

Genetic sequencing and habitat modelling of the Australasian bittern (*Botaurus poiciloptilus*) for enhanced conservation

Prabu Raju¹, Prof. Mike Taylor¹, and Prof. Dianne Brunton¹

¹School of Biological Sciences, The University of Auckland, Auckland.

Genetic sequencing of the Australasian bittern was successfully achieved using sanger DNA sequencing following DNA extraction, PCR amplification, and purification of tissue samples. The resulting sequences were verified through BLAST analysis in *Geneious Prime*, showing a 100% match with the only other published Australasian bittern reference (GeneBank Accession MZ148271) (Figure 1).

Habitat suitability modelling of the Australasian bittern using MaxEnt showed good performance across both historical (1901-2000) and current (2001-2020) periods, achieving high predictive accuracy (AUC~0.85-0.86) with reliable omission patterns (Figure 2). Temperature-related predictors, particularly mean annual temperature and mean temperature of the driest quarter, were the most influential, followed by moderate contributions from precipitation seasonality and annual rainfall, while distance to rivers contributed least. Historically, extensive-high suitability zones were observed across the Northland, Waikato-Hauaki, and Bay of Plenty wetlands, with smaller clusters in Gisborne, Hawke's Bay and Marlborough. In contrast, current predictions indicate a contraction and fragmentation of suitable habitats, particularly within central and southern regions, reflecting a significant decline in optimal wetland for the species. Together, these outcomes demonstrate significant progress toward understanding both the genetic detectability and ecological requirements of the Australasian bittern. The integration of molecular (eDNA) and spatial modelling approaches provides a robust framework for identifying remaining strongholds and guiding future wetland restoration. Ongoing sequencing and future predictive modelling will further refine these insights, supporting targeted conservation management for this nationally critical species.

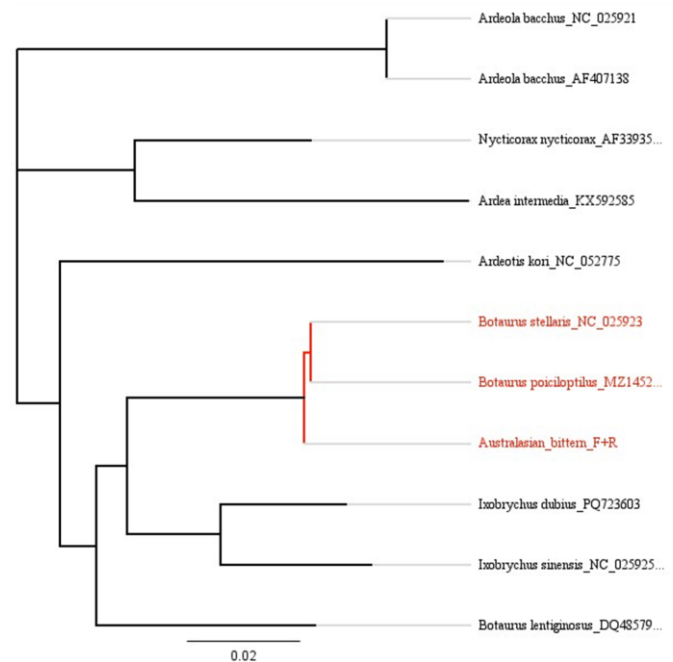


Figure 1: Neighbour-Joining phylogenetic tree based on 12S rRNA sequences of *B. poiciloptilus*

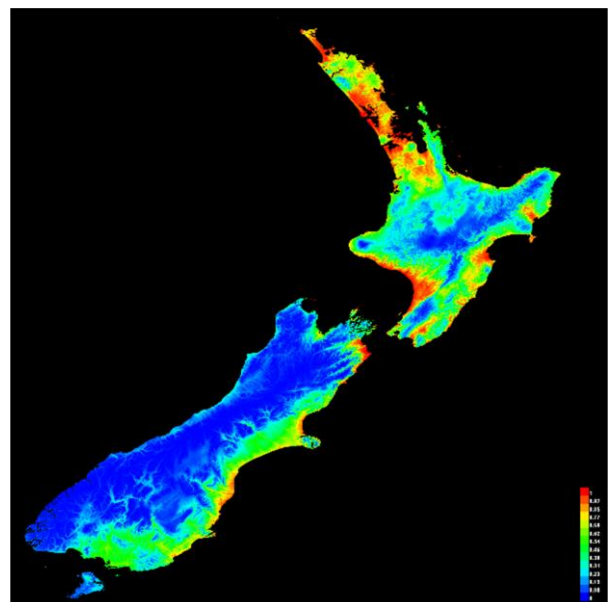


Figure2: Habitat suitability maps of Australasian bittern for historic periods (1901-2000)