

Conservation genomics and phylogeography of mohua

Johanna Kann, Dr Ludovic Dutoit, Professor Bruce Robertson
Department of Zoology, University of Otago

The mohua (*Mohoua ochrocephala*) is endemic to Aotearoa New Zealand. The species was once abundantly found across the South Island of New Zealand and Rakiura/Stewart Island. However, mohua now exist in only 75% of their former range and populations are fragmented. The primary causes for this decline and the fragmentation of populations are habitat loss and predation by introduced mammals. Today's mohua populations are small and isolated, making them vulnerable to genetic drift (the random fluctuation of allele frequencies) and inbreeding (the mating between relatives). Both factors can lead to genetic diversity being lost. Conservation efforts include predator control as well as translocations, primarily to establish mohua populations on predator-free islands. Translocations can lead to further loss of genetic diversity when a new population is established by a small number of individuals (a founder effect). Genetic diversity across the genome is essential to allow populations to adapt to changing environmental conditions. Adaptation needs genetic variation to act on, the absence of such variation can restrict how well populations respond to selection and lead to higher risk of extinction in populations with low genetic diversity.



Blood sample taken from a mohua by DOC staff.

Using genome-wide single-nucleotide-polymorphism (SNP) data generated via genotyping-by-sequencing (GBS) our project investigated population structure and levels of genetic diversity and inbreeding in mainland and island birds. We aimed to understand how genetically 'healthy' island birds are. We further evaluated whether island populations are suitable sources for translocations to supplement declining mainland populations. Our analyses of population structure found that island birds clustered away from mainland birds, indicating a loss of the genetic signature found on the mainland. Our findings further revealed reduced genetic health (i.e., higher inbreeding and decreased genetic diversity) in island birds, calling for caution when establishing new populations with birds sourced solely from

one island.

Additionally, we used the mitochondrial cytochrome b gene and the control region to resolve the phylogeography of mohua. By gaining insights into past demographic distribution and patterns of geneflow historical relationships between population can be discovered, which can have implications for conservation management. Our GBS analysis divided present-day mainland mohua into three groups (roughly west, south and east). In contrast, the analysis of mtDNA did not reveal structured distribution patterns thus indicating continuous geneflow between populations in the past. In the absence of historic structure, mohua could be translocated across populations to restore previously naturally occurring migration, should this become necessary in the future.