Nig. J. Wildlife Management, 2017 (SPECIAL EDITION) 1(1): 11 - 18
© Wildlife Society of Nigeria

Nigerian Journal of Wildlife Management

Importance of genetics in conservation of biodiversity

Coker, O.M.
Department of Wildlife and Ecotourism Management, University of Ibadan, Ibadan, Nigeria
E-mail: liftingup2003@gmail.com Phone: +234 805 4150 061

Abstract

Genetic diversity is the centre pillar for species and ecosystem diversities and the main goal of conservation genetics is to apply the knowledge of genetics to reduce the risk of extinction. Unfortunately, it has not received its deserved place in the biodiversity conservation efforts. This review is aimed at highlighting the need for the application of genetics in the conservation of natural resources and as well to assess the successes recorded so far while also identifying some challenges of conservation genetics. Non-invasive DNA sampling have been used to trace the origin of seized ivory tusk, detect hybridization, evaluate social structures in organisms, estimate population size and identify predator of kills. Poor adaptation of captive-bred endangered species when they are reintroduced to the wild, solving the problem of inbreeding and the high cost of conducting researches were identified as some of the challenges in the field of conservation genetics.

Keywords: Conservation genetics, biodiversity, genetic diversity, natural resources

Introduction

One of the major duties of man is to ensure the proper management and conservation of all the natural resources around him, without which his own existence is threatened. Unfortunately, a vast number of these resources are threatened with extinction due to habitat destruction, environmental pollution, climate change, over-exploitation, environmental variation and natural disasters (Frankham et al., 2010). Most of these are due to the activities of man. Many wildlife populations have been reduced to small isolated fragmented populations with reduced potentials for survival as a result of the afore-mentioned activities of man. Small populations are potentially at risk and the main goal of conservation genetics is to apply the knowledge of genetics to reduce the risk of extinction (Frankham et al., 2010). This review highlights the need for the application of genetics in the efforts of conservation of natural resources, assessed some successes recorded so far with conservation genetics and identified the challenges facing conservation genetics.

The need for conservation of biodiversity

The attempt to protect the vast biological diversity is referred to as conservation (Eisner et al., 1995; Allendorf et al., 2013). There are three forms of biodiversity that are recognized by the International Union for Conservation of Nature (IUCN): Ecosystem diversity, Species diversity and Genetic diversity (McNeely *et al*., 1990; Allendorf et al., 2013). Genetic diversity is the centre pillar of the other two. Unfortunately, according to Laikre et al. (2010), member countries of the Convention on Biological Diversity (CBD) have generally ignored genetics in their National Biodiversity Strategy and Action Plans. There is no doubt that the vast biological resources in the world needs adequate protection especially those that are vulnerable and endangered. Currently, a large but unknown number of species are going into extinction at an alarming rate, a situation that has been termed "the sixth extinction" (Leakey & Lewin, 1995). The rate of extinction in vertebrates had increased with time (Hruska, 2015; Frankham et al., 2010) (Figure 1). Many species may be going extinct even before they are discovered and described (Gentry, 1986). Extinction is a natural evolutionary process which leads to the formation of other numerous species as it was the case in the previous five extinctions. However, the current rate at which species are lost far outruns that of speciation (Leakey & Lewin, 1995; Frankham et al., 2010). This calls for more than a double effort in the conservation of biodiversity.

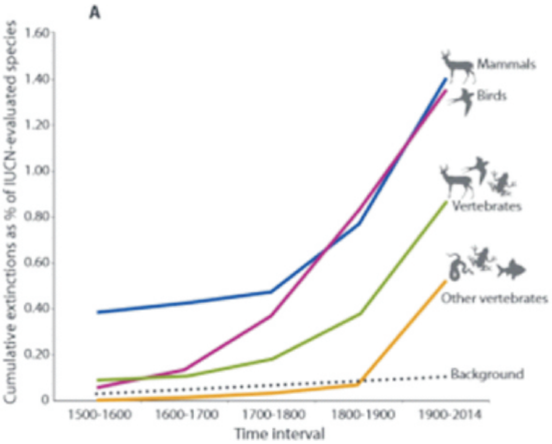

Figure 1: Cumulative vertebrate species recorded as extinct or extinct in the wild by the IUCN (2012)
Source: Hruska, 2015

Conservation biology is a multidisciplinary field that requires contributions from several areas of study (Figure 2). The field of genetics has been recognized as key in the efforts of biodiversity conservation (Soulé & Wilcox, 1980; Frankel & Soulé, 1981; Schonewald-Cox et al., 1983). Since its recognition in the field of conservation, genetics has increasingly been proven as an integral discipline in the field of conservation of biodiversity (Frankham et al., 2010; Allendorf *et al.*, 2013).

Figure 2: Structure of conservation biology and the position of genetics in it
Source: Frankham *et al.* (2010)

Conservation genetics

One important and constant factor facing the world's biodiversity is environmental change. Species have to cope with the ever-changing environment in order to survive. As such, adaptation to environmental changes becomes paramount in order to avoid extinction (Hansen et al., 2012). Maintenance of biodiversity is one of the most important current concerns of humankind, as wild species and domestic breeds and strains are disappearing at an alarming rate, and an increasing number of these require human intervention to guarantee their survival (Frankham et al., 2002). It has been estimated that about 99% of species that had ever lived are now extinct (Raup, 1994; Freeland et al., 2011) and over the past 400 years or so, several hundreds of species had disappeared (Freeland et al., 2011). Genetic diversity is the building block for other higher levels of biodiversity (populations, species) and it is the basis of evolutionary potential of species to respond to environmental changes and as such becomes an essential pillar in conservation genetics (Geffen et al., 2007).

Conservation genetics applies the principles of genetics to preserve/conserve species as dynamic units that can cope with environmental change (Frankham et al., 2010). Knowledge of genetics aids conservation by helping in the genetic management of small populations, resolution of taxonomic uncertainties, defining management units within species, the use of molecular genetics analyses in forensics and understanding species' biology (Sikes et al., 2008; Freeland et al., 2011) .It deals with the genetic factors that affect extinction risks and genetic management regimes required to minimize these risks. Conservation genetics itself is an applied science which thrives on the knowledge of molecular ecology and population genetics (Frankham et al., 2010; Allendorf et al., 2013).

Population genetics

The science of population genetics deals with Mendel's laws and other genetic principles as they apply to populations of organisms (Hartl & Clark, 2007). A population is the group of organisms of the same species living together in the same environment at a particular time (King et al., 2006). Members of a population are able to interact sexually and produce offspring. Population genetics cuts across many fields of modern biology. A working knowledge of population genetics has become essential in genetics, genomics, evolutionary biology, computational biology, systematics, plant breeding, animal breeding, ecology, natural history, forestry, horticulture, conservation, and wildlife management (Hartl & Clark, 2007).

Population genetics is aimed at three goals. The first aim is to explain the origin and maintenance of genetic variation. Second is to explain the patterns and organization of genetic variation and the third is to understand the mechanisms that cause changes in allele frequencies (Conner & Hartl, 2004). To achieve these aims, population genetics studies the genetic differences within and among populations and how these differences change from one generation to next.

Molecular ecology

Broadly speaking, the application of molecular genetic methods to ecological questions is termed molecular ecology. This term was rarely used prior to1990, although many earlier studies could reasonably be described as molecular ecology. The emergence of this field of study hinges on systematics, evolutionary theory, genetics and behavioral ecology (Beebee & Rowe, 2008).

The subject of ecology itself studies the interactions between organisms and its physical environment. The environment also interacts with genotypic composition of a species to bring about its phenotypic expressions. These give rise to arrays of phenotypic data based on one or more aspects of an organism's biochemistry, behaviour, morphology or physiology. But phenotypic data on their own are limited (Freeland et al., 2011). The potential of a single genotype to develop into multiple alternative phenotypes under different environmental conditions (phenotypic plasticity) is a major short fall making phenotypic data inadequate for diversity studies. Genetic data which allows direct quantification of genetic variation is more reliable (Freeland et al., 2011).

Also, increasing availability and scope of genetic markers has immensely contributed to the success of molecular ecology (Beebee & Rowe, 2008). With molecular markers, quantification of genetic diversity, tracking of the movement (gene flow) patterns of organisms, measure of inbreeding, identification of individuals and populations, new species characterization, retracing historical patterns of dispersal, resolution of population structure, resolution of taxonomic uncertainties, detection of hybridization and wildlife forensics are all possible with high accuracy (Freeland et al., 2011).

Genetic variation and diversity

Genetic diversity has been defined as the variety of alleles and genotypes present in a population and this is reflected in morphological, physiological and behavioural differences between individuals and populations (Frankham et al., 2002). From a functional point of view, genetic diversity can be classified as neutral, deleterious or adaptive (Hedrick, 2001). Generally, neutral variants are used for conservation applications, but deleterious and adaptive variations are also important in the contexts of population survival and economically important traits in domestic plants and animals (Toro & Caballero, 2005). Genetic diversity is usually measured by the frequencies of genotypes and alleles, the proportion of polymorphic loci, the observed and expected heterozygosity or the allelic diversity (Allendorf et al., 2013). The most widely used parameter to measure diversity within populations is the expected heterozygosity, or gene diversity, defined as the probability that two alleles chosen at random from the population are different. In monitoring conservation programmes, a key parameter is the rate of change in gene diversity or inbreeding (Toro & Caballero, 2005).

Genetic variation and diversity depend on the levels of gene flow between and among populations. The degree of differentiation among populations (F_{ST}) is usually greater for species with lower migration rates among subpopulations compared to those of higher dispersal rates. Differentiation is also expected to be greater for subdivided habitat compared with continuous habitat (Conner & Hartl, 2004; Frankham et al., 2010). Gene flow among populations is particularly important for evolutionary processes, but the mechanisms are not fully understood yet (Pilot et al., 2006).

Quantitative genetic variation is the basis of productive and reproductive traits and therefore of greatest concern in conservation biology. Analysis of data from families allows estimates of the amount of additive genetic variance or heritability for polygenic traits to be obtained (Falconer & Mackay, 1996).

Most populations of endangered species are commonly subdivided into different breeding groups, either in different fragments of habitats, natural reserves, arboreta or zoos, or in different breeds or strains in the case of domestic plants and animals, which are, in turn, subdivided into smaller reproductive units more or less interconnected. Thus, characterization and management of genetic diversity has to be assessed, considering distinct nature of population structures (Toro & Caballero, 2005). This will help to determine species that need to be managed in order to preserve the genetic diversity (Grobler et al., 2004).

Genetic Exploits in Conservation and Management of Biodiversity

The discovery of the Polymerase Chain Reaction (PCR) techniques has revolutionized the field of molecular studies. This has made the use of small number of samples useful in conservation genetics. Even samples that are considered poor in quality can still be used. This is a great achievement since endangered species can be effectively studied non-invasively, using, hair, urine, faeces, regurgitates, egg shells, saliva and sloughed skin (Waits & Paetkau, 2005). Noninvasive genetic sampling has been used to trace the origin of seized ivory tusk (Wasser et al., 2004), detect hybridization (Adams et al., 2003), study genetic diversity and gene flow (Lucchini et al., 2002), evaluate social structures in organisms (Garnier et al.,2001), estimate population size (Mowat & Strobeck, 2000) and identify predator of kills (Farrell et al., 2000) (Table 1).

Table 1: Some Applications of Genetics to Conservation

Application	Species	Citation
Ivory tusk region of origin	Elephant	Wasser et al. (2004)
Estimating population size	Elephant, Grey Wolf	Mowat & Strobeck (2000)
Genetic diversity and gene flow	Grey Wolf, Brown Bears, Elephants	Lucchini et al. (2002)
Detecting hybridization	Red Wolf	Adams et al. (2003)
Evaluating social structure	Chimpanzee, Rhinocerous	Garnier et al. (2001)
Predator identification of kills	Coyote, Dingo	Farrell et al. (2000)

Source: Waits & Paetkau, 2005.

Information about the genetic structure of a population provides a platform to evaluate the level of inbreeding and its possible impact on biodiversity. This information is also important to understanding how diseases may spread among wildlife populations (Ernest, 2000*)*. Genetic structure and genetic differentiation are the results of natural processes like migration, genetic drift, natural selection and historical events. Studies of these structures and differentiation usually focus on isolated and partially isolated small populations where evolutionary forces such as founder effect, drift, inbreeding and selection are expected to cause genetic changes (Templeton, 1987), as a result of limited gene flow (Epperson, 1992 cited in Jones et al., 2007). However, continuous landscape may differ characteristically as to inform interesting genetic structure of some species of organisms. Environmental differences are likely to cause differences in selection among sub-populations which is likely to lead to local adaptation and genetic variation at loci that affect adaptations to these local conditions (Coker, 2016).

Pilot et al. (2006), using mtDNA and microsatellite loci established that the genetic differentiation among local populations of European grey wolves correlates with climate, habitat types, and diet composition. This suggests that ecological processes may strongly influence the amount of gene flow among populations. They therefore suggested that natal-habitat-biased dispersal is an underlying mechanism linking population ecology with population genetic structure.

Genetic studies on North American wolf populations revealed a pattern of isolation by distance on a continental scale (Geffen et al., 2004) and regional scale (Forbes & Boyd, 1997; Carmichael et al., 2001), although previous studies failed to establish a significant isolation by distance (Roy *et al.,* 1994; Vilà *et al*., 1999). Vegetation type along with climate and habitat type have been suggested to play a role in the genetic dissimilarities among populations (Geffen et al., 2004) in addition to the distance between populations. Natural barriers, such as rivers, mountains, swamps, and deserts impede gene flow and therefore play a key role in the genetic structure of populations (Wayne *et al*., 1991; Wayne *et al*., 1992; Carmichael et al., 2001). Other determinants of gene flow and genetic structure includes habitat fragmentation, anthropogenic activities and prey distribution (Wayne et al., 1992, Young & Clarke, 2000).

Investigating the genetic structure of the populations of cattle (*Bos taurus*) in northern Eurasia and the neighbouring regions using microsatellite markers, it was discovered that populations of modern commercial origin are genetically distinct from those of native origin (Li et al., 2007).

Cane rat (grasscutter) is an economically important rodent in West Africa based on the preference of its meat as an alternative source of protein in the area. Majority of these are usually sourced from the wild. According to the IUCN, the status of this animal is "least concern". Adenyo et al. (2013) used mitochondrial D-loop sequence to investigate diversity among cane rats in Guinea Savanna, Forest and Coastal Savanna in Ghana. They suggested that the Ghanaian populations of cane rats are highly diverse but less distinctive and that there is no evidence of isolation by distance among the populations. A similar study on cane rats in Southwestern Nigeria using microsatellite markers confirmed a high level of genetic variation among this species (Coker et al., 2017). This high level of genetic variation is suspected as the reason why they are not yet threatened in any way.

The application of DNA forensic techniques to wildlife management had increased over the years amidst global concern over the loss of biodiversity and the suspicion that organized crime is involved in illegal wildlife trade (Ogden, 2010). Following its success in the field of human crime investigations, DNA forensics was extended to the field of wildlife crime investigation with great potential to successfully curb illegal wildlife trades (DeSalle & Birstein, 1996; Wasser et al., 2004) and poaching (Sweijd et al., 1998). Wildlife DNA forensics had been effective in identifying an individual, a species and the geographic origin of wild species (Ogden et al., 2009; Ogden, 2010).

When poachers are captured, the evidences from the crime scene are the remains (meat, fur, bone and skin) of the animal. Precise identification of wildlife is therefore necessary (Sanches et al., 2012). According to Grobler et al. (2005), the resolution power of microsatellite markers and assignment tests have been applied to determine species identity and to trace their geographical origins. Wildlife forensics has helped to identify both endangered and non-endangered wildlife species in some traditional East Asian medications (Tobe & Linacre, 2011).

Wasser et al. (2007), in their work on "using DNA to track the origin of the largest seizure since the 1989 trade ban" examined the tusk seized from Singapore and confirmed that the tusks originated from the savanna habitats. They were also able to estimate that locations of origin for the tusks spread east and west from Zambia and may include regions of Mozambique and savanna Angola. It has also been used to verify captive breeding claims where bird theft was suspected (Shorrock, 1998).

Wildlife DNA forensics is a very important aspect of conservation genetics which has the potential to unravel high profiled wildlife crimes committed in the past and in the present. The field is becoming increasingly popular just as the wildlife crime is also increasing.

Challenges of Managing Biodiversity with Genetic Tools

Managing biodiversity with genetic tools is not without its challenges. One of such is finding a lasting solution to the poor adaptation of captive bred endangered/threatened species when they are reintroduced to the wild. It will be good to establish explicit management strategies (including genetic pedigree documentations of the species) that will minimize genetic adaptation to captivity. This can help maximize successful reintroduction (Frankham, 2010). Inbreeding has been identified as a major challenge in biodiversity conservation. Inbred populations are known to exhibit some genetic weaknesses known as inbreeding depression. Species exhibiting inbreeding depression in the wild include, golden lion tamarins (*Leontopithecus rosalia*), lions (*Panthera leo*), greater prairie chicken (*Tympanuchus cupido*), song sparrow (*Melospiza melodia*), reed warbler (*Acrocephalus scirpaceus*), and many species of plants (Saccheri et al., 1998; Frankham et al., 2010). Signs of inbreeding depression in endangered Florida panthers include heart defects, kinked tail, undescended testes and poor semen quality. This was addressed in Florida Panthers by the introduction of its closely related population from Texas in other to increase their genetic diversity (Frankham et al., 2010). But how can inbreeding be reversed in a population that does not have any relative in any other part of the world° We may have to depend on mutation which is the only source of genetic diversity. This looks far from reach since the rate of mutation in natural populations is extremely slow.

Also, the cost of conducting research in the field of conservation genetics is high. There is a need to develop a low cost genome sequencing regime which is believed will ease researches in the field of conservation genetics and thereby increase research output in the field. According to Frankham (2010), a major challenge is to be able to assess genetic diversity of adaptive values on a genome-wide scale. High cost is a major bottleneck to this venture. Development of simple inexpensive means is necessary in monitoring genetic diversity of species.

Conclusion

The importance of genetics in conservation of renewable natural resources cannot be overstressed, yet there has been limited application of genetics to management of biodiversity and their habitats. Knowledge of genetics have aided conservation efforts by reducing extinction risk, minimizing inbreeding and loss of genetic diversity, identifying populations of conservation concern, resolving population structure, resolving taxonomic uncertainties, defining management units within species, detecting hybridization, defining sites for reintroduction, choosing the best populations for reintroduction and forensics. There is therefore no doubt that the field of conservation genetics is key in the efforts of biodiversity conservation.

Acknowledgement

I want to appreciate Prof. Abosede O. Omonona (Department of Wildlife and Ecotourism Management, University of Ibadan) for her advice and suggestions in the course of the review. Also, I thank Mr. A. T. Adetuga ((Department of Wildlife and Ecotourism Management, University of Ibadan) for his useful suggestions in the buildup of this review and helping to proof read the manuscript.

References

Adams, J. R., Kelly,B. T., & Waits, L. P. (2003). Using fecal DNA sampling and GIS to monitor hybridization between red wolves (*Canis rufus*) and coyotes (*Canis latrans*). *Molecular Ecology,* 12, 2175–2186.

Adenyo, C., Hayano, A., Kayang, B. B., Owusu, E. H. & Inoue-Murayama, M. (2013). Mitchondrial D-loop diversity of grasscutter(Thryonomys swinderianus Rodentia: Hystricomorpha) in Ghana. *Open Journal of Animal Sciences,* 3, 145-153

Allendorf, F. W., Luikart, G. & Aitken, S. N. (2013). Conservation and the genetics of populations. John Wiley and Sons Ltd, West Sussex, UK. Pp 97-134

Beebee, T. J. C. & Rowe, G. (2008). An Introduction to Molecular Ecology (2nd Ed). Oxford University Press. Pp 90-120

Carmichael, L. E., Nagy, J. A., Larter, N. C., & Strobeck, C. (2001). Prey specialization may influence patterns of gene flow in wolves of the Canadian Northwest. *Molecular Ecology*, 10, 2787–2798.

Coker, O. M. (2016) Molecular Characterisation of Wild and Captive- Reared Cane Rats (Thryonomys swinderianus Temminck, 1827) in Southwestern Nigeria Unpbl. PhD thesis, University of Ibadan

Coker, O. M., Omonona, A.O., Fagbohun, A. O., Pylant, C. &d Austin, J. (2017). Genetic structure of wild and domesticated grasscutters (*Thryonomys swinderianus*) from Southwestern Nigeria. *African Zoology*, 52(3): 155-162

Conner, J. K. & Hartl, D. L. (2004). A primer of ecological genetics. Sinauer Associates, Inc. USA

DeSalle, R. & Birstein, V. J. (1996). PCR identification of black caviar. *Nature*, 381:197–8.

Eisner, T., Lubchenco, J., Wilson, E. O., Wilcove D. S. & Bean, M. J. (1995). Building a scientifically sound policy for protecting endangered species. *Journal of Science,* 269(5228), 1231–1233.

Epperson, B. K. (1992). Spatial structure of genetic variation within populations of forest trees. *New Forests,* 6, 257–278.

Ernest, H.B. (2000). DNA sampling and research techniques. *Outdoor California*. May-June. 61(3), 20-21.

Falconer, D.S. & Mackay, T.F.C. (1996). Introduction to quantitative genetics. In Longman 4th ed. Harlow, UK. Longman

Farrell, L. E., Roman, J.& Sunquist, M. E. (2000). Dietary separation of sympatric carnivores identified by molecular analysis of scats. *Molecular Ecology,* 9, 1583–1590.

Forbes, S. H., & Boyd, D. K. (1997). Genetic structure and migration in native and reintroduced Rocky Mountain wolf populations. *Conservation Biology*, 11, 1126–1234.

Frankel, O. H., & Soulé, M. E. (1981). Conservation and Evolution. Cambridge University Press, Cambridge.

Frankham, R. (2010). Challenges and opportunities of genetic approaches to biological conservation. *Biological Conservation,* 143(9), 1919-1927

Frankham, R., Ballou, J. D. & Briscoe, D. A. (2002). Introduction to Conservation Genetics. Cambridge University Press, Cambridge, UK.

Frankham, R., Ballou, J. D., & Briscoe, D. A. (2010). Introduction to conservation genetics (2nd ed.) Cambridge University press.

Freeland, J. R., Kirk, H., & Petersen, S. D. (2011). Molecular Ecology (2nd Ed). John Wiley & Sons, Ltd. West Sussex, UK. Pp 135

Garnier, J. N., Bruford,M. W. & Goossens, B. (2001).Mating system and reproductive skew in the black rhinoceros. *Molecular Ecology,* 10, 2031–2041.

Geffen, E., Anderson, M. J. & Wayne, R. K. (2004). Climate and habitat barriers to dispersal in the highly mobile grey wolf. *Molecular Ecology*, 13(8), 2481–2490

Geffen, E., Luikart, G. & Waples, R. S., (2007). Impacts of modern molecular genetic techniques on conservation biology. In: Macdonald, D. W. and Service, K. (Eds) Key Topics in Conservation Biology. Blackwell Publishing Ltd

Gentry, A.H. (1986). Endemism in tropical versus temperate plant communities. In: M.E. Soulé, ed. Conservation Biology: The Science of Scarcity and Diversity. Sinauer, Sunderland, MA. Pp. 153–181

Grobler, J. P., Hartl, G. B., Grobler, N., Kotze, A., Botha, K. & Tiedemann, R. (2004). The genetic status of an isolated black wildebeest (Connochaetes gnou) population from the Abe Bailey Nature Reserve, South Africa: Microsatellite data on a putative past hybridization with blue wildebeest (C. taurinus). *Mammalian Biology*, 70(1), 35-45.

Grobler, J. P., Kotze, A., Swart, H. & Hallerman, E. M. (2005). The application of microsatellite DNA markers for forensic analysis of koi carp (Cyprinus carpio). *South African Journal of Science*, 101, 19-21.

Hansen, M. M., Olivieri, I., Waller, D. M., Einar E. Nielsen, E. E. & The Gem Working Group (2012) Monitoring adaptive genetic responses to environmental change. *Molecular Ecology,* 21, 1311–1329

Hartl, D. L. & Clark, A. G. (2007). Principles of population genetics (4th edition). Sinauer Associates, Inc. Publishers, USA

Hedrick P. W. (2001). Conservation genetics: where are we now° . *TREE,* 16, 629–636.

Hruska, J. (2015). More evidence suggests Earth is entering a sixth extinction-level event. ExtremeTech Newsletter June 22, 2015 at 3:00pm.https://www.extremetech.com/extreme/208739-more-evidence-suggests-earth-is-entering-a-sixth-extinction-level-event accessed on 23rd Nov., 2017

IUCN (2012). IUCN Red List Categories and Criteria: Version 3.1. Second edition. Gland, Switzerland and Cambridge, UK: IUCN. 32pp

Jones, T. H., Vaillancourt, R. E., & Potts, B. M. (2007). Detection and visualization of spatial genetic structure in continuous Eucalyptus globulus forest. *Molecular Ecology,* 16(4), 697–707.

King, R. C., William D. Stansfield, W. D. & Pamela K. Mulligan, P. K. (2006) *A Dictionary of Genetics*. (7th ed) Published by Oxford University Press, Inc.

Laikre, L., Allendorf, F. W., Aroner, L. C., Baker, C. S., Gregovich, D. P., Hansen, M. M., Jackson, J. A., Kendall, K. C., McKelvey, K., Neel, M. C., Olivieri, I., Ryman, N., Schwartz, M. K., Bull, R. S., Stetz, J. B., Tallmon, D. A., Taylor, B. L., Vojta, C. D., Waller, D. M.& Waples, R. S.(2010). Neglect of genetic diversity in implementation of the Convention on Biological Diversity. *Conservation Biology,* 24, 86–88.

Leakey, R. and Lewin, R.(1995). The Sixth Extinction: Biodiversity and its Survival. Phoenix, London.

Li, M., Tapio, I., Vilkki, J., Ivanova, Z., Kiselyova, T., Marzanov, N., Cinkulov, M., Stojanovic, S., Ammosov, I., Popov, R., & Kantanen, J. (2007). The genetic structure of cattle populations (Bos taurus) in northern Eurasia and the neighbouring Near Eastern regions: implications for breeding strategies and conservation. *Molecular Ecology*, 16, 3839–3853

Lucchini, V., Fabbri,E., Marucco,F., Ricci,S., Boitani,L. & Randi, E. (2002). Non-invasive molecular tracking ofcolonizing wolf (Canis lupus) packs in the western ItalianAlps. *Molecular Ecology,* 11, 857–868.

McNeely, J. A., McNeely, J. A., Miller, K. R., Reid, W. V., Mittermeier, R. A. & Werner, T. B. (1990). Conserving the world's biological diversity. IUCN. Gland, Switzerland. 193 pp.

Mowat, G., & Strobeck, C. (2000). Estimating populationsize of grizzly bears using hair capture, DNA profiling,and mark–recapture analysis. *Journal of Wildlife Management,* 64,183–193.

Ogden, R. (2010). Forensic science, genetics and wildlife biology: getting the right mix for a wildlife DNA forensics lab. Forensic Sci Med Pathol DOI 10.1007/s12024-010-9178-5

Ogden, R., Dawnay, N. & McEwing, R. (2009). Wildlife DNA forensics—bridging the gap between conservation genetics and law enforcement. *Endangered Species Research,* 9, 179–195

Pilot, M., Jedrzejewski, W., Branicki, W., Sidorovich, V. E., Jedrzejewska, B., Stachura, k. & Funk, A. M. (2006). Ecological factors influence population genetic structure of European grey wolves. *Molecular Ecology*, 15(14), 4533–4553.

Primack, R.B. (1998). Essentials of Conservation Biology, 2nd edn. Sinauer, Sunderland, MA.

Raup, D. M. (1994). The role of extinction in evolution. *Proceedings of the National Academy of Sciences,* 91, 6758- 6763

Roy, M. S., Geffen, E., Smith, D., Ostrander, E. & Wayne, R. K. (1994). Patterns of differentiation and hybridization in North American wolf-like canids revealed by analysis of microsatellite loci. *Molecular Biology and Evolution*, 11, 553–570.

Saccheri, I., Kuussaari,M., Kankare,M., Vikman,P., Fortelius, W. & Hanski, I. (1998) .Inbreeding and extinction in a butterfly metapopulation. *Nature,* 392, 491–494.

Sanches, A., Tokumoto, P. M., Peres, W. A. M., Nunes, F. L., Gotardi, M. S. T., Carvalho, C. S., Pelizzon, C., Godoi, T. G. & Galetti, M. (2012). Illegal hunting cases detected with molecular forensics in Brazil. *Investigative Genetics,* 3, 17-22.

Schonewald-Cox, C. M., Chambers, S. M., MacBryde, B. & Thomas, W. L.(1983). Genetics and Conservation. Benjamin/ Cummings, Menlo Park, CA.

Shorrock, G. (1998). The success of DNA profiling in wildlife law enforcement. *Int J Biosci Law,* 1,327–341

Sikes, D.S., Vamosi, S.M., Trumbo, S. T., Ricketts, M. & Venables, C. (2008). Molecular systematics and biogeography of Nicrophorus in part-The investigator species group (Coleoptera: Silphidae) using mixture model MCMC. *Molecular Phylogenetics and Evolution,* 48, 646–666

Smith, T.B., Freed, L.A., Lepson, J. K.& Carothers, J. H.(1995). Evolutionary consequences of extinctions in populations of a Hawaiian honeycreeper. *Conservation Biology,* 9, 107–113.

Soulé, M. E., & Wilcox, B. M.(1980). Conservation Biology: An Evolutionary–Ecological Perspective. Sinauer, Sunderland, MA.

Sweijd, N. A., Bowie, R. C. K., Lopata, A. L., Marinaki, A. M., Harley, E. H. & Cook, P. A. (1998). A PCR technique for forensic, species level identification of abalone tissue. *J Shellfish Res,* 17, 889–895.

Templeton, A. R. (1987).Animal Species and Evolution. Harvard Univ. Press, Cambridge, MA Evolution 41, 233

Tobe, S. & Linacre, A. (2011). A new assay for identifying endangered species in Traditional East Asian Medicine. Forensic Science International: *Genetics Supplement Series,* 3: 232–233.

Toro, M. A. & Caballero, A. (2005). Characterization and conservation of genetic diversity in subdivided populations. *Phil. Trans. R. Soc. B Biol. Sci.*, 360,1367–1378.

Vilà, C., Amorim, I. R., Leonard, J. A., Posada, D., Castroviejo, J., Petrucci-Fonseca, F., Crandall, K. A., Ellegren, H. & Wayne, R. K. (1999). Mitochondrial DNA phylogeography and population history of the grey wolf Canis lupus. *Molecular Ecology*, 8, 2089–2103.

Waits, L. P. & Paetkau, D. (2005) Noninvasive genetic sampling tools for wildlife biologists: A review of applications and recommendations for accurate data collection. *Journal of Wildlife Management,* 69(4), 1419–1433

Wasser, S. K., Mailand, C. Booth, R., Mutayoba, B., Kisamo, E., Clark, B. & Stephens, M. (2007). Using DNA to track the origin of the largest ivory seizure since the 1989 trade ban. *PNAS,* 104(10),4228–4233

Wasser, S. K., Shedlock, A. M., Comstock, K., Ostrander, E. A., Mutayoba, B. & Stephens, M. (2004). Assigning African elephant DNA to geographic region of origin: applications to the ivory trade. *Proc Natl Acad Sci.,* 101,14847–52.

Wayne, R. K., Gilbert, D. A., Lehman, N., Hansen, K., Eisenhawer, A., Girman, D., Peterson, R. O., Mech, L. D. & Gogan, P. J. P. (1991). Conservation genetics of the endangered Isle Royale gray wolf. *Conservation Biology*, 5, 41–51.

Wayne, R. K., Lehman, N., Allard, M. W. & Honeycutt, R. L. (1992). Mitochondrial DNA variability of the gray wolf — genetic consequences of population decline and habitat fragmentation. *Conservation Biology*, 6, 559–569.

Young, A. G. & Clarke, G. M. (Eds.) (2000). Genetics, Demography, and Viability of fragmented populations. Cambridge University Press, Cambridge, UK.