

Conservation genetics 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 the South Island of New Zealand. While the species could historically be found throughout the majority of unmodified forests on the South Island and Rakiura, present-day 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 translocations, primarily to establish mohua populations on predator-free islands. These can lead to further loss of genetic diversity when a new population is established by a small number of individuals (a founder effect).

As island populations of mohua are stable the Mohua Recovery Group and the Department of Conservation (DOC) are interested in using these populations as source populations for future translocations. Supplementing declining mainland populations with additional individuals could help the recovery of the species. Island populations were established using one founding population only and their subsequent genetic make-up has not been investigated yet. This however is important to ensure these island source populations are in good genetic health.

Using genotyping-by-sequencing (GBS) our project will analyse mohua from mainland populations as well as from translocated populations on Kā Huru-huru-o-Koekoeā (Breaksea), Te Kāhahu-o-Tamatea (Chalky), Whenua Hou (Codfish) and Anchor island to investigate the genetic diversity and genetic structure of the mohua. This research aims to determine whether the island populations are suitable sources for translocations back to the mainland. Our preliminary results indicated slightly reduced genetic diversity in the island populations.

The Bird NZ Research Grant will allow the additional analysis of mitochondrial DNA (mtDNA, cytochrome b gene (cytb), and control region), thereby further resolving the phylogeography of mohua. This will provide knowledge of maternal lineages (which are another proxy of genetic diversity) and insights into how representative the mohua populations on islands are of those on the mainland. Understanding the phylogeography of the mohua will further provide valuable insights into female dispersal (typically the dispersing sex in birds) and historical abundance, which are essential for the conservation management of the current mohua populations.

This project is a collaboration between the University of Otago, the Department of Conservation, and the Mohua Recovery Group. Outcomes of our research will strongly aid the future management of the mohua by clarifying genealogical lineages, characterising genetic diversity within the species and its populations, and highlighting the most suitable source populations for future translocations.



Mohua captured in the Glenorchy area during a DOC sampling trip.