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**GENETICS AND CONSERVATION OF
YELLOW-EYED PENGUIN:**

AN INTERIM REPORT

by

Sue Triggs and John Darby

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Science & Research Directorate,
Department of Conservation,
P.O. Box 10-420, Wellington,
New Zealand

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GENETICS AND CONSERVATION OF YELLOW-EYED PENGUIN
AN INTERIM REPORT

Sue Triggs¹ and John Darby²

¹ Science & Research Directorate, Department of Conservation,
P O Box 10-420, Wellington.

² Otago Museum, Great King Street, Dunedin.

SUMMARY

Analysis of the genetics of yellow-eyed penguin populations in the subantarctic and South Island suggests that there are three discrete populations of yellow-eyed penguin. Recovery of penguin numbers in the South Island will have to be achieved without input from the subantarctic, as migration rates between subantarctic and mainland populations are very low. Migration between Campbell and Enderby Islands, although an order of magnitude higher than that between the subantarctic and mainland, is insufficient to prevent significant genetic differentiation between the two subantarctic populations. The present low numbers in the South Island and possibly in the Auckland Islands are likely to lead to loss of genetic variation within these populations and hence decreased long-term viability. Genetic variation in the Enderby Island population is already less than half that found on Campbell Island. Samples from Stewart and Codfish Islands are essential to complete this analysis of genetic structure in yellow-eyed penguins.

1. INTRODUCTION

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 variation and hence levels of fitness and adaptability (Triggs 1988). Biochemical genetic techniques can be used to define discrete populations or management units and to assess genetic diversity within species by determining diversity among populations and genetic variation within populations. Genetic techniques provide a rapid and relatively inexpensive alternative to traditional banding methods for estimating migration (gene flow) between populations.

The yellow-eyed penguin *Megadyptes antipodes*, the world's rarest penguin and the sole representative of its genus, has a total population size of less than 3000 breeders (McKinlay in prep., P J Moore pers. comm.). It is one of only three species of penguin to breed on the New Zealand mainland and thus has aroused considerable public interest. The present range of yellow-eyed penguins extends from southern New Zealand to the subantarctic. Since the arrival of humans to New Zealand yellow-eyed penguin numbers have decreased as a result of predation by introduced mammals, disturbance by humans and domestic animals, and habitat A dramatic decline in numbers from approximately 600 to 200 pairs has occurred on the southeast coast of the South Island since 1986, possibly as a result of a collapse in the marine food chain.

Low penguin numbers raise concern for the long-term genetic viability and the potential for population recovery in the South Island. The aim of the present research was to determine the potential role of immigration from the subantarctic in population recovery in the South Island, and to suggest strategies for maintaining genetic viability in yellow-eyed penguins based on an assessment of genetic structure and diversity within the species.

2. METHODS

The genetic structure of yellow-eyed penguin populations was determined by electrophoresis, a biochemical technique that estimates genetic variation from proteins in blood samples. (Research is also underway using mitochondrial DNA techniques to determine the genetic structure of yellow-eyed penguin populations. This work is being done by Dr Allan Baker of the Toronto Museum, Canada). Genetic variation was estimated at 29 protein loci for samples from two South Island and two subantarctic sites: Otago Peninsula (21 individuals), Catlins (24), Enderby Island, Auckland Islands (24) and Campbell Island (24).

The genetic variation within populations is estimated by the statistic H (heterozygosity). The amount of genetic differentiation between populations, or the genetic diversity, is given by F_{ST} . Samples that are part of a single inter-mixing population have $F_{ST} = 0$, whereas completely isolated populations have $F_{ST} = 1.0$. The number of migrants exchanged per generation, (effective population size \times migration rate), can also be estimated from F_{ST} , using the following equation:

$$F_{ST} = (4N_e m + 1)^{-1}$$

Estimation of effective population size N_e requires information on sex ratio, variance of reproductive success, generation time, and fluctuations in population size. For the purposes of this interim report N_e was assumed to be approximately equal to the number of breeders (N_b) for each population. The average of N_e for two populations x and y is given by the harmonic mean: $1/N_e = 0.5 (1/N_{BX} + 1/N_{BY})$.

3. RESULTS

The level of genetic variation (heterozygosity, H) in yellow-eyed penguins averaged 0.03. This is lower than the average ($H = 0.05$), but within the known range, for other bird species. Enderby Island had the lowest level of variation ($H = 0.02$), possibly reflecting the small size of the Auckland Islands population (estimated at 150-200 pairs), whereas Campbell Island had the highest level of variation ($H = 0.04$).

Significant genetic differentiation was found among the four samples (Table 1). Enderby and Campbell Islands were significantly divergent from each other, as were Enderby and the South Island, and Campbell and the South Island. No significant genetic differences were found between the Catlins and Otago samples.

Table 1: Genetic structure and migration between populations of yellow-eyed penguin [$N_e m$ is the actual number of migrants exchanged per generation (estimated from F_{ST}), N_e is the effective population size (estimated from censuses and historic information), m is the migration rate, the proportion of the population exchanged, (estimated from $N_e m$).

	F_{ST}	Significant differentiation?	$N_e m$	N_e	m
Among all 4 samples	0.243	Yes	0.8	570	0.001
Campbell Is. vs South Is.	0.138	Yes	1.6	460	0.001
Enderby Is. Vs South Is.	0.333	Yes	0.5	1000	0.001
Campbell Is. Vs Enderby Is.	0.052	Yes	4.6	470	0.01
Catlins vs Otago	0.008	No	31	500	0.06

The amount of genetic differentiation (or genetic differences) between yellow-eyed penguin populations is an order of magnitude higher than that estimated for most other species of bird (F_{ST} averaged 0.022 for 15 geographically-widespread species of birds; Barrowclough 1983). The genetic differentiation between these populations is a natural population structure developed over thousands of years. Thus, F_{ST} and $N_e m$ estimates are valid for average population sizes over the past few thousand years. Recent declines in yellow-eyed penguin numbers, assuming that migration rates remain constant, will decrease $N_e m$ and lead to even greater divergence between populations.

Significant genetic differentiation between populations can only occur when either population size or migration rate or both are small (low $N_e m$ value). $N_e m$ the actual number of migrants exchanged between locations per generation. When this value greater than approximately 1-4 the locations sampled can be treated as a single management unit for genetic conservation (Varvio et al. 1986). Yellow-eyed penguins thus form at least two discrete populations (the subantarctic and South Island). Enderby and Campbell Islands are on the borderline of genetic isolation. Although migration between these two populations is an order of magnitude higher than between subantarctic and mainland populations, significant differences in gene frequency and amount of genetic variation between Enderby and Campbell Islands suggest that these two locations could be treated as discrete populations. This will be particularly true if penguin numbers decrease on either island in the future or have decreased substantially in the recent past. The large value of $N_e m$ between Catlins and Otago samples indicate that migration has, in the past, been more than sufficient to maintain these as a single genetic population. The decline of penguin numbers in the South Island by at least an order of magnitude in recent decades suggests that $N_e m$ may now be approximately 3 rather than 31, as given in Table 1. If so, the Catlins and Otago populations may soon begin to show effects of genetic isolation.

4. MANAGEMENT IMPLICATIONS

The genetic diversity within the species is high. Thus, each of the three discrete populations is an important component of the total genetic diversity to be conserved.

Immigration to the South Island from the subantarctic is very low and thus is unlikely to play a significant role in population recovery on the South Island.

The present population size of at least one of the three defined populations, the South Island, is lower than the recommended minimum of 500-1000 breeding individuals needed to maintain genetic variation within populations. In addition, low numbers in the South Island may result in genetic isolation between the Catlins and Otago Peninsula, thus disrupting the natural population structure of yellow-eyed penguins. Accurate census information is not available for the Auckland Islands, but present estimates suggest that numbers may be fewer than 500-1000 (McKinlay in prep.). Active management to increase numbers in the South Island and perhaps the Auckland Islands, if possible, is recommended.

Two major strategic breeding areas, Stewart Island and Codfish Island, have not as yet been sampled. Their large size and geographic position make them vital components of the analysis of genetic structure and diversity.

Calculations of effective population size are an important part of conservation genetics. An accurate census of the Auckland Island population, as well as an analysis of life history information, will be required before accurate estimates of N_e can be made.

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