Population genetics of Weka (*Gallirallus australis*) with respect to a translocated population on Rakitu nr Aotea, North Island using mitochondrial and microsatellite variation

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Introduction

The weka (*Gallirallus australis*) is a flightless bird endemic to Aotearoa New Zealand. Before humans arrived, weka lived over the whole country and as opportunistic omnivores played a key role in the New Zealand ecosystem as a native predator (Trewick et al. 2017). Previously weka were managed as four subspecies based on their separate geographic ranges and plumage variation: North Island Weka (*Gallirallus australis greyi*); Western Weka (*G. a. australis*); Buff Weka (*G. a. hectori*); and Stewart Island Weka (*G. a. scott*). However, population genetic analysis using nuclear (microsatellite) and mitochondrial DNA sequence data (Trewick et al. 2017) revealed signal for only two lineages; one in North Island and one in South Island. The available sample of weka, mostly collected ~2004, showed a higher level of genetic diversity within the restricted extant range of the North Island subspecies than the more abundant and widespread South Island subspecies.

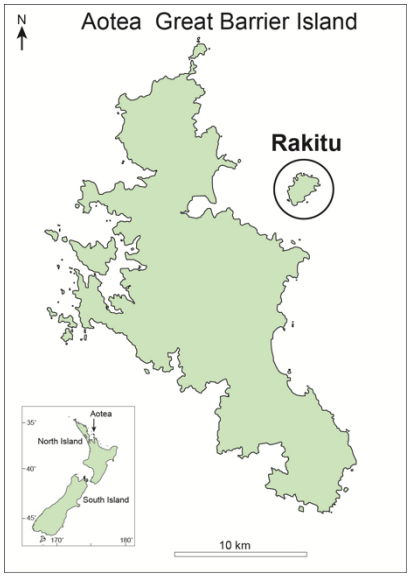

Figure 1. Location of Rakitu Island weka population

Rakitu Island near Aotea supports a small population of weka thought to have originated from near Gisborne. Translocation in 1951 (Miskelly & Powlesland 2013) involved 13 individuals. When in 2018 weka were temporarily removed from the island for rat eradiation, feather samples were obtained from >60 individuals to provide an opportunity for later analysis (Department of Conservation, 2018). In order to make inferences about the conservation genetic significance of Rakitu weka, a comparison has to be made with weka populations from elsewhere. This can be done using existing genetic markers and published data (Trewick et al. 2017), however we have also taken the opportunity to develop a new set of species-specific markers that should provide better resolution in future management of weka.

Feather samples are not ideal for genetic analysis but are often sufficient and their collection is simple and causes minimal distress to birds. We extracted DNA from the feather samples and obtained mitochondrial Control Region DNA sequence after amplification.

Results

We were able to successfully amplify Control Region from all 66 samples. From DNA sequences we found 24 individuals with haplotype B, 10 individuals with haplotype E and 32 individuals with haplotype F. Haplotypes B, E and F belong to the North Island weka lineage and have previously been reported from weka sampled from Gisborne (B), Mokoia Island (B, E, F), Opotiki (F) and Kawau Island (F). The relationships of the haplotypes is shown in Figure 2. Based on these data, the Rakitu population was, when sampled in 2018, genetically most similar to the Mokoia Island population sampled in 2004.

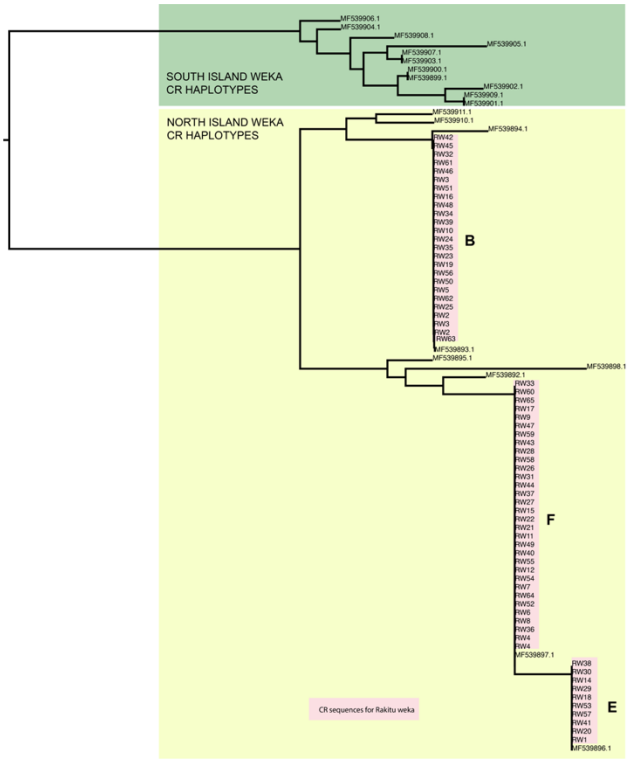

Figure 2. Phylogenetic tree of mitochondrial Control Region DNA sequences from Weka. The mtDNA haplotypes characteristic of the North Island subspecies are within the yellow box, new data from Rakitu population sample are highlighted pink. Published haplotypes (Trewick et al. 2107) found in the Rakitu weka were B, E, F.

Future work

The Control Region is part of the maternally inherited mitochondrial genome so it tends to give a conservative estimate of genetic variation. Therefore we have applied microsatellite markers to the DNA from Rakitu weka feathers, to target several different parts of the nuclear genome. These are functionally neutral markers but of a type routinely used to provide estimates of population genetic structure in animals. Previously we applied a set of microsatellite markers to weka (Trewick et al. 2017) that gave limited resolution; i.e. only five reliable loci were available. Although the resulting data supported observations from CR mtDNA sequencing, we have sought to improve the type of data we can obtain for weka, before applying the revised marker set to the Rakitu sample.

We therefore developed new microsatellite primers for weka from a complete genome for weka generated by our group (2023/2024). This approach allowed in-silico testing of the new primers and careful management of size ranges to optimised downstream multiplexing of 12 loci, rather than working with each locus separately. That should mean that all the loci can be screened for each individual sample in a single event.

We were able to successfully amplify 17 weka samples from around New Zealand. Results from genotyping indicate that most of the loci include useful polymorphism (about 2-7 alleles per locus), a low amount of scatter and relatively clear alleles that help scoring. Using this new set of markers we now have data for approximately 120 weka that includes representatives of the Rakitu population sample and existing sampling of North Island and South Island weka for comparison. However, scoring and analysis of these data has been on hold as our student will continue the work starting July 2024. From that time we will be able to provide more details. We envisage a science paper that includes information on the development of novel markers and their application. We will also be in a position to report specifically on the Rakitu population data.

Summary

What is already clear from the Control Region mtDNA sequence data, is that the Rakitu weka sampled in 2018 included three different haplotypes. These haplotypes are also found in the weka on Mokoia Island, suggesting the two populations are very similar. Given the small founder population of 13 individuals moved to Rakitu Island (Beauchamp et al. 1993), and relatively small size of the island (250 ha), the mtDNA genetic diversity is high. That means that at least the same level of variation existed in the original source population and the Rakitu founders, and that the population on Rakitu grew rapidly and so retained founding diversity. Although no new CR haplotypes were found, the Rakitu population included good representation of North Island weka diversity previously sampled. Assuming that the weka returned to Rakitu re-established successfully after rodent eradication, and all contributed to subsequent generations we can assume that the diversity in 2018 has persisted. However, given the size of the island (250ha) and using an intermediate density estimate of about 0.5 birds/ha (Beauchamp 1987, Beacuhamp et al. 2009) would suggest carry capacity of about 125 individuals, although density appears to have fluctuated since first introduction this could be higher (~0.9/ha Beauchamp et al. 1993). The genetic data from nuclear genes that will be generated will be used to estimate inbreeding. A population of this size is expected to lose genetic diversity each generation so human mediated gene flow (moving birds between populations) would be sensible long term strategy.

References

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