodiversity resources. But a statistically robust Population Viability Analysis (PVA) has yet to be developed to assess the ecological and genetic risks faced by the Essential Evolutionary Unit (ESU) which is the unit of biodiversity that is of concern to conservation geneticists. Though, International Union for Conservation of Nature (IUCN) has recognized the need to manage and conserve biodiversity resources at three levels; genetic diversity, species diversity, and ecosystem diversity. Genetic information is involved in all of these three levels. Thus, geneticists (specifically known as conservation geneticists) are playing an increasingly important role in the management and conservation of biodiversity resources — identifying and monitoring the genetic variability that directly relates to evolutionary factors of biodiversity units.

Conservation geneticists deal with evolutionary factors causing rarity; endangerment and extinction of threatened population and species, and genetic management to minimize impacts of evolutionary factors in threatened population and species, as well as resolving taxonomic uncertainties in threatened species, understanding the biology of threatened population and species through their genomic, and wildlife forensics. All of these are important research courses in conservation genetics with the ultimate goal to manage biodiversity resources with utmost care through preserving and maintaining the ability of populations and species to evolve. Thus, reducing the extinction risk of population and species, while ensuring a functioning community and ecosystem services. All research courses in conservation genetics can be disentangled by using molecular genetics methods through the use of various molecular markers. The common molecular markers which have been used are single-locus markers (allozymes), DNA minisatellite fingerprints, random amplified polymorphic DNA (RAPD), mitochondrial DNA (mtDNA) sequences, chloroplast DNA (cpDNA) sequences, genic sequences such as Major histocompatibility complex (MHC) genes, and nuclear DNA (nDNA) sequences including microsatellites and single nucleotide polymorphism (SNP). To date, conservation geneticists also have started to use whole-genome sequence which offers a more powerful assessment to disentangle evolutionary factors and their implications towards population/species rarity and survival to manage biodiversity.

Yet, efforts to implement conservation genetics for managing biodiversity have been done for very few threatened species. Therefore, the aim of this chapter is to briefly highlight the importance of assimilating conservation genetics to manage biodiversity with a review of the relevant literature. This chapter is comprised of three parts. The first part introduces readers to the genetic management of biodiversity units that are seldom been misinterpreted. The second part points out the essence of genetic variability in managing biodiversity due to its importance for determining future population/species evolution. The final section hopes to engage readers with an appreciation of research courses in conservation genetics by briefly describing evolutionary factors influencing genetic variability of threatened populations/species including mutations, non-random mating, gene flow, genetic drift, and natural selection.

2. Genetic management of biodiversity unit

Poorly planned conservation management plans can significantly cause local adaptation damage (overcoming depression) and reduce the viability of the population, especially the threatened population. PVA is a methodology that has been used by conservation geneticists to assess the ecological and genetic risks faced by wildlife or captive population, and thus appropriate conservation management plan can be developed. PVA refers to a group of mathematical models that are useful for predicting the probability of population extinction at some point in the future. The early PVA models considered demographic data (growth rate, current population size, and birth rate) and environmental stochastic data. But Gilpin and Soulé [2] has been further enhanced the ability of the PVA model in predicting the extinction of a species by including genetic factors. Genetic factors including mutation, genetic drift, non-random mating, gene flow, and natural selection have significantly influenced genetic variability. It is clearly expressed through its effects on demographic factors that influence population dynamics, especially in small isolated/threatened populations. This shows that genetic factors contribute to extinction probabilities through a very complex manner of interactions affecting the genetic variability and fitness of a population [3, 4]. Unfortunately, little is understood regarding genetic

factors' linkage to ecological factors. Thus, statistically strong PVAs have not yet been developed sufficiently to provide comprehensive biodiversity management.

The biodiversity unit of concern by conservation geneticists in PVA is ESUs. ESUs represent genetically differentiated populations whereby depicting deep phylogenetic subdivisions typically within a species (i.e., subspecies) or occasionally as entire species in the case of local endemics or distinct population segments (DPS - Endangered Species Act 1973). ESUs are classified based on genetic criteria; both genetic diversity and multilocus genetic similarity using multilocus mtDNA or nDNA (preferably microsatellites) variation. mtDNA shows evidence for significant long-term genetic divergence and reciprocal monophyly. Whereas microsatellites show evidence for the significant recent divergence of allele frequencies at nuclear loci. A refine ESUs in wildlife conservation include pedigree analysis. Pedigree analysis has been used to understand the established kinship and individual founder contributions, to determine genetically desirable and undesirable individuals as well as their descendants, to elucidate population structure and mating system, and to designate appropriate individuals for translocation or reintroduction. Hence, pedigree management programs based on mean kinship or minimal founder contributions are commonly used to minimize inbreeding in local subpopulations and metapopulations. Delineating refine ESUs is important when considering long-term conservation actions especially translocations and captive breeding programs. Translocation between ESUs should be avoided in order to successfully replenish the diversity and viability of severely declining and nearly monomorphic populations with severe inbreeding depression (low heterozygosity, low fertility (e.g., poor sperm and ovum quality and cryptorchidism), and low disease susceptibility). Whereas captive breeding programs between ESUs may lead to reduce genetic variability and increase populations' susceptibility to extinction.

3. Genetic variability as the heart of managing biodiversity

Conservation of the genetic variability within a species is necessary as a part of global efforts to manage and conserve biodiversity. High levels of genetic variability in most natural populations of plants and animals are determinants of future population/species evolution. Genetic variability which is determined by genetic diversity can be interpreted at several levels including karyotypic variation (usually low within a species), allozyme variation (usually high within a species), and DNA sequence variation (maybe very high within a species at nongenic region e.g., short repeat sequences (microsatellites/SSR) of nuclear DNA, and maybe low within a species at genic region).

Genetic diversity can be assessed by determining kinship lineage and home range within and between a particular species/population of wildlife by using DNA analyses. Through DNA analyses, crucial information including identification of parentage, distant relatives, founders of a population, unidentified individuals, and population structure (mating system, sex ratio, estimate past population size and patterns of variability over periods time) can be correctly done to ensure genetic effective population size (N_e) is present in a particular wildlife population/species. DNA analysis expressed as genetic distance allows interpopulation comparisons to uncover spatial structuring and historical patterns of gene flow within a species. The absolute values of genetic distances which can be calculated from dissimilarities in genetic diversity vary between species, and they are increased over geological time. Therefore, accurate ESUs for effective conservation management purposes can be justified. Widely use DNA analyses by conservation geneticists are allozymes, DNA minisatellite fingerprints, RAPD, mtDNA sequences, cpDNA sequences,

genic sequences such as MHC genes, and nDNA sequences including microsatellites and SNP. The recent DNA analysis used by conservation geneticists involves the investigation of a whole-genome that is typically challenged with a huge amount of DNA base. Both nuclear and mitochondrial sequence data still provide the most informative characterizing variability at or above the level of populations. Whereas for characterizing variation within populations, polymorphic nuclear microsatellite loci and SNP are ideal markers. The various DNA analyses provide different resolutions of pedigree, population, and species-level answers and all methods are correct. Most importantly, DNA analyses can be performed for wildlife populations without requiring plants to be disturbed and animals to be seen and disturbed, as well as for museum and fossil specimens (e.g., dodo, moa, thylacine, and quagga). This can be done by using non-invasive (shed tissues, faeces, urines, and scent markings) and non-destructive (toe, tail and ear clips, and fish scales) samples. Nevertheless, DNA of some types of non-invasive and non-destructive samples may deteriorate rapidly, and hence be very difficult to work with, but it is possible with extra technical care and patience.

DNA sequence variation at the genic region is the focus of conservation geneticists. This is due to in natural populations, much of genetic variability at genic region have been discovered are appeared to be selectively neutral or near-neutral in their effects on the phenotypes (i.e., cryptic variations). Hence, the individuals carrying these allelic variants/genetic diversities appear phenotypically normal. In addition, some cryptic variations have shown circumstantial evidence that they are beneficial — provide long-term population perseverance and evolvability [5]. However, their relationship between genetic variability and individual fitness is not well understood. In a world whose change is unpredictable, alleles that are selectively neutral for thousands of generations can suddenly become a saviour for the individual who carries it. Experiments and field observations on several species have shown that there is a positive relationship between genetic variability at the genic region and individual adaptability or evolvability in important ecological aspects and significant phenotypes. The phenotypes are including body size, symmetry of body parts, growth rate, size at maturity, fecundity, hatching date, predator avoidance behaviour (e.g., escape speed, defence method, aggression, etc.), and health as measured by parasite load. Hence, conservation genetics have been putting efforts to understand genetic variability at these phenotypes through understanding the genetic diversity to explain the cause of rarity, endangerment, and extinction of a genetically deteriorate species/population. For example, cheetah (*Acinonyx jubatus*) with a low level of genetic diversity has been proved to have reduced genetic variability and hence has increased susceptibility to diseases [6, 7]. Genetic variability in these phenotypes; quantitative trait loci (QTL) are controlled by several to many genes (i.e., oligogenic and polygenic) that work additively in dominance/recessive relationships or epistatically, and their expression profiles are usually induced by environmental factors as consequences of local adaptation known as phenotypic plasticity (i.e., an adaptive mechanism). According to Fisher's fundamental theorem of natural selection, additive genetic variation (i.e., innate genetic variability; heritability (h^2)) in QTL fitness is positively related to a population's ability to respond to natural selection (i.e., evolutionary success; the ability of a species to persist despite changes in climate and environment as well as exposure to new challenges including new competitors, diseases and predators). Therefore, the heritability of such phenotypes is of conservation geneticists' interest. High heritabilities of a QTL on a trait demonstrate that a population has a great potential for evolution. Whereas low heritabilities demonstrate a more limited ability of a population to respond to environmental change. Unfortunately, such heritability is difficult to measure because it requires pedigree studies over several generations or

long-term manipulative experiments such as laboratory-raised plants and animals. Heritability is the ratio of the variance of a genetically inherited proportion of a trait (additive genetic variance, V_A ; a component in genetic variance (V_G)) which response to directional selection) to the total phenotypic variance (V_P) measured in a particular population and time. Estimating V_A is complicated by the need to estimate environment variance (V_E) as well as other genetic components in V_G that are nonadditive genetic variances including dominance (V_D) and epistasis (V_I). However, QTL analyses using studbook records for captive populations of plants and animals, and the comparison of laboratory-raised offspring to their parents in the wild have allowed conservation geneticists to predict a reliable population's risk of extinction. This provides conservation biologists with important information on how biodiversity can be best protected against climate change and anthropogenic impacts.

On the other hand, management of genetic diversity at a large number of neutral polymorphic sites (nongenic region) has provided a useful scientific assistant to clarify for setting a species/population recovery priorities and protection. Whereby it allows more explicit estimates of N_e , migration rate, populations dynamics, and population structure (units of management). It also permits better assessment of introgression concerning management against the breeding of hybrid organisms and closely related individuals. Thus, de-extinction that is bringing back extinct wildlife species and reintroducing them to their previously inhabited landscapes with optimum N_e can be successfully done. Asexually reproducing species including clonal plants, hermaphrodite invertebrates, fish, and lizards, as well as threatened species are mostly genetically invariant in their nongenic region although they may exhibit a great ecological success [8]. Therefore, they are more prone to become extinct when their environment changes than their closely related sexually reproducing species. This has been proved in several threatened species — e.g., cheetah and ice-breeding seals whereby they are ecologically successful in the wild because of their innate genetic variability despite low absolute levels of genetic diversity; both genic and nongenic genetic diversity and being classified as threatened wildlife [8, 9].

Evolution is largely dependent on genetic variability; both genic and nongenic genetic diversity, whereby the conservation and survival of species significantly depend on the conservation of their innate genetic variability [5]. Different types of genetic variability will respond differently to evolutionary factors, population collapse, and habitat fragmentation. Hence, genetic variability is an important biological factor to determine the presence of genetic diversity or it lost, understand the causes of the loss and make recommendations to overcome its ultimate effects in wildlife conservation.

4. Evolutionary factors influencing genetic variability

4.1 Mutation

Mutations encompass a wide range of phenomena; from a change of a single base pair in the genetic code to an inadvertent doubling of the number of chromosomes. Many mutations are deleterious or lethal, some are near neutral and a small number may be beneficial (usually exist as rare alleles). A large number of mutations are completely invisible in the phenotype and can only be detected with various genetic techniques. Hence, mutations are of concern for conservation geneticists in a couple of circumstances. First, mutations in small, remnant, or isolated populations with deleterious effects. Second, whether the emergence of new mutations will replace

variability lost due to population extinction and genetic erosion. Mutation rates are usually in the order of one per 10⁵ cell divisions with time for the accumulation of new variants in a population taking tens of thousands of years.

Deleterious alleles (alleles that are accountable for genetic defects such as albinism) are usually very rare and have a frequency less than 0.0001. In a large population, natural selection purges very rare alleles of deleterious mutations from the population almost immediately. However, in a small, remnant, or isolated population, purging for such deleterious alleles in the context of the conservation of threatened species breeding program should be controlled or eliminated instantly artificially because natural selection is inefficient. Even though extinction due to the presence of deleterious mutations is almost unknown, but their contribution to the extinction process should not be ignored. Theoretically, the accumulation of deleterious mutations can significantly induce inbreeding depression and genetic erosion of fitness [10]. Deleterious alleles if not eliminated in a population, will gradually increase in frequency and become a serious problem when the frequency exceeds 0.05 or $1/(2N_e)$. Fortunately, this process took hundreds of generations.

On the other hand, conservation geneticists are often being demanded to save rare alleles including mildly deleterious alleles in threatened populations as they may be important for the population's adaptation towards environmental changes. The maintenance of desirable rare alleles including mildly deleterious alleles require very large population sizes and is simply not possible in most captive management programs. The risk of extinction due to fixation of rare alleles including mildly deleterious mutations of equal importance to environmental stochasticity and can reduce the long-term viability of populations with N_e of less than a few thousand. An optimum $N_e = 10,000$ is required to ensure genetic and demographic factors act synergistically for avoiding inbreeding depression and for suppressing genetic erosion of fitness [11]. Small populations ($N_e < 500$) can decline fitness rapidly with the accumulation of mildly deleterious mutations, called mutational meltdown [11–13]. However, many threatened species currently have insufficient individuals to ensure long-term viability if $N_e = 10,000$ is strictly required.

Therefore, conservation geneticists are often left with conflict to design conservation plans that will further maintain rare alleles including mildly deleterious alleles, and eliminate deleterious alleles in threatened populations without jeopardizing populations' fitness. If the purpose of a conservation program is to return captive populations to the wild, then managers should maximize the genetic variability of rare alleles including mildly deleterious mutants. On the other hand, if the population cannot be returned to the wild and must be sustained in captivity for many generations, managers should either purge or rigorously control deleterious mutations and maintain rare alleles including mildly deleterious mutants as they are identified. For example, the homozygous recessive rare allele of White tigers (*Panthera tigris*) show no severe physiological defects but are needed to be strictly controlled in the captive populations and curbed from transmission to the wild populations to maintain the wild tiger populations [14].

4.2 Non-random mating

The ideal population genetic theory is based on random mating. It is widely accepted that random mating in sexual reproduction species evolved in part because of chromosomal crossing over and recombination facilitated by outbreeding. Most plants and animals species have effective immunological and behavioural mechanisms to favour outbreeding. These include asynchronous maturation of male and female gametes, sex-biased dispersal of the juvenile from their natal population, complex courtship behaviours, and the evolution of diverse self-incompatibility

systems. Though, such mating behaviour is rarely observed in the nature of non-random mating species. The three extreme modes of non-random mating species are self-fertilized hermaphroditic, obligate outbreeding dioecious, and females preferentially mate (also known as selective breeding).

The most extreme consequence of non-random mating is the rise of inbreeding. Inbreeding refers to the mating of close relatives — matings between father and daughter, brother and sister, or first cousins. Many species of plants and animals have evolved mechanisms to minimize close inbreeding. Species differ greatly in their tolerance to inbreeding; for example, some trees and dioecious plants are obligate outcrosses. In wild populations, the occurrence of gradual inbreeding allows natural selection to purge the first generation but the partially recessive near-neutral mutations continue to increase in frequency and significance. Inbreeding results in increased homozygosity of recessive partially deleterious mutants and by chance, in small isolated populations, these alleles can become fixed. In the simplest genetic example of a trait under the control of this recessive allele, there is an increased risk that the offspring of two related healthy but heterozygous individuals will inherit the harmful allele from each parent and die. Although the risk, in this case, is only one in four, this is a very strong fitness difference in which natural selection will act. Generalizing from this simplest single-locus example, geneticists discuss inbreeding depression as an overall manifestation of the genomic effects of mating between close relatives. These effects may involve outright genetic disease (congenital abnormalities) but are more often subtle and appear as decreased growth rate, behavioural abnormalities, and reduced fertility and fecundity. Inbreeding is rare in typically outbreeding populations but becomes a serious problem in small isolated populations. In small isolated populations and fragmented populations, inbreeding depressions can intimidate population viability. Animal and plant breeders have learned this lesson from their centuries of experience with artificial selection, and therefore they limit inbreeding rates to less than 2% per generation. The genetic underpinnings of inbreeding depression (i.e., reduced viability and fecundity) are best studied and understood in inbred strains of laboratory-reared *Drosophila* and Mice, in which recessive lethal mutations and mildly deleterious mutations arise due to non-random mating [5].

There is abundant evidence that isolated wildlife populations suffer inbreeding depressions. Inbreeding depression can be avoided in the short term if $N_e > 50$ [12]. The inbreeding coefficient (F) increases by $1/2N_e$ per generation and centuries of animal breeding experience show that a 1% increase in F per generation is tolerable. Thus, $N_e = 50$ is necessary to avoid inbreeding depression [12]. Jamieson and Allendorf [12] further concluded that $N_e > 500$ was necessary to enable a population to continue to evolve in the long term. Although this 500 number has been revised upwards, the theory behind the 50 number is still accepted [15]. But it is important to realize that its derivation was based on controlled laboratory experiments; larger N_e ($N_e = 10,000$) are required in nature, where environmental fluctuations are more severe and stressful.

4.3 Gene flow

One of the fundamental agents in evolution that interest conservation geneticists are the dispersal of genes (i.e., gene flow) between populations of a species. Gene flow can be either active or passive, often gender-biased and limited to certain phases of the life cycle. It may be accelerated under certain climatic conditions that occur at frequencies of many years or irregular intervals of many years apart. Gene flow is typically can be estimated from allele frequency data and presented in terms of the number of successful establishment migrants per generation in the new

population. In theory, one migrant per generation between two populations will ensure the two populations remain genetically homogeneous and related, as well as reduce inbreeding depression. In the future, overcoming genetically depauperate populations. Whereas lack of gene flow allows interpopulation differentiation. Hence, understanding historical patterns and rates of gene flow in a conserved population are crucial. Particularly if previously continuous populations become fragmented, the patterns of historical dispersal and gene flow may be disrupted with potentially serious consequences for population viability. For example, if young female orangutans can no longer migrate and confine from their natal social group due to habitat destruction in the surrounding area, their isolated natal populations will experience significantly increased inbreeding. On the other hand, if previously fragmented populations with each population have the unique genetic basis for adapting to local conditions become interacted, gene flow can erode the genetic differences between populations. Consequently, the two populations become one and some unique genes/alleles may be lost (see genetic drift).

In nature, widespread interspecific gene flow may occur between members of two different but related species (i.e., semispecies) or between very distantly related conspecific individuals in hybrid zones and produce hybrids. Hybrids are commonly sterile, or partial sterile in one sex or have high neonate mortality or have genetic disorders, and rarely are fertile. However, if fertile interspecific hybrids (also known as introgressive hybridization) exist, it causes a dilemma in conservation management. Because their occurrence reduces the value of the taxon. But at the same time, it is interesting because they show that the evolution of many groups of species involves both lineage splitting and lineage anastomosis. Hybridization is more common observe in plants than in animals; therefore, not surprisingly in plants, there are many examples of rare species being hybridized with the more common sympatric congeners (genetic assimilation) and become extinct (e.g., [16]).

4.4 Genetic drift

Genetic drift is referring to the loss of alleles from a population by chance due to a sudden reduction in N_e . This results in loss of fitness unless there is a rapid and continuous recovery. Often in nature, genetic drift happens almost clocklike regularly [5, 7] and followed by a rapid population recovery is referred to as a demographic bottleneck. They can have an immediate impact on variability at molecular genetic loci as genetic drift snatch the innate variation in a population. The evidence of a demographic bottleneck may persist for hundreds of thousands to millions of generations in low levels of variation in the loci of allozyme and molecular genetic markers. On the other hand, a demographic bottleneck can result in a short-term increase in population variation because epistatic variation (due to interactions among genes controlling a trait) is transformed into additive variation. However, whether it is beneficial or harmful to population viability is unknown.

The rate at which alleles are lost from a population by genetic drift can be statistically estimated. Sewall Wright theoretical model showed analytically how the rate of allele loss varies with population size, and concluded that census population size (N) is not important but rather the N_e . N_e is almost always less than N under some populations. N_e taking into account the fact that closely related individuals will share alleles with the same lineage, unequal numbers of males and females, increased variances in family size, and temporal fluctuations. N_e can be defined and estimated in a variety of ways using temporal ecological data, DNA sequences, and a variety of methods to estimate migration rates. Some estimation methods have theoretical value but little operational utility. Even so, by estimating N_e the effects of different population management strategies can be evaluated.

In many threatened populations, N_e is only 10–30, and at such levels, genetic variation becomes significant for the viability of the population.

Very low genetic variability has been known in many sexually reproductive species whose currently large populations have recovered from one or recurrent demographic bottleneck or extinction. Meanwhile, in a large continuously distributed population (metapopulation) with frequent extirpation and recolonization of subpopulations, reduce metapopulation N_e orders of magnitude below than N can mimic the genetic effects of a demographic bottleneck. In small isolated populations with the absence of factors driving genetic variation (mutation and gene flow), the impacts of demographic bottlenecks are severe. Whereby demographic bottleneck reduces genetic variation (loss of heterozygosity), leading to increased homozygosity and loss of evolutionary adaptability to change (genetic variability or selectively neutral variation). The genetic variability is expected to be lost $\frac{1}{2}N_e$ per generation and mostly lost within $2N_e$ generations. N_e of 10 is predicted to lose heterozygotes five times faster than N_e of 100. This is because 50% of heterozygosity in $N_e = 10$ will be lost in approximately 20 generations. Therefore, in theory, small isolated populations have a higher rate of loss of heterozygosity and faster loss of variability by genetic drift than large populations and metapopulations).

4.5 Natural selection

In nature, differences in the survival and reproduction of some genotypes over others as the major agents of microevolutionary changes are known as natural selection. Natural selection attracts the interest of conservation geneticists for two reasons. First, human activities can radically alter selection coefficients in both natural and control populations. Such evolutionary changes of human influence are referred to as artificial selection whether intentional or not. This can be seen in many commercially exploited wildlife species, whereby has resulted in rapid behavioural and natural history changes and consequently reduced fitness. Examples include reduced body size in the game and commercial fish and the impact of hunting only horned or tusked male mammals on social behaviour.

Second, the major challenges to assist wildlife species adapt to ongoing global climate change. In the past, in the absence of humans, natural selection favoured individuals adapted to change and many species shifted their ranges towards accommodating major changes. The rate of directional selection that a population can control in response to some environmental change is in part, is determined by its inherent variability. Unfortunately, in the 21st century, environmental change and destruction such as those associated with global warming are happening too quickly for many species to respond to it. Hence, effective conservation management is necessary to ensure that many species survive.

5. Conclusions

The importance of incorporating conservation genetics in managing biodiversity is undeniable. This is because the understanding of the relationship between evolutionary factors including mutations, non-random mating, gene flow, genetic drift, and natural selection in population/species survival is very important in the current situations where many natural populations are declining towards species extinctions. Therefore, with the relevant literature review in this chapter, it is hoped to provide brief explanations of the importance of assimilating conservation genetics to manage biodiversity. Especially to those who are less aware of the scope of genetic conservation studies.

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Conflict of interest

The authors declare no conflict of interest.

Appendices and nomenclature

N	Census population size
cpDNA	Chloroplast DNA
DPS	Distinct population segments
Ne	Effective population size
ESU	Essential Evolutionary Unit
IUCN	International Union for Conservation of Nature
MHC	Major histocompatibility complex
mtDNA	Mitochondrial DNA
nDNA	Nuclear DNA
PVA	Population Viability Analysis
RAPD	Random amplified polymorphic DNA
allozymes	Single-locus markers
SNP	Single nucleotide polymorphism
QTL	Quantitative trait loci

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