

Filling out the family tree - conservation genetics of the Chatham Island taiko (*Pterodroma magentae*)

Once the most abundant burrowing petrel on the Chatham Island, the Chatham Island taiko (*Pterodroma magentae*) is today one of the world's rarest seabirds. Following the arrival of introduced predators, the taiko suffered a dramatic population decline and was considered extinct for almost 100 years until its rediscovery in 1978. Since then, extensive conservation efforts have allowed the taiko population to increase to 31 breeding pairs in 2017 although the species is still classified as critically endangered. Taiko spend most of their lives at sea, only coming to land to breed. When on land they are nocturnal and breed in long underground burrows situated in dense bush in challenging terrain. As such, taiko are difficult to locate and observe. Since 1996 almost every taiko caught has been blood sampled (289 individuals). Many taiko are first caught as adults and consequently, their parentage remains unknown. Furthermore, some individuals have only ever been caught in flight using spotlighting techniques and so even less is known about their origins.

The aim of this project was to 1) develop a set of genetic markers specific to taiko and 2) use these markers to determine familial relationships between individuals in order to inform management decisions.

DNA from a single individual was sequenced using massively parallel technology. Using computer software, I searched the thousands of resulting DNA sequences for microsatellites (short tandem repeats 1-6 base pairs in length). The number of repeats in a microsatellite differ between individuals and these differences are passed from parents to offspring. In this way we can use microsatellites to establish kin relationships as is done in human paternity tests.

I developed a total of 18 microsatellite loci that varied in the number of repeats between individual taiko. I also utilised two microsatellite loci previously shown to amplify in taiko. DNA was extracted from 157 taiko blood samples. These included nearly all individuals ever known to have bred ($n = 101$ of which 93 were used in this study) and all individuals of unknown parentage ($n = 64$) including those birds only ever caught in flight. I used my 20 microsatellite loci to genotype all of these DNA samples. I then analysed these genotypes to determine kinship between individuals and examine any structuring within the population.

I was able to assign many first-degree relationships with high confidence, expanding upon the known taiko pedigree. Seven individuals were found to be offspring of known breeders, some of which were likely breeding for over 20 years prior to the discovery of their burrow. There was also strong evidence that active burrows remain undiscovered, justifying ongoing efforts to locate them. Additionally, there was evidence that inbreeding is occurring as breeding pairs were on average more closely related than expected by chance. This is likely a consequence of a reduced population size combined with strong natal philopatry. Analysis of population structure confirmed the hypothesis that all sampled taiko belong to the single Chatham Island breeding colony.

Further work is being undertaken to increase the number of microsatellite loci available for taiko and to genotype the remaining 132 individuals which would increase the power of the analysis and may uncover more unknown relationships. I am very grateful for the Birds New Zealand Research fund which helped make this project possible by funding lab consumables such as primers, fluorescent labels for primers and PCR reagents.

