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**The Ecology and Evolution of New Zealand's Endemic  
Alpine Grasshoppers**

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## Abstract

Anthropogenic climate change has stimulated interest in how species distributions are influenced by climate and how they might respond to global warming. The alpine zone is a harsh ecosystem to inhabit, as it experiences climate extremes daily and seasonally, whilst also exhibiting a steep environmental gradient linked to elevation. This makes it a particularly vulnerable environment in light of anthropogenic climate change, but also an informative situation to explore evolutionary ecology. Flora and fauna inhabiting alpine environments are predicted to be most strongly impacted by future climatic changes, when compared with other global ecosystems. The alpine zone of New Zealand stretches the length of the South Island, and is represented in south and central North Island. It is the result of mountain building since the late Miocene, and is home to a diverse array of endemic flora and fauna. As a relatively large component of native New Zealand habitats that has so far been preserved in higher proportion to other systems, the alpine zone will not be exempt from the effects of global anthropogenic climate change. To date, little research has directly investigated the impact worldwide climate shifts might have on this ecosystem.

I investigated the impact that climate change has had, and will have, on New Zealand's endemic alpine short-horn grasshoppers (Orthoptera: Acrididae), as representatives of New Zealand's alpine fauna. Four endemic genera contain 13 endemic species that are all freeze-tolerant, open ground specialists. To assess how these species will be affected by future climate change, it was necessary to examine how they have likely responded to past climatic cycles. Phylogenetic relationships were investigated using high-throughput Next Generation Sequencing. The current classification of 13 species into four monophyletic genera was not supported by this study, and the re-classification of members within this group would be appropriate. The mitochondrial (mtDNA) genomes assembled in this analysis, were combined with mitochondrial genome data of Acrididae species from around the world. This allowed identification of species most closely related to the New Zealand alpine taxa and to estimate the timing of divergence using fossil calibration. New Zealand's alpine grasshoppers form a monophyletic group and share a common ancestor with alpine species from Tasmania. Molecular phylogenetic analysis established that the split of the New Zealand clade from their

Tasmanian ancestor probably occurred ~17–19Mya, which is about 12My prior to alpine habitat being available in New Zealand. Thus, the radiation of New Zealand grasshoppers predates the availability of alpine habitat, suggesting they retained shared ancestral cold tolerance for 12 million years or they independently converged on their alpine adaptations.

Using the current distributions of New Zealand's alpine grasshoppers, potential niche spaces were projected for three time periods (Last Glacial Maximum (LGM), current and future). Ecological niche models predict that suitable niche space has been reduced for most grasshopper species since the LGM, and that with future climate change, the suitable niche spaces of these species will be reduced further still. Fine-scale niche partitioning and population dynamics of species inhabiting five mountains were investigated using field sampling data and population genetics. On a fine scale the presence of particular species of grasshopper was found to correlate with habitat patches (e.g. rock or tussock) and elevation. Each species contained high levels of mtDNA genetic diversity, as expected of large stable populations, but the most common grasshopper species collected had the lowest genetic diversity of the three examined (*Sigaus australis*, *Paprides nitidus*, *Brachaspis nivalis*), suggesting it may have been more restricted in the past (perhaps due to microhabitat preferences) compared to the other species. The sampled mountain populations of each species have apparently existed in isolation long enough to accumulate unique clusters of mtDNA haplotypes, suggesting very low gene flow between populations. The fact that regional populations are already segregated could make them vulnerable to future climate warming, but might have the opportunity to adapt independently of one another.

The loss of alpine habitat due to climate change is likely to be more pronounced on islands than continental systems. I modelled the expected alpine area lost due to anthropogenic climate warming for eight island systems around the world. In each case the size of the alpine habitat is predicted to shrink, potentially leading to the extinction of species as a consequence of their insularity. The grasshopper species in New Zealand provide evidence that predictions of range shifts require knowledge of current large scale climatic limitations on species distributions and an understanding of fine scale biotic and habitat interactions as well as species specific potential for dispersal.





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