

# Evaluating mate choice in Brown Kiwi and its implications for conservation.

## Summary article

Eliana Ramos, Dr Isabel Castro, and Dr Gillian Gibb.

School of Natural Sciences, Massey University, Palmerston North

Genetic diversity is closely tied to species' adaptive potential as it supplies the range of phenotypes for selection to act upon, playing an important role in the conservation of any species. A key aspect of maintaining genetic diversity is the pattern of mating and mate choice of a species. We have recently found that the translocated North Island (NI) kiwi (*Apteryx mantelli*) population on Ponui Island underwent genetic rescue and has higher genetic diversity than its two parental populations. We now want to understand how genetic rescue was achieved and whether it can be replicated in other kiwi species translocations as this would be ideal to safeguard the group. In this project we examine the possible role of mate choice in this process. One hypothesis is that kiwi select partners that are dissimilar in terms of their genetics. This would lead to their offspring having higher genetic diversity especially when two different populations mix as was the case on Ponui Island. Kiwi's nocturnal habit suggests that they could use olfaction for mate selection. The Major Histocompatibility Complex (MHC) is a series of genes that are associated to immunity and many species can 'smell' these differences using them to choose partners that could provide better immunity to their offspring. If our hypothesis that mate choice is based on smell and that this results in genetic rescue, this would suggest that kiwi translocations would be best when done using two (or more) sources of birds.

Thanks to BirdsNZ support, we were able to (i) characterise the genomic organisation of the MHC II  $\beta$  region and (ii) estimate MHC genes diversity and (iii) compare our estimates to other kiwi species. Briefly, we found that the MHC II  $\beta$  region in NI brown kiwi has at least three different loci and contains typical functional elements found in other kiwi species (*Apteryx owenii*). Regarding the structural characteristics of the  $\beta$ 1 domain, we found all amino acid residues that are conserved among tetrapods, characteristics of a functional molecule. When compared to kiwi pukupuku and rowi (*Apteryx rowi*) there was (i) absence of species grouping, (ii) extensive recombination between sequences, and (iii) no shared alleles between kiwi species. However, a single year was not enough to complete all of the proposed outcomes, which has delayed the completion the third aim of this study (i.e., determine if brown kiwi exhibit a genetic MHC-based mate choice). We have designed a set of primers which successfully amplify exon 2 MHC class II  $\beta$ , (Figure 1) and we are using these primers to genotype all kiwi pairs being monitored at Ponui Island. Results are expected later this year. We look forward to being able to provide a full update after completing this chapter of my PhD research. This project would not be possible without the support of BirdsNZ my supervisors Professor Isabel Castro, and Dr Gillian Gibb. We also thank all volunteers who have made data collection possible.

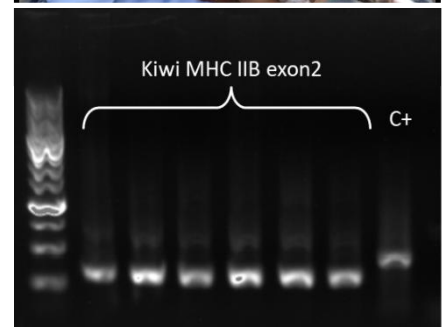


Figure 1. Male north island brown kiwi (top). PCR products of exon 2 MHC class IIB (bottom). Photos by E. Ramos and I. Castro