

Where are we in conservation genetics and where do we need to go?

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Introduction

Conservation genetics is an applied science, involving the application of evolutionary and molecular genetics to biodiversity conservation. There are often disconnects between the highest priority scientific needs in applied disciplines and what is technologically feasible, and what is being implemented. Consequently, I will briefly address the questions ‘Where are we now in conservation genetics and where do we need to go?’ Since resources are limited, I will also address priorities for future research in conservation genetics, and for practical applications in the discipline. Most of the issues are reviewed in the 2nd edition of ‘Introduction to Conservation Genetics’ (Frankham et al. 2009).

Where are we now and what do we need to do?

There has been substantial progress in conservation genetics since its foundation in the late 1970s (see Frankel and Soulé 1981; Frankham et al. 2009). Within Europe, there have been substantial advances in the quality of the discipline during the last 5 years that seem partially attributable to the ConGen program.

Most of the theories underlying genetic concerns in conservation biology have been experimentally validated.

Practical application of genetic principles to management of captive populations of threatened species has been instituted and is being done in a scientifically rational manner. The most pressing change required is to explicitly manage populations to minimize genetic adaptation to captivity so that its deleterious impacts on reintroductions are minimized. We know in broad outline how to do this, but procedures need to be optimised based upon simulations and laboratory experiments. Genetic management of groups (where pedigrees are unavailable) needs to be widely applied in managing group-breeding threatened species.

By contrast, the application of genetics in the management of threatened species in the wild is in its infancy. This is not due to a lack of scientific guidelines, but due to failure to consider genetic issues in wild management. The most important unresolved issue in conservation biology is to address genetic issues in the management of fragmented wild populations of threatened species. There are two reasons for this shortcoming. First, wildlife managers often do not have adequate genetics training. All future conservation and wildlife biologists need to receive adequate genetics training. Second, fears of outbreeding depression are impeding the rational genetic management of fragmented populations. Thus, there is an urgent need for means to predict the risk of outbreeding depression. Many conservation geneticists believe that the risks of outbreeding depression are being overemphasized.

Arguably the greatest genetic effort in conservation biology is directed towards resolving taxonomic uncertainties. This effort is seriously compromised by the lack of an agreed definition for species in conservation biology. There are at least 22 definitions of species. The use of different definitions leads to considerable controversy and this undermines our credibility in the broader community. There is an urgent need for an IPPC-like organisation in

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conservation biology to reach a consensus on the definition of species for our purposes. On the scientific side, it would be highly beneficial if ‘speciation genes’ could be identified that allow prediction of the degree of reproductive isolation in crosses between populations. Interestingly, a recent paper has suggested that sequence differences in a region of the internal transcribed spacer 2 (ITS2) of nuclear rRNA genes predict the occurrence of reproductive isolation (Coleman 2009). If this is verified it will be a ‘holy grail’ in relation to molecular tests to distinguish species. Searching for speciation loci should be a high priority pursuit within conservation genomics.

A closely related pursuit is to define units with species that are sufficiently differentiated to require separate management. Several attempts have been made to define evolutionary significant units and management units within species and these concepts are being applied in conservation biology. Again, there is need for agreed definitions for each of the units within species.

Population viability analyses (PVAs) are commonly applied to estimate extinction risk and aid in prioritising management options in species conservation. There is now extensive evidence that inbreeding has deleterious effects on reproductive fitness. However, inbreeding depression is included in models used for only some such assessments. For example, CBSG usually apply a default of 3.14 lethal equivalents to juvenile survival. PVAs need to routinely include genetic factors, as inbreeding depression typically has sizeable impacts on median times to extinction (O’Grady et al. 2006). Further, more realistic costs of inbreeding in the wild need to be included (approximately 12 lethal equivalents). There are few estimates of the full impacts of inbreeding depression in the wild and a need for many more estimates. There is almost no empirical information on the long-term impacts of loss of genetic variation (as distinct from inbreeding depression) on extinction risk. Such information is sadly needed. In general, there is only limited information on the relative impacts of genetic versus other factors on extinction risk and much need for quantitative estimates in a broad array of taxa.

Addressing the impacts of global climate change on biodiversity is a major challenge that requires both research and management actions. Genetic issues are involved in these. A crucial question is what proportion of species can adapt genetically to projected future environments. Genetic issues need to be included when designing means to alleviate the impacts of climate change e.g. by managed translocations to ‘keep pace with’ climate change.

Conservation genomics is a new discipline that has become possible with the sequencing of genomes (Primmer 2009). It allows estimates of many parameters to be obtained with much greater precision e.g. genetic diversity, introgression and gene flow. In addition, it greatly

enhances opportunities to study multi-locus effects such as associative overdominance, selective sweeps and background selection. It also provides realistic opportunities for detecting loci subject to natural selection, and for identifying loci involved in speciation. Inevitably, improved markers and analytical tools will arise from this work. It is to be hoped that genomic tools will be wisely used to address important issues in conservation genetics, rather than becoming a bandwagon with a substantial proportion of trivial work, as happened subsequent to the introduction of allozymes. Two groups doing innovative and relevant work in population genomics are those of Ilkka Hanska (see Wheat et al. 2009) and Volker Loeschcke (see Kristensen et al. 2010).

Many estimates of molecular genetic diversity have been obtained in threatened and non-threatened species. However, the ability of species to evolve is more closely related to quantitative genetic variation than molecular variation and the two are, at best, weakly correlated. We have very few estimates of quantitative genetic variation in threatened species and many more are required (e.g. for body weight and fecundity).

Invasion biology has recently become much more prominent and genetic studies in the field have increased. For example, levels of genetic diversity have been documented in invasive species. Evolutionary changes have been documented in several invasive species and in several native species responding to introduction of invasive species. Continued genetic inputs are required to understand genetic factors affecting evolution of invasiveness and genetic susceptibilities that can aid in designing control measures for invasive species.

The consequences of different breeding systems on genetic management of threatened species have received limited attention. The consequences of selfing are fairly clear. Further, we now have growing understanding of the unique consequences of loss of genetic diversity on self-incompatible and haplo-diploid species. However, the special features associated with different breeding systems justify more serious consideration and more research. For example, theory suggests that polyploids will be less affected by inbreeding depression than diploids, but empirical evidence is insufficient to confirm this.

Priorities in research and applications

In general, we can expect incremental future advances in all areas of conservation genetics. However, resources are limited, so it is important to decide upon priorities. Table 1 lists my priorities for applying genetics within conservation biology. My list of research priorities in conservation genetics is provided in Table 2.

Table 1 Priorities in applying genetics in conservation biology

1. Institute rational genetic management of threatened species in the wild, especially for fragmented populations
2. Explicitly manage captive populations of threatened species to minimize genetic adaptation to captivity (along with minimizing loss of genetic diversity).
3. Apply genetic principles in efforts to alleviate impacts of global climate change on biodiversity.
4. Apply genetic principles in assessing impacts of invasive species and in the control of invasive species
5. Routinely include genetic factors (especially inbreeding depression) in PVAs and apply realistic levels of inbreeding depression to all aspects of the life cycle
6. Apply genetic principles to management of species with diverse breeding systems.
7. Apply group management to populations of threatened species that breed in multimale, multifemale groups (without pedigrees).

Table 2 Top priority scientific needs in conservation genetics

1. Develop methods to predict the risk of outbreeding depression
2. Agree upon a definition of species for conservation purposes
3. Collect an extensive body of information on the occurrence of outbreeding depression and evaluate predictors of risk
4. Investigate impact of global climate change on biodiversity, its adaptive consequences and the desirability of translocations to cope with it.
5. Agree on definitions of ESUs and MUs for conservation purposes
6. Optimise management procedures for minimizing genetic adaptation to captivity
7. Obtain many more quantitative estimates of the cost of inbreeding in wild populations in nature
8. Obtain much more information on the relative contribution of genetic versus other factors to extinction risk in the wild
9. Define and test means to manage adaptive variation in threatened species
10. Obtain many estimates of quantitative genetic variation in threatened species
11. Update meta-analyses of N_e/N ratio in wild and tests for variables affecting the ratio (especially fecundity)
12. Incremental improvements in wildlife forensics
13. Improve molecular methods for obtaining information on biological attributes of threatened species that are important to their conservation

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