Leveraging genomics for distribution and fitness monitoring of kākāpō and takahē

Lara Urban & The Kākāpō/Takahē Recovery Teams

The kākāpō (*Strigops habroptilus*) and takahē (*Porphyrio hochstetteri*) are critically endangered flightless bird species endemic to Aotearoa New Zealand that have become central to the development of national institutional and societal conservation consciousness. Given that the current habitat of both species is limited to managed predator-free territories that have nearly reached capacity, the expansion of kākāpō and takahē to their original habitat will require detailed monitoring of their population development, reproduction success, and resilience to thus far circumvented threats such as predation and anthropogenic impact. Together with the Kākāpō/Takahē Recovery Teams, we leveraged environmental DNA (eDNA) research as a cost-efficient, non-invasive and scalable monitoring approach to obtain insights into both, distribution and genetic diversity, of the two species.

eDNA monitoring is a powerful approach to determine the presence of a species due to detection of its DNA in environmental samples such as water, soil or faeces. To benchmark the sensitivity of this approach for kākāpō detection, we collected soil samples at various distances from kākāpō hotspots on Whenua Hou in 2019. By examining a tiny DNA region, we were able to determine the island's biodiversity just from these soil samples: We detected species such as the lesser short-tailed bat and various bird species, including kākāriki, ruru, kākā, pīwakawaka and tuī. At many locations, we also found kākāpō DNA, showing us that a soil-based eDNA approach is feasible for monitoring the critically endangered parrot.

We then used soil samples that contained kākāpō DNA to extract as much species-specific DNA as possible – more than just a tiny DNA region, but ideally the entire genome of the species! To do so, we used revolutionary technique by combining selective real-time nanopore sequencing with the kākāpō high-quality reference genome to enrich for kākāpō DNA – and not sequence the DNA of all the dominant bacteria, fungi and other species in the soil. This approach and targeted bioinformatic analyses allowed us to identify the presence of kākāpō individuals. Thanks to the Recovery Team's extensive metadata, we were then able to confirm that we had indeed correctly predicted the presence of an individual kākāpō. For example, we could determine just based on soil samples that one of the kākāpō mating structures we had sampled belonged to Merv, one of our male kākāpō on the island. This is an exciting finding since it shows that we are able to retrieve more information than just species presence from environmental samples; in the long term, we will develop this approach further to assess the genetic diversity and fitness of any species at risk from environmental samples.

We furthermore sampled takahē faeces in the remote and rugged Murchison Mountains in 2020. We firstly confirmed that we could detect takahē DNA in the faeces and then repeated the approach of extracting species-specific DNA. Please stay tuned for these results by following Lara's research.

We thank Birds New Zealand very much for providing us with a generous research grant that has allowed us to initiate non-invasive and efficient eDNA monitoring of both, kākāpō and takahē.

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