Improving eDNA monitoring of Australasian Bittern: genetic sequencing of bittern and testing methodologies in lab and field.

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Native and endemic species encounter a variety of threats, including habitat loss and fragmentation, invasive species, disease, and climate change. Effective monitoring of species is critical to understanding these impacts and the success of mitigations aimed at reducing biodiversity loss. Among the distinctive ecosystems of Aotearoa New Zealand, wetlands are among the most biodiverse and vulnerable to human impacts. Of all wetland species, the Australasian Bittern/Matuku is one of New Zealand's most iconic and elusive native bird species. Northland, with its extensive wetland systems, is deemed a crucial habitat for this species. However, due to its elusive behaviour and infrequent observations, current understanding of Matuku distribution and population trends remains limited. Traditional survey methods, including visual and auditory surveys, provide useful information on bittern locations but are time consuming and face challenges due to the inaccessibility of the habitat. Further, as only males vocalise, it is also difficult to know if habitats contain breeding pairs or solitary males.

The matuku-hūrepo/Australasian bittern.
Photo: Fran Bell

Photo: Gavin Klee

Recent advances in molecular techniques, such as eDNA can assist in the identification of rare and endangered species even when their populations are sparse. Such techniques complement traditional survey methods and may enhance detection capability. eDNA technology is considered a potential game changer in conservation; however, to be effective, it requires species-specific genetic sequences and rigorous experimental validation of field methods. Sequences for Australasian bitterns are not yet available. In our study we will 1) extract DNA from archival Matuku tissue samples (University of Auckland), 2) perform genetic sequencing on these samples using various methodologies, and 3) experimentally assess (in the lab) the sensitivity of eDNA methods for detecting bitterns across a range of 'realistic' dilutions and substrates. To verify our findings, we will then test our methodology in the field by employing our sequences and eDNA techniques to detect bitterns at the Tara-iti wetlands in Mangawhai Heads; a site known to host bitterns throughout the year. At the conclusion of our study, we aim to have developed genetic sequences for the identification of the Australasian bittern, evaluated different eDNA methodologies to develop guidelines for eDNA application, and provide recommendations on sample substrates, sampling designs, and the limitations of this technique for monitoring bittern populations.