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**The Ecology and Molecular Ecology of the New Zealand  
Lesser Short-tailed Bat *Mystacina tuberculata***

**A thesis presented in partial fulfilment of the requirements for the  
degree of Doctor of Philosophy**

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**Brian Donald Lloyd**

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**GENERAL ABSTRACT**

The distribution, ecology, and molecular ecology of short-tailed bats *Mystacina tuberculata* were investigated in the central North Island, New Zealand. Special emphasis was given to providing information for conservation management of the species. Seven large populations containing between 2000 and 10 000 bats were found to persist in the area. Populations require numerous large cavities in the main trunk of mature trees for colonial roosts and are therefore restricted to extensive stands of tall old-growth forest. There was no evidence of predation by introduced mammals at roosts where the bats are most vulnerable. In summer, large group size, aggressive behaviour, and frequent movement between colonial roosts reduce the probability of predation. During winter, roosting bats remain in torpor for long periods and are vulnerable to predators, but the entrances to winter roosts are usually too small for predators to enter. Although field trials demonstrated that the bats may be at risk of secondary poisoning during pest control operations, close monitoring of a bat population during a control operation revealed no mortality. The species' intraspecific phylogeny was investigated using a 2878 bp sequence alignment from multiple mitochondrial genes. Six sympatric phylogroups were identified with estimated divergences of 0.93–0.68 My ago. The phylogroups do not correspond to the existing subspecific taxonomy. The phylogeographic structure and demographic history of the phylogroups were investigated using control region sequences modified by removing homoplastic sites. Phylogeographic structure was generally consistent with an isolation-by-distance dispersal model. The observed pattern is not typical of microbats, which generally exhibit low levels of genetic structure over continental ranges. Coalescent based analyses (mismatch distributions, skyline plots, lineage dispersal analysis, and nested clade analysis) indicated the three phylogroups found in central and southern North Island expanded before the last glacial maximum, presumably during interstadials when *Nothofagus* forest was most extensive. Genetic structure within a central North Island hybrid zone was consistent with range expansion from separate refugia following reforestation after catastrophic volcanic eruptions. Discrepancies between estimates of historic and current population size (> 12 million cf. 50 000) indicate the species has undergone a massive population decline.

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