

CASE STUDY



MAINTAINING GENETIC DIVERSITY IN NEW ZEALAND'S KAKAPO POPULATION OFFERS NEW OPTIONS FOR CONSERVATION MANAGEMENT

Photo courtesy of Ian Jamieson

HELPING THE KAKAPO'S LONG-TERM SURVIVAL

RESEARCH has revealed genetic diversity in the immune systems of New Zealand's kakapo that could help the population's long-term survival.

University of Otago zoology doctoral student Gabrielle Knafler says that, although endangered populations can rebound – especially when immediate threats to reproduction and survival are reduced – inbreeding and genetic drift can detrimentally impact on the species' long-term viability.

“It's therefore a high priority to maintain genetic diversity, alongside minimising the external threats and enhancing habitats.”

The kakapo (*Strigops habroptilus*) was once abundant on the mainland, but over several hundred years, the population was reduced to a single adult male, known as Richard Henry, discovered in Fiordland. Between 1977 and 1997, another 62 birds were located on Stewart Island and transferred to predator-free island sanctuaries. In 2014, there are 123 adult kakapo.

Ms. Knafler wanted to identify variation in immunity genes and to incorporate this variation into conservation management practices. “To achieve this, we compared the immunity genes between kakapo originating from Stewart Island to those of kakapo originating from the mainland – more specifically Richard Henry.”

Using NZGL's MiSeq technology to extract the necessary genetic data, the research determined that there was a degree of immune gene diversity between the two populations.

However, maintaining this diversity in the species' gene pool remains a challenge, especially if individuals are allowed

to reproduce randomly. “The solution may be to prioritise mating between specific individuals with the appropriate immunity gene combinations, using artificial insemination, to ensure unique genetic diversity is not lost forever.”

CLIENT:

Gabrielle Knafler, University of Otago

NZGL SERVICES:

MiSeq sequencing of data

GREGORY GIMENEZ BIOINFORMATICIAN UNIVERSITY OF OTAGO

“This project was challenging, because so little is known about the kakapo DNA. We meet with the client very early in the project to define the experimental design. We also included our genomics colleagues for the molecular biology construction. The MiSeq sequencing was done in Auckland and I carried out the analysis of the genetic diversity of 138 kakapo individuals. It is a rare opportunity to analyse data from last living individuals of a species. We compared the observed genetic diversity with the kakapo pedigree data and discussed how this could influence kakapo breeding.”