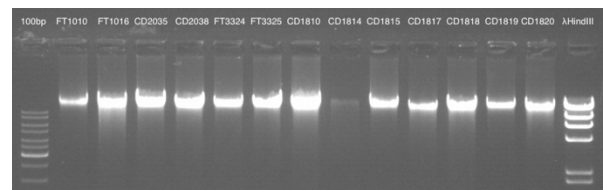


Resolving a genetic mash-up: reconstructing an accurate evolutionary history of kākārīki



Prioritising species conservation and over-stretched government funding is built on an accurate understanding of evolutionary relationships and taxonomy. But what if that evolutionary history is wrong, and what are the consequences for endangered taxa if conservation funding and resources are re-assigned? The Department of Conservation (DoC) Te Papa Atawhai does not have enough government funding to save all our unique taonga species from extinction. Kākārīki (*Cyanoramphus* spp.) are one of our iconic avian groups and are spread throughout the Aotearoa New Zealand region, including the far-flung Rangitāhua Kermadec, sub-Antarctic and Rēkohu Chatham Islands. While some kākārīki are of less conservation concern, the kākārīki karaka orange-fronted parakeet (*C. malherbi*) is nationally critical and the subject of intense conservation efforts. Likewise, the nationally endangered Forbes' parakeet (*C. forbesi*) would have become extinct through hybridization with the Chatham Islands red-crowned parakeet (*C. novaezelandiae chathamensis*) if not for the efforts of the DoC.

The evolution and taxonomy of kākārīki was seemingly resolved over 20 years ago using the fast evolving mitochondrial DNA control region (CR). This work established, for example, that Forbes' and orange-fronted parakeets are distinct from the yellow-crowned parakeet (*C. auriceps*), and a number of insular island populations of red-crowned parakeet (nominate *C. novaezelandiae*) were actually distinct species (e.g. Norfolk Island parakeet *C. cookii*).



Genomic DNA, still well-preserved after 40 years in a freezer.

Birds, especially parrots, are known to have gene duplications within the mitochondrial genome, including the CR. These duplications range from nearly identical to differing from the original sequences by as much as 80%. Contrary to previous assertions of a single CR in kākārīki (i.e. no duplication), our preliminary modern and ancient DNA data indicate kākārīki do in fact have a duplicated CR. The vital questions are, what is the nature of the duplication, how divergent are the two CR's, and has a mix-up of two divergent CR's been used previously to infer kākārīki evolution and taxonomy? Answering these questions could have serious implications for the conservation management of kākārīki.

We have used the Birds New Zealand (NZ) funding to characterise the CR duplications within kākārīki, and have started to reconstruct the accurate evolutionary history (and taxonomy) of *Cyanoramphus* using whole mitochondrial genomes and nuclear genotyping-by-sequencing (GBS). Our research has confirmed that a mix-up of two markedly divergent CR's was previously used to infer kākārīki evolution. From thousands of blood samples we sourced from numerous collections dating back to the mid 1980's, we have managed to assign robust metadata (e.g. species, location) to several hundred samples. Our preliminary GBS data of nearly one hundred individuals covering the majority of kākārīki taxa shows most island populations are genetically distinct (e.g. Reischek's parakeet *C. hochstetteri*) but evolutionary relationships between taxa are likely to change. The situation on mainland NZ is more complicated, clouded by hybridisation. This has highlighted where we need to focus future research efforts to tease apart this story. Additional sampling by collaborators over the next year, including from the Kermadecs with Ngāti Kuri and Auckland Museum, will fill out the picture.

Our ongoing research will provide vital data to help inform evidence-based conservation management of these important New Zealand taonga. We look forward to being able to provide a full update in the near future on the biological heritage of kākārīki.