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**CONSERVATION GENETICS IN NEW ZEALAND:
A BRIEF OVERVIEW OF PRINCIPLES AND
APPLICATIONS**

by

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SUMMARY

Maintaining genetic diversity is an important component of conservation. Minimum population sizes of a few hundred to a few thousand are necessary to maintain natural levels of genetic variation and hence viability and fitness (survival and reproductive success) and adaptability to environmental changes. Genetic principles should also be applied to loss of genetic variation when establishing new populations. Genetic techniques are available to quantify genetic diversity and population structure (including breeding systems and migration rates). Several examples are given of applications of conservation genetics to management of New Zealand fauna.

INTRODUCTION

One of the three major objectives of conservation as defined by the World Conservation Strategy (1980) is the preservation of genetic diversity: that is, the preservation of the full range of species, and the genetic variability of those species, characteristic of each ecosystem. This recent recognition of the importance of incorporating genetic principles into conservation theory and practice is in line with the concept of conservation as the "long-term retention of natural communities under conditions which provide the potential for continuing evolution" (Frankel and Soule 1981).

The aims of this report are to highlight some of the genetic principles and problems relevant to conservation and to outline examples of current genetic research of relevance to conservation management in New Only the genetic aspects of conservation are considered, although clearly management strategies must be based on an integration of population and community ecology, biogeography, behaviour, and economics, as well as genetics. This report is intended as no more than an overview of a relatively new field of conservation biology: further information on theoretical and practical conservation genetics can be found in Frankel and Soule (1981) and Schonewald-Cox et al. (1983).

AIM OF CONSERVATION GENETICS

The main aim of conservation genetics is the preservation of genetic diversity within ecological communities, as well as within species and populations. Conservation genetics is particularly concerned with rare and endangered species: that is, species with a restricted distribution and low numbers or species with higher numbers but separated into a number of small, isolated populations. This concern arises from the rapid loss of genetic variation, and thus the increased probability of extinction, in small and isolated populations.

Genetic principles should form part of management to
1. protect natural diversity
2. manage natural populations of rare and endangered species
3. establish new populations of any species
4. breed any species in captivity.

PRINCIPLES OF CONSERVATION GENETICS

Maintenance of Natural Diversity

The need to preserve intact communities representing the full range of
natural diversity is already well accepted by conservationists and forms
the basis of the PNA and other reserve programmes. The question of reserve
size and whether one large reserve is better than several small reserves
can be resolved (at least in theory) by considering the species-composition
to be maintained within the reserve (Soule and Simberloff 1986). By
identifying 'target' or 'keystone' species with the largest area
requirements and by determining the minimum size of reserve needed to
maintain sustainable populations of these species, the area required to
maintain the intact community is automatically defined. Several small
reserves will thus be better than one large reserve only if the area of a
'small' reserve is larger than the minimum area necessary to maintain the
community and its keystone species. Keystone species include large
carnivores and herbivores and species with important roles in maintaining
ecological processes, such as pollinators and organisms which create
habitat. Even the largest available reserves may not be sufficiently large
to maintain viable populations of all species and many species will be at
risk of extinction due to other factors, such as predation and competition
from introduced species. Therefore, active management of some species will
always be needed to maintain the full diversity of the ecosystem.

Estimation of the minimum number of individuals needed to maintain a viable
population is an extremely complex issue. However, as stated by Soule and
Simberloff (1986): "Thoughtful estimates of minimum viable population sizes
for many animal species are rarely lower than an effective size of a few
hundred". Effective population size refers to 'ideal' populations, which
have no fluctuations in population size, equal numbers of each sex, and an
equal reproductive success for every individual in the population. As real
populations do not meet these 'ideal population' criteria, any population
with an actual size of less than about a thousand individuals should be
considered to be at risk. 'Viable', in this sense, relates not only to the
need for self-sustaining populations (in terms of numbers), but also to the
maintenance of levels of genetic variation and thus 'evolutionary or
adaptive potential' within populations. Minimum viable population size
(MVP) should be calculated separately for each species, with reference to
the demographic characteristics (age structure, sex ratio, individual
variation in reproductive success, population growth rate, and fluctuations
in population size) and the population structure (number, size, and
distribution in space of populations making up a species) of each species.
Calculations of MVP need only be done for keystone species, so that minimum
reserve size for ecosystem maintenance can be estimated, and for endangered
species, for which special reserves may be set aside. It must be stressed
that calculation of a minimum reserve area using genetic criteria is only
part of reserve design. Other criteria to be considered include local
geography and geology, the probability of local catastrophe (for example,
fire, drought, avalanche), and spatial relationships between reserves.

Small, isolated populations lose genetic variation as a result of
'inbreeding' and 'genetic drift'. Inbreeding (mating between related
individuals), which usually occurs in very small populations (less than 50
individuals) because of limited mate choice, is commonly associated with an
increase in lethal or harmful genetic disorders and a decrease in
productivity, including decreased fertility and increased juvenile
mortality. Genetic drift is the random change in gene frequencies that
results from sampling a small subset of a larger population. For example,
two people shipwrecked on a desert island might, by chance, both be tall,
green-eyed, and red-headed, with a B blood group. Obviously, they do not
represent all the possible genetic types of humans and nor will their

children. This is an extreme example of how genetic drift can lead to loss of variation in small populations. The smaller the population and the longer it remains small, the greater the loss of variation. Loss of variation may affect the long-term adaptability of the species to environmental changes. For example, the evolution of resistance to disease, pesticides, and environmental pollution has been shown in many cases to result from selection of rare genetic variants already present within populations. Such rare variants are rapidly lost in small populations by genetic drift. Levels of genetic variation may also be related to components of fitness, such as survival, growth rate, and productivity (Frankel and Soule 1981, Mitton and Grant 1983). One example of a species with very low variation is the cheetah. Detailed studies (O'Brien et al. 1983, 1985: Wayne et al. 1986) have shown that cheetahs have several physiological handicaps, as well as a high rate of juvenile mortality and a high susceptability to disease.

Maintaining a single viable population of any species does not, of course, preserve the total genetic diversity of that species, because a significant proportion of the genetic diversity of each species is spread between its various populations. The actual ratio of within-population to between-population variation depends on the population structure, movements and distribution of the species.

Establishing New Populations

In New Zealand and elsewhere, an important technique for managing endangered and rare species, particularly those under threat from habitat destruction and predation in their present range, is the establishment of new populations. This may include reintroductions to previously occupied areas, translocations to predator-free or other suitable sanctuaries, or breeding in captivity. A variety of genetic principles should be considered, in conjunction with ecological or behavioural requirements, when establishing new populations.

(i)   Maximise the number of founders: If possible, 50-100 pairs, although in practise this will often not be possible for endangered species. Species with a slow growth rate are particularly susceptible to loss of variation and therefore need a large founder size.
(ii) If possible, choose founders that are not inbred and are unrelated.
(iii) Do not release founders from uncertain genetic stock, such as captive-bred stock of unknown history.
(iv) Maximise genetic variation. If the target species is divided into genetically distinct populations, maximum genetic variation can be achieved by mixing individuals from different sources to form a new population. However, problems may arise from mixing very different genetic, ecological or behavioural types. In practice, it is often difficult to determine the optimal composition of a new population. As a guideline, a new population should be established with individuals from one or more geographically close or ecologically similar areas and, preferably, with individuals from large populations that have no history of bottlenecks (periods of very small population size). If the new population is to be established outside the present range of the species or in a modified habitat the best strategy may be to introduce founders from a range of donor populations.
(v)   To minimise loss of variation and inbreeding before the new population reaches a viable population size, make further introductions or exchanges of individuals between populations at a rate of 1-5 additions per generation.
(vi) Further opportunities for genetic manipulation are possible in captive breeding programmes. However, captive breeding should be considered a backup for natural populations in case of extinction, rather than an alternative to management of natural populations, because of the technical,

behavioural and genetic problems associated with captive breeding programmes. As well as inbreeding and loss of variation, such genetic problems include selection for undesirable characteristics (such as tameness) and lack of natural selection against deleterious genes (such as inherited deformities that reduce feeding efficiency or ability to escape predators).

EXAMPLES OF RESEARCH IN CONSERVATION GENETICS

Population Structure of Blue Duck

Ecological and behavioural research by Murray Williams (Science and Research Directorate, DOC) suggests that blue ducks form very small and isolated populations in modified habitats. Thus these birds may be more threatened than is suggested by their present total numbers of about 2000-4000 individuals. Recently, Murray and I began a study of the genetic structure of blue duck populations, attempting to answer the following questions:

a) What is the effective size of blue duck populations?
b) How much genetic variation occurs within populations?
c) How much inbreeding is occurring as a result of small population size?
d) How much migration occurs among blue duck populations a) within a river system and b) between catchments?
e) Do populations in less modified habitats have a different population structure from populations in modified habitats?
f) What proportion of the total genetic diversity of blue ducks occurs among different geographic isolates of blue duck?

A biochemical technique known as protein electrophoresis will be used to determine levels of variation within and among populations and another technique, DNA fingerprinting (very recently developed for human forensic tests) will be used to assess inbreeding and migration. All genetic analyses can be done from small blood samples taken at very low risk to the animal.

Initial results indicate that levels of inbreeding are extremely high within the blue duck population on the Manganui-a-te-Ao River, suggesting that this population is both extremely small and isolated. In genetic terms, this means that blue ducks populations, at least in modified habitats, may be rapidly losing genetic variation and therefore losing adaptability and viability. They are also at risk from the harmful effects of inbreeding. If this is common to other populations of blue duck, then the conservation status and management of blue ducks will need redefining. Management designed to increase population sizes and promote contact among populations may be necessary. This could include, for example, protection and enhancement of habitats (water and riverbed quality, riparian vegetation) and population enhancement by adding blue duck to small populations or adjacent rivers. The importance of maintaining large populations in relatively unmodified habitats should be emphasised, as these have the best long-term survival prospects if protected. Management should aim to maintain blue duck populations of a minimum size, which can be calculated using MVP (minimum viable population) theory and the known biology of blue duck. The necessary genetic research to determine MVP and answer the above questions will continue during 1988-89.

Genetics of New Zealand Parakeets

Hybridisation between Forbes and Chatham Island red-crowned parakeets.
Protein electrophoresis was used to establish the extent of gene exchange
between the endangered Forbes parakeet and the Chatham Island red-crowned
parakeet. The two species have been hybridising on Chatham Island for at
least two decades, probably as a result of drastic habitat modification to
Mangere and Little Islands, which comprise the entire range of the Forbes
parakeet.

The genetic data suggest that Forbes parakeet, which is presently
considered a subspecies of yellow-crowned parakeet, is actually more
closely allied to red-crowned parakeets, and should be considered a
separate (and endangered) species. Despite extensive and continuing
hybridisation with Chatham Island red-crowned parakeets, the Forbes
parakeets on Island appear to have remained a distinct genetic unit. This
may have resulted partly from the active management programme to remove
hybrids, but also from the apparent preference of hybrids to mate with red-
crowned rather than Forbes parakeets, as suggested by the greater
morphological and genetic similarity between hybrids and red-crowned
parakeets than between hybrids and Forbes parakeets. Removal of hybrids and
enhancement of habitat seem to have been successful management techniques
to rescue the Forbes parakeet from the verge of extinction. Further
increase in the population size is now needed to achieve a viable long-term
population.

Release of Captive-bred Parakeets
Captive-bred parakeets have been used as a source of founders for releases
onto several islands. However, genetic analysis suggests that several
captive-bred stocks of red-crowned parakeets have the genetic
characteristics of red-crowned x yellow-crowned hybrids and some also have
very low levels of genetic variation, indicating that the present captive
stocks of parakeets are not suitable for release programmes.

Status of Orange-fronted Parakeets The rare orange-fronted parakeet was
examined genetically to determine whether it is a separate species from or
a colour morph of the yellow-crowned parakeet. Although the sample size was
insufficient to answer this question, the results clearly indicated an
unexpected diversity among yellow-crowned parakeets from northern and
southern populations. Thus, the present orange-fronted breeding programme,
which interbreeds orange-fronted parakeets with the genetically different
captive yellow-crowned parakeets, is not a suitable programme to maintain
the orange-fronted type.

Management of the orange-fronted parakeet will be extremely difficult until
more is known about the numbers, distribution, and biology of this parakeet
in the wild. Further surveys for parakeets, particularly during the
breeding season, are recommended.

Translocation Programme for Whitaker's Skink

A programme to establish a new population of the endangered Whitaker's
skink has been designed by Dave Towns (Science and Research Directorate,
and Charles Daugherty (Victoria University) to incorporate genetic, as well
as ecological, behavioural, and physiological, principles. Whitaker's skink
is known only from two tiny offshore islands and one highly vulnerable
mainland site. Korapuki Island, in the Mercury group, was chosen as the
release site because of its close proximity and ecological similarity to
the present island locations of the species. Genetic aspects of the release
programme include:
(i) A survey of the genetic diversity of the species and levels of
variation in each natural population, in order to identify and characterise

potential source populations.
(ii) Release of sufficient numbers of skinks (50 individuals, over a four-year period) to minimise loss of variation through inbreeding and genetic drift.
(iii) Release of a high proportion of gravid females to maximise the effective number of animals released (Towns et al. in press).

Stock Structure of Smelt in Lake Taupo

Genetic techniques can also be applied to fisheries and game management. For example, a genetic study using electrophoresis is presently underway to determine the stock structure of smelt in Lake Taupo. Morphological studies by Theo Stephens (Science and Research Directorate, DOC) suggest that smelt in Lake Taupo may return to breed in the stream in which they were hatched. Thus, there may be several independent stocks (management units) rather than a single, interbreeding stock of smelt in Lake Taupo. Hence, removal of large numbers of smelt from any single stream may jeopardize the future productivity of that stream. This has obvious implications for the management of smelt, which are not only the main food of rainbow trout, but are considered by the local Maori to be a potential substitute for their traditional whitebait fishery. The genetic study will test for genetic differences between samples of smelt from different streams. If significant genetic differences are found the theory of independent stocks centred on different streams will be supported.

CONCLUSION

Conservation genetics thus provides not only the theory essential for every biological management programme, but also a technology to enable the necessary information to be collected. Overseas, genetic principles and data have already been included in many management plans for species protection (for example, spotted owls, Barrowclough and Coats 1985: grizzly bears, Shaffer 1983). New Zealand has played a role in exporting these concepts; management plans with a significant genetic component are being formulated for the Galapagos following recent workshop discussions attended by several New Zealand scientists (D. Towns, pers. comm.).

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