

Portable sequencing in aid of fast genetics-based conservation decision making

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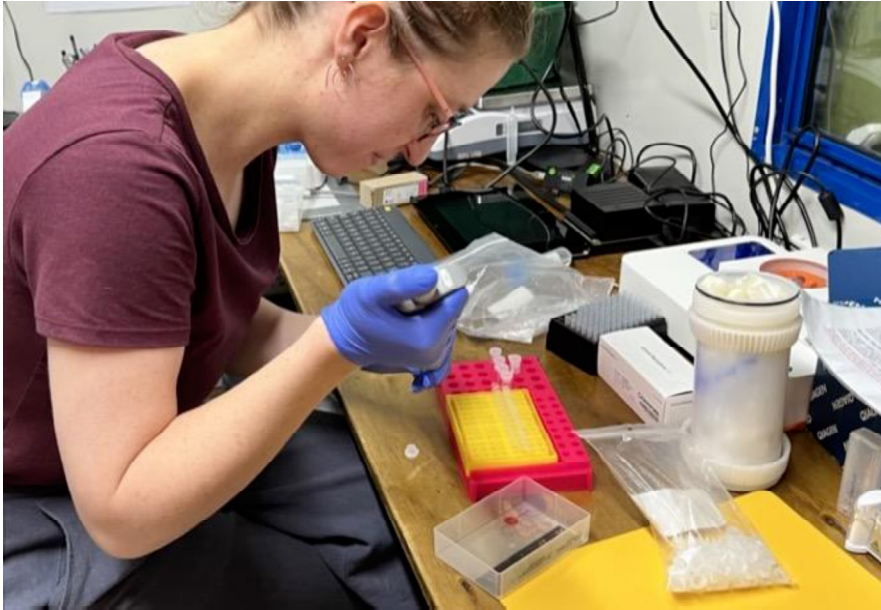
Kākāpō (*Strigops habroptilus*) are nocturnal, flightless parrots, and one of Aotearoa New Zealand's iconic bird species. They have been pushed to the brink of extinction, primarily as a result of introduced mammalian predators. However, the kākāpō population is now increasing, thanks to an intensive recovery programme. One of the many facets of this recovery programme is the use of genetic information. For example, genetics are used to determine the sex of each bird, how they are related to each other, and to ensure the genetic diversity of the species is maintained.

Unfortunately, genetics results are not always very accessible for conservation, and can be slow to obtain, given the need to send samples to a lab. Faster genetic results after kākāpō chicks hatch would substantially help how they are managed, in several ways. For example, sex information based on genetic data is used in combination with weight data as a proxy for chick health status. Weight differs slightly between the sexes, so it can be impossible to distinguish between a healthy female chick or an underweight male chick. Determining the sex of chicks as soon as possible would allow sick chicks to be identified early, meaning they could receive veterinary care promptly and have a better chance of survival.

Parentage information in kākāpō is also very important, as it is used to help manage genetic diversity of the species and limit inbreeding. This information is useful to have early on to ensure that when chicks are translocated to manage the population genetic diversity, full information is available, and they won't need to be moved unnecessarily later on. Finally, both sex and parentage are used to identify high-priority chicks, which are particularly valuable to allow the kākāpō population to grow and be genetically healthy.

We aimed to provide these rapid genetics-based results to the conservation managers during the kākāpō breeding season. To do so, we trialled the use of recent genetic sequencing technology (Oxford Nanopore), in the field. We first tested and developed the methods in the lab using known sex and parentage samples. Then, we took the sequencing set up out into the field, where kākāpō were breeding, on Whenua Hou. We were able to determine the sex of 57 kākāpō chicks which hatched this year, as well as the parentage for 12 chicks for which it was uncertain. These results informed chick veterinary care, prioritisation, and translocations during the 2022 breeding season. It also showed that artificial insemination in kākāpō had a record number of successes this season, producing 8 surviving chicks.

The generous support of the Birds NZ Research Fund allowed us to develop this sequencing methodology, which has the potential to become standard part of the toolkit for kākāpō conservation in future. However, it also has potential to better understand other species, including many of New Zealand's threatened native birds. Portable sequencing using the method we developed could reduce the barrier to obtaining genetic information such as sex or parentage in other species, which could also be very valuable for their conservation.



Marissa preparing blood samples from kākāpō chicks for sequencing, on Whenua Hou. Photo by Andrew Digby



Kākāpō chick. Photo by Marissa Le Lec