

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 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 Department of Conservation.

The evolution and taxonomy of kākārīki was seemingly resolved over 20 years ago using the fast-evolving mitochondrial DNA control region. 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*).



Red-crowned parakeet. Photo by Bernard Spragg.

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

We will use the Birds New Zealand funding to characterise the control region duplications within kākārīki, and reconstruct the accurate evolutionary history (and taxonomy) of *Cyanoramphus* using whole mitochondrial genomes and nuclear genotyping-by-sequencing. These datasets, combined with external kākārīki morphology and ecology, will also allow us to determine what role hybridization has played in the recent evolutionary history of *Cyanoramphus*. To date, conservation management decisions for kākārīki (and other New Zealand birds) have been based on little genetic data. This collaborative (including scientists from the University of Otago, Massey University and the British Museum of Natural History) and multifaceted approach will provide vital data to help prioritise species conservation funding and inform evidence-based conservation management of these important New Zealand taonga.

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